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(54) Title: METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in ovarian cancer. Related methods and compositions that can be used for diagnosis and treatment of ovarian cancer are disclosed. Also described herein are methods that can be used to identify modulators of ovarian cancer.

WO 02/102235 A2

METHODS OF DIAGNOSIS OF OVARIAN CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF OVARIAN CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS.

5 This application is related to USSN 60/299,234, filed June 18, 2001; USSN 60/315,287, filed August 27, 2001; USSN 60/317,544, filed September 5, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2002, each of which is incorporated herein by reference for all purposes.

10 FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in ovarian cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of ovarian cancer. The invention further relates to methods for
15 identifying and using agents and/or targets that inhibit ovarian cancer.

BACKGROUND OF THE INVENTION

Ovarian cancer is the sixth most common cancer in women, accounting for 6% of all female cancers. It ranks fifth as the cause of cancer death in women. The American Cancer
20 Society predicts that there will be about 23,100 new cases of ovarian cancer in this country in the year 2000 and about 14,000 women will die of the disease. Because many ovarian cancers cannot be detected early in their development, they account for a disproportionate number of fatal cancers, being responsible for almost half the deaths from cancer of the female genital tract; more deaths than any other reproductive organ cancer.

25 Most patients with epithelial ovarian cancer, the predominant form, are asymptomatic in early-stage disease and usually present with stage III or IV disease. Their five-year survival is less than 25%, with lower survival among African-American women. The minority of patients discovered with early-stage disease have a five-year survival rate of 80%-90%. See, Parker, et. al., (1997) "Cancer Statistics, 1997" CA Cancer J. Clin. 47:5-27.

30 In the absence of a family history of ovarian cancer, lifetime risk of ovarian cancer is 1/70. Risk factors include familial cancer syndromes (risk of up to 82% by age 70 in women

- with hereditary breast/ovarian syndrome); family history (1.4% lifetime risk with no affected relatives, 5% with one affected relative, 7% with two affected relatives; Kerlikowski, et. al. (1992) Obstet. Gynecol. 80:700-707); nulliparity; advancing age; obesity; personal history of breast, endometrial, or colorectal cancer; fewer pregnancies; or older age (>35 years) at first pregnancy. However, 95% of all ovarian cancers occur in women without risk factors. Use of hormonal contraceptives, oophorectomy, and tubal sterilization reduce risk of ovarian cancer (Kerlikowski, et. al. (1992) Obstet. Gynecol. 80:700-707; Grimes (1992) Am J. Obstet. Gynecol. 166:1950-1954; Hankinson, et. al. (1993) JAMA 270:2813-2818); however, even bilateral oophorectomy may not be completely effective in preventing ovarian cancer.
- 10 Treatment of ovarian cancer consists largely of surgical oophorectomy, anti-hormone therapy, and/or chemotherapy. Although many ovarian cancer patients are effectively treated, the current therapies can all induce serious side effects which diminish quality of life. Deciding on a particular course of treatment is typically based on a variety of prognostic parameters and markers (Fitzgibbons, et al. (2000) Arch. Pathol. Lab. Med. 124:966-978;
- 15 Hamilton and Piccart (2000) Ann. Oncol. 11:647-663), including genetic predisposition markers BRCA-1 and BRCA-2 (Robson (2000) J. Clin. Oncol. 18:113sup-118sup).

- The identification of novel therapeutic targets and diagnostic markers is essential for improving the current treatment of ovarian cancer patients. Recent advances in molecular medicine have increased the interest in tumor-specific cell surface antigens that could serve
- 20 as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated. Examples of such antigens include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu
- 25 (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. Ross and Fleischer (1998) Stern Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

- 30 Potential immunotherapeutic targets have been identified for ovarian cancer. One such target is polymorphic epithelial mucin (MUC1). MUC1 is a transmembrane protein, present at the apical surface of glandular epithelial cells. It is often overexpressed in ovarian cancer, and typically exhibits an altered glycosylation pattern, resulting in an antigenically

distinct molecule, and is in early clinical trials as a vaccine target. Gilewski, et al. (2000) Clin. Cancer Res. 6:1693-1701; Scholl, et al. (2000) J. Immunother. 23:570-580. The tumor-expressed protein is often cleaved into the circulation, where it is detectable as the tumor marker, CA 15-3. See, e.g., Bon, et al. (1997) Clin. Chem. 43:585-593. However, many
5 patients have tumors that express neither HER2 nor MUC-1; therefore, it is clear that other targets need to be identified to manage localized and metastatic disease.

Mutations in both BRCA1 and BRCA2 are associated with increased susceptibility to ovarian cancer. Mutations in BRCA1 occur in approximately 5 percent (95 percent confidence interval, 3 to 8 percent) of women in whom ovarian cancer is diagnosed before
10 the age of 70 years. See Stratton, et al. (1997) N.E.J. Med. 336:1125-1130. And, in BRCA1 gene carriers, the risk for developing ovarian cancer is .63. See Easton (1995) Am. J. Hum. Genet. 56:267-xxx; and Elit (2001) Can. Fam. Physician 47:778-84.

Other biochemical markers such as CA125 have been reported to be associated with ovarian cancer, but they are not absolute indicators of disease. Although roughly 85% of
15 women with clinically apparent ovarian cancer have increased levels of CA125, CA125 is also increased during the first trimester of pregnancy, during menstruation, in the presence of non-cancerous illnesses, and in cancers of other sites.

While industry and academia have identified novel gene sequences, there has not been an equal effort exerted to identify the function of these novel sequences. The elucidation of a
20 role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is essential for improving the current treatment of ovarian cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in ovarian and other cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of ovarian cancer. Further provided are methods that can
25 be used to screen candidate bioactive agents for the ability to modulate ovarian cancer.

SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in ovarian cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate ovarian cancer, such as hormones or antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins can be used for many purposes, e.g., early detection of ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for postoperative chemotherapy or radiation therapy, selecting therapy, determining tumor prognosis, treatment, or response to treatment (of primary or metastatic tumors), and early detection of pre-cancerous lesions. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting an ovarian cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the present invention provides a method of determining the level of an ovarian cancer associated transcript in a cell from a patient.

In one embodiment, the present invention provides a method of detecting an ovarian cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-26.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat ovarian cancer. In another embodiment, the patient is suspected of having metastatic ovarian cancer.

In one embodiment, the patient is a human.

In one embodiment, the ovarian cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids

before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of ovarian cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of an ovarian cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic ovarian cancer. In a further embodiment, the patient has a drug resistant form of ovarian cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the ovarian cancer-associated transcript to a level of the ovarian cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

Additionally, provided herein is a method of evaluating the effect of a candidate ovarian cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1-26.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-26.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting an ovarian cancer cell in a biological sample from a patient, the method comprising contacting the biological

sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to ovarian cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from

5 Tables 1-26.

In another aspect, the present invention provides a method for identifying a compound that modulates an ovarian cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with an ovarian cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26; and (ii) determining the functional effect of the compound upon the polypeptide.

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In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

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In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of an ovarian cancer-associated cell to treat ovarian cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

20

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having ovarian cancer or to a cell sample isolated from; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of ovarian cancer.

25

In one embodiment, the control is a mammal with ovarian cancer or a cell sample that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal, or is non-malignant tissue.

30

In one embodiment, the test compound is administered in varying amounts or

concentrations. In another embodiment, the test compound is administered for varying time periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

In one embodiment, the levels of a plurality of polynucleotides that selectively
5 hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1-26 are individually compared to their respective levels in a control cell sample or mammal. In a preferred embodiment the plurality of polynucleotides is from three to ten.

In another aspect, the present invention provides a method for treating a mammal having ovarian cancer comprising administering a compound identified by the assay
10 described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having ovarian cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

In one aspect, the present invention provides a method of screening drug candidates
15 by providing a cell expressing a gene that is up- and down-regulated as in an ovarian cancer. In one embodiment, a gene is selected from Tables 1-26. The method further includes adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

In one embodiment, the method of screening drug candidates includes comparing the
20 level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary when present, and wherein the comparison can occur after addition or removal of the drug candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided is a method of evaluating the effect of a candidate ovarian cancer drug
25 comprising administering the drug to a transgenic animal expressing or over-expressing the ovarian cancer modulatory protein, or an animal lacking the ovarian cancer modulatory protein, for example as a result of a gene knockout.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments
30 of Tables 1-26, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably, at least two nucleic acid segments are included. More preferably, at least three nucleic acid segments are included.

Furthermore, a method of diagnosing a disorder associated with ovarian cancer is

provided. The method comprises determining the expression of a gene of Tables 1-26 in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected individual. A difference in the expression indicates that the first individual has a disorder
5 associated with ovarian cancer.

In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in ovarian cancer.

In one embodiment a method for screening for a bioactive agent capable of interfering with the binding of an ovarian cancer modulating protein (ovarian cancer modulatory protein)
10 or a fragment thereof and an antibody which binds to said ovarian cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining an ovarian cancer modulatory protein or fragment thereof, a candidate bioactive agent and an antibody which binds to said ovarian cancer modulatory protein or fragment thereof. The method further includes determining the binding of said ovarian cancer modulatory protein or
15 fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits ovarian cancer.

Also provided herein are methods of eliciting an immune response in an individual. In one embodiment a method provided herein comprises administering to an individual a
20 composition comprising an ovarian cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1-26.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises an ovarian
25 cancer modulating protein, preferably encoded by a nucleic acid of Table 1-26 or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding an ovarian cancer modulating protein, preferably selected from the nucleic acids of Tables 1-26, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of an ovarian cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded
30 by a nucleic acid selected from those of Tables 1-26.

In another aspect of the invention, a method of treating an individual for ovarian cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of an ovarian cancer modulating protein. In another embodiment, the method comprises administering to a patient having ovarian cancer an antibody to an ovarian cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for ovarian cancer (OC), including metastatic ovarian cancer, as well as methods for screening for compositions which modulate ovarian cancer. Also provided are methods for treating ovarian cancer and related conditions, e.g., ovarian carcinoma (e.g., epithelial (including malignant serous tumors, malignant mucinous tumors, and malignant endometrioid tumors), germ cell (including teratomas, choriocarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, and gonadoblastoma), and stromal carcinomas (e.g., granulosa stromal cell tumors)), fallopian tube carcinoma, and peritoneal carcinoma.

Tables 1-26 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in ovarian cancer samples. Tables 1-26 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

15

Definitions

The term "ovarian cancer protein" or "ovarian cancer polynucleotide" or "ovarian cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-26; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-26, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-26 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-26. A polynucleotide or polypeptide

sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. An "ovarian cancer polypeptide" and an "ovarian cancer polynucleotide," include both naturally occurring or recombinant forms.

- 5 A "full length" ovarian cancer protein or nucleic acid refers to an ovarian cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type ovarian cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.
- 10 "Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of an ovarian cancer protein, polynucleotide or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes,
- 15 blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of
- 20 particular interest.

- "Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the
- 25 methods of the invention in vivo. Archival tissues, having treatment or outcome history, will be particularly useful.

- The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same
- 30 (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default

parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Lippincott.

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990)

J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a word length of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Nat'l Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l Acad. Sci. USA 90:5873-5887). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells, such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogenous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (2001) Molecular Biology of the Cell (4th ed.) Garland Pub.; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the non-covalent association of independent tertiary units. Anisotropic terms are also known as energy terms. "Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds,

- although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and
- 5 linkages. Other analog nucleic acids include those with positive backbones, non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of
- 10 nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.
- 15 A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986),
- 20 Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucl. Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-2322), O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-897;
- 25 Meier, et al. (1992) Angew. Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature, 365:566-568; Carlsson, et al. (1996) Nature 380:207, each of which is incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpocy, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141 and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Jung, et al. (1994) Nucleoside and Nucleotide 13:1597; Chapters 2 and 3, in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs,
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et al. (1994) J. Biomolecular NMR 34:17-xx; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (p. 35 June 2, 1997) C&E News. Each of these references is hereby expressly incorporated by reference.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched base pairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic,

photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the ovarian cancer nucleic acids, proteins and antibodies at any position. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945-xxx; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or non-covalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or non-covalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the

stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or
5 subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic
10 acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using
15 polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or
20 organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic
25 acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes
30 arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target

sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are available, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press, N.Y.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided, e.g., Ausubel, et al. (ed. 1991 and supplements) Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that

modulate activity of an ovarian cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the ovarian cancer protein or nucleic acid, e.g., a functional, physical, physiological, or chemical effect, such as the ability to decrease ovarian cancer. It includes ligand binding activity; cell growth on soft agar; anchorage
5 dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of ovarian cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

10 By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an ovarian cancer protein sequence, e.g., functional, enzymatic, physical, physiological, and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence,
15 absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the ovarian cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on ovarian cancer can also be performed using ovarian
20 cancer assays known to those of skill in the art such as an in vitro assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of ovarian cancer
25 cells. The functional effects can be evaluated by means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for ovarian cancer-associated sequences, measurement of RNA stability, or identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence,
30 colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of ovarian cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of ovarian cancer polynucleotide and

polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of ovarian cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate ovarian cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of ovarian cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Assays for inhibitors and activators include, e.g., expressing the ovarian cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of ovarian cancer can also be identified by incubating ovarian cancer cells with the test compound and determining increases or decreases in the expression of one or more ovarian cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more ovarian cancer proteins, such as ovarian cancer proteins encoded by the sequences set out in Tables 1-26.

Samples or assays comprising ovarian cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25% or less. Activation of an ovarian cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (e.g., 2-5 fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to a change in cell growth and proliferation characteristics in vitro or in vivo, e.g., cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, change in contact inhibition or density limitation of growth, loss of growth factor or serum requirements, change in cell morphology, gain or loss of immortalization, gain or loss of tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss.

“Tumor cell” refers to pre-cancerous, cancerous, and normal cells in a tumor.

“Cancer cells,” “transformed” cells or “transformation” in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is typically associated with phenotypic changes, such as immortalization of cells, aberrant growth control, non-morphological changes, and/or malignancy. See, Freshney (1994) Culture of Animal Cells.

“Antibody” refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See, e.g., Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one “light” (about 25 kD) and one “heavy” chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H -CH1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody,

one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries. See, e.g., McCafferty, et al. (1990) Nature 348:552-554.

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al., pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Transgenic mice, or other organisms, e.g., other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; and Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

Identification of ovarian cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is

characteristic of the state of the cell. That is, normal tissue (e.g., normal ovarian or other tissue) may be distinguished from cancerous or metastatic cancerous tissue of the ovarian, or ovarian cancer tissue or metastatic ovarian cancerous tissue can be compared with tissue samples of ovarian and other tissues from surviving cancer patients. By comparing
5 expression profiles of tissue in known different ovarian cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

The identification of sequences that are differentially expressed in ovarian cancer
10 versus non-ovarian cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate ovarian cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, does existing treatment induce expression of a target. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known
15 expression profiles. Metastatic tissue can also be analyzed to determine the stage of ovarian cancer in the tissue or origin of the primary tumor. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the ovarian cancer expression profile. This may be done by making biochips comprising sets of
20 the important ovarian cancer genes, which can then be used in these screens. These methods can also be based on evaluating protein expression; that is, protein expression levels of the ovarian cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the ovarian cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense or RNAi nucleic acids, or the
25 ovarian cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in ovarian cancer relative to normal tissues and/or non-malignant tissues, herein termed "ovarian cancer sequences." As outlined below, ovarian cancer
30 sequences include those that are up-regulated (e.g., expressed at a higher level) in ovarian cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the ovarian cancer sequences are from humans; however, as will be appreciated by those in the art, ovarian cancer sequences from other organisms may be useful

in animal models of disease and drug evaluation; thus, other ovarian cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Ovarian cancer sequences, e.g., counterpart genes, from other organisms may be obtained using the techniques outlined below.

Ovarian cancer sequences can include both nucleic acid and amino acid sequences. Ovarian cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids. Screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the ovarian cancer sequences, are also provided.

An ovarian cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the ovarian cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying ovarian cancer-associated sequences, the ovarian cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing ovarian cancer samples with metastatic cancer samples from other cancers, such as lung, ovarian, gastrointestinal cancers, etc. Samples of different stages of ovarian cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal ovarian, but also including, and not limited to, lung, heart, brain, liver, ovarian, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the ovarian cancer screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, expression in non-essential tissues may be tolerated. That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side

effects by interaction with target present in other organs.

In a preferred embodiment, ovarian cancer sequences are those that are up-regulated in ovarian cancer; that is, the expression of these genes is higher in the ovarian cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Other embodiments are directed to sequences up regulated in non-malignant conditions relative to normal.

Unigene cluster identification numbers and accession numbers herein refer to the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, et al. (1998) Nucl. Acids Res. 26:1-7; and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, e.g., FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, ovarian cancer sequences are those that are down-regulated in ovarian cancer; that is, the expression of these genes is lower in ovarian cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three-fold change, with at least about five-fold or higher being preferred.

Informatics

The ability to identify genes that are over or under expressed in ovarian cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. Expression profiles can be used in diagnostic or prognostic evaluation of patients with ovarian cancer. Subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA) or in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable

exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database, and can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for any assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing ovarian cancer, e.g., the identification of ovarian cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, and outcome data, among others. Although data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method

using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

Fundamentals of bioinformatics are provided, e.g., in Mount, et al. (2001) Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge Univ. Press; Baxevanis and Ouellette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d ed.) Wiley-Liss; Rashidi and Buehler (1999) Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford Univ. Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for ovarian cancer. In another variation, assay records cross-tabulate one or more of the following parameters for a target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or

characteristic separation coordinate (e.g., electrophoretic or genomic position coordinates); (2) sample source; and (3) absolute and/or relative quantity of target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells)

composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, e.g., which typically comprises one or more of: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by methods of the inventions, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of ovarian cancer-associated proteins

Ovarian cancer proteins of the present invention may be categorized as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the ovarian cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes. See, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity, and the like. Intracellular proteins can also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are often involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-

322.

In another preferred embodiment, the ovarian cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their

cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules, or may be processed or shed to the blood stream. In this respect, they can mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Ovarian cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeabilized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful ovarian markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the ovarian cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to an adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus, secreted molecules often find use in modulating or altering numerous aspects of physiology. Ovarian cancer proteins that are secreted proteins are particularly preferred as good diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be

antibody or small molecule therapeutic targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms, as protein or DNA vaccines.

Use of ovarian cancer nucleic acids

5 As described above, ovarian cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the ovarian cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on
10 the same molecule.

The ovarian cancer nucleic acid sequences of the invention, e.g., in Table 1-26, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein,
15 extended sequences, in either direction, of the ovarian cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

20 Once the ovarian cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire ovarian cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised as a linear nucleic acid segment, the recombinant ovarian cancer nucleic acid can be further-used as a probe to identify and isolate other ovarian cancer
25 nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant ovarian cancer nucleic acids and proteins.

The ovarian cancer nucleic acids of the present invention are useful in several ways. In a first embodiment, nucleic acid probes to the ovarian cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for
30 administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, the ovarian cancer nucleic acids that include coding regions of ovarian cancer proteins can be put into expression vectors for the expression of ovarian cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to ovarian cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the ovarian cancer nucleic acids, e.g., the target sequence (either the target
5 sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations
10 is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole
20 genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a
25 particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the
30 solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent

attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds.

- 5 Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

- 10 In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

- The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See, e.g., WO0055627 Reusable Low Fluorescent Plastic Biochip.
- 15
- 20

- Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.
- 25

- In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxyl groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using
- 30

functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo- or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of ovarian cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, an ovarian cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of ovarian cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are available. See, e.g., Innis, et al.(1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be

extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of

5 amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR; see Wu and Wallace (1989) Genomics 4:560-569; Landegren, et al. (1988) Science 241:1077-1980; and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Nat'l Acad. Sci. USA 86:1173-1177), self-sustained
10 sequence replication (Guatelli, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of ovarian cancer proteins from nucleic acids

In a preferred embodiment, ovarian cancer nucleic acids, e.g., encoding ovarian
15 cancer proteins are used to make a variety of expression vectors to express ovarian cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known and are used to express proteins. See, e.g., Ausubel, supra; and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press. The expression vectors may be either self-replicating extrachromosomal vectors or
20 vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the ovarian cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an
25 operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a pre-sequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a pre-protein that participates
30 in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation; and two sequences may be operably linked when they are physically part of the same polymer. Generally,

“operably linked” means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the ovarian cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences typically encode constitutive or inducible promoters. The promoters may be naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, *supra*.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The ovarian cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding an ovarian cancer protein, under the appropriate conditions to induce or cause expression of the ovarian cancer protein. Conditions appropriate for ovarian cancer protein expression will vary with

the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculovirus systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the ovarian cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048, both of which are hereby expressly incorporated by reference. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter. See, e.g., Fernandez and Hoeffler, *supra*. Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, ovarian cancer proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters

are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences.

Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable.

- 5 The expression vector may also include a signal peptide sequence that provides for secretion of the ovarian cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been
- 10 transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and
- 15 include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others. See Fernandez and Hoeffler, *supra*. The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

- In one embodiment, ovarian cancer proteins are produced in insect cells. Expression
- 20 vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

- In a preferred embodiment, an ovarian cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*,
- 25 *Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

- The ovarian cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the ovarian cancer protein may be fused to a carrier protein to form an
- 30 immunogen. Alternatively, the ovarian cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the ovarian cancer protein is an ovarian cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the ovarian cancer protein is purified or isolated after expression. Ovarian cancer proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the ovarian cancer protein may be purified using a standard anti-ovarian cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the ovarian cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the ovarian cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

15

Variants of ovarian cancer proteins

In one embodiment, the ovarian cancer proteins are derivative or variant ovarian cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative ovarian cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at most any residue within the ovarian cancer peptide.

Also included within one embodiment of ovarian cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the ovarian cancer protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant ovarian cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the ovarian cancer protein amino acid sequence. The variants typically exhibit the same

qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to
5 optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed ovarian cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using
10 assays of ovarian cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the ovarian cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution
20 relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the ovarian cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the ovarian cancer protein is
25 altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure;
30 the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine,

valine, or alanine; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Covalent modifications of ovarian cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of an ovarian cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of an ovarian cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking ovarian cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-ovarian cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutamine and asparagine residues to the corresponding glutamic and aspartic acid residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serine, threonine, or tyrosine residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1983) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the ovarian cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence ovarian cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence ovarian cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express ovarian cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to ovarian cancer polypeptides may also be

accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence ovarian cancer polypeptide (for O-linked glycosylation sites). The ovarian cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the ovarian cancer polypeptide at pre-selected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the ovarian cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330, and pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem. CRC Press.

Removal of carbohydrate moieties present on the ovarian cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57; and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases. See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of ovarian cancer comprises linking the ovarian cancer polypeptide to one of a variety of non-proteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylene. See, e.g., U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; or 4,179,337.

Ovarian cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules, e.g., comprising an ovarian cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of an ovarian cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl-terminus of the ovarian cancer polypeptide. The presence of such epitope-tagged forms of an ovarian cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the ovarian cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of an ovarian cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of

the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; His6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Mol. Cell. Biol. 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3:547-553). Other tag polypeptides include, e.g., the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other ovarian cancer proteins of the ovarian cancer family, and ovarian cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related ovarian cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the ovarian cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art (e.g., Innis, PCR Protocols, supra).

Antibodies to ovarian cancer proteins

In a preferred embodiment, when the ovarian cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the ovarian cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller ovarian cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known to the skilled artisan (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a

mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495-497. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-26 or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at

least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Table 1-26 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is
5 tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to ovarian cancer protein are capable of reducing or eliminating a biological function of an ovarian cancer protein, as is described below. That is, the addition of anti-ovarian cancer protein antibodies (either polyclonal or preferably monoclonal) to ovarian cancer tissue (or cells containing ovarian cancer) may
10 reduce or eliminate the ovarian cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the ovarian cancer proteins are humanized antibodies (e.g., Xenerex Biosciences; Medarex, Inc.; Abgenix, Inc.; Protein
15 Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary
20 determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the
25 imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise
30 at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. Humanization can be essentially performed following the method of Winter and co-workers, e.g., by substituting rodent CDRs or CDR sequences for the

corresponding sequences of a human antibody. See, e.g., Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; Presta (1992) Curr. Op. Struct. Biol. 2:593-596; and Verhoeven, et al. (1988) Science 239:1534-1536). Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries (see, e.g., Hoogenboom and Winter (1991) J. Mol. Biol. 227:381-388; and Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (see, e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. See, e.g., U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016; Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Neuberger (1996) Nature Biotechnology 14:826 commenting on Fishwild, et al. (1996) Nature Biotechnology 14:845-51; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of ovarian cancer, e.g., with an antibody raised against ovarian cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the ovarian cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby

inactivating the secreted ovarian cancer protein.

In another preferred embodiment, the ovarian cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the ovarian cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane ovarian cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the ovarian cancer protein. The antibody is also an antagonist of the ovarian cancer protein. Further, the antibody prevents activation of the transmembrane ovarian cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the ovarian cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, ovarian cancer is treated by administering to a patient antibodies directed against the transmembrane ovarian cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be any number of molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the ovarian cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the ovarian cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase or protein kinase activity associated with ovarian cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to ovarian cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with ovarian cancer. Cytotoxic agents are numerous and varied and include, but are not limited to,

cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against ovarian cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane ovarian cancer proteins not only serves to increase the local concentration of therapeutic moiety in the ovarian cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the ovarian cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the ovarian cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto contains a signal for that target localization, e.g., a nuclear localization signal.

The ovarian cancer antibodies of the invention specifically bind to ovarian cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding is also important.

Detection of ovarian cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the ovarian cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing ovarian cancer) and in ovarian cancer tissue (and in some cases, for varying severities of ovarian cancer that relate to prognosis, as outlined below, or in non-malignant disease are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states,

information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

5 “Differential expression,” or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus ovarian cancer tissue. Genes may be turned on or turned off in a particular
10 state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is modulated, either up-regulated, resulting in an increased amount of
15 transcript, or down-regulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, e.g., Lockhart (1996) *Nature Biotechnology* 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis, and RNase
20 protection. As outlined above, preferably the change in expression (e.g., up-regulation or down-regulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

 Evaluation may be at the gene transcript, or the protein level. The amount of gene
25 expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the ovarian cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass
30 spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to ovarian cancer genes, e.g., those identified as being important in an ovarian cancer or disease phenotype, can be evaluated in an ovarian disease diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed, or on an individual basis.

In this embodiment, the ovarian cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of ovarian cancer sequences in a particular sample. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

5 In a preferred embodiment nucleic acids encoding the ovarian cancer protein are detected. Although DNA or RNA encoding the ovarian cancer protein may be detected, of particular interest are methods wherein an mRNA encoding an ovarian cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined
10 herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method
15 permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding an ovarian cancer protein is detected by binding the digoxigenin with an anti-digoxigenin
20 secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells
25 containing ovarian cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

30 As described and defined herein, ovarian cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as prognostic or diagnostic markers of ovarian disease. Detection of these proteins in putative ovarian cancer tissue allows for detection, diagnosis, or prognosis of ovarian disease, and for selection of therapeutic strategy. In one

embodiment, antibodies are used to detect ovarian cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the ovarian cancer protein is detected, e.g., by immunoblotting with antibodies raised against the ovarian cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the ovarian cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai (ed. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. Cells are contacted with from one to many antibodies to the ovarian cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the ovarian cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of ovarian cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing ovarian cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of ovarian cancer proteins. Antibodies can be used to detect an ovarian cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology, and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous ovarian cancer protein.

In a preferred embodiment, in situ hybridization of labeled ovarian cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including ovarian cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It

is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to ovarian cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of a plurality of genes being preferred. As above, ovarian cancer probes may be attached to biochips for the detection and quantification of ovarian cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing ovarian cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, et al. (1998) *Science* 279:84-88; and Heid (1996) *Genome Res.* 6:986-994.

In a preferred embodiment, the ovarian cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified ovarian cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the ovarian cancer phenotype or an identified physiological function of an ovarian cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, *supra*.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in ovarian cancer, test

compounds can be screened for the ability to modulate gene expression or for binding to the ovarian cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing ovarian cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in ovarian cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in ovarian cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the ovarian cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the ovarian cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of ovarian cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more ovarian cancer-associated sequences, e.g., a polynucleotide sequence set out in Tables 1-26. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate ovarian cancer, modulate ovarian cancer proteins, bind to an ovarian cancer protein, or interfere with the binding of an ovarian cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the ovarian cancer phenotype or the expression of an ovarian cancer sequence,

e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses an ovarian cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced an ovarian cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of an ovarian cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to an ovarian cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that

display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks. See, e.g., Gallop, et al. (1994) J. Med. Chem. 37:1233-1251.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175; Furka (1991) Pept. Prot. Res. 37:487-493; and Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6909-913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), non-peptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14:309-314; and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522; and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33, Baum (Jan. 18, 1993) C&E News; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available.

See, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY; Symphony, Rainin, Woburn, MA; 433A Applied Biosystems, Foster City, CA; 9050 Plus, Millipore, Bedford, MA.

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, MA; Orca, Hewlett-Packard, Palo Alto, CA), which mimic the manual synthetic operations performed by a chemist. Any of the above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J.; Asinex, Moscow, RU; Tripos, Inc., St. Louis, MO; ChemStar, Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD; etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of ovarian cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide

detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or
5 fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly
10 useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring
15 proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be
20 designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some
25 positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains,
30 serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of ovarian cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids.

For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

5 After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example,
10 an in vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as,
15 alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin
20 is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702; 5,597,909; 5,545,730; 5,594,117;
25 5,591,584; 5,571,670; 5,580,731; 5,571,670; 5,591,584; 5,624,802; 5,635,352; 5,594,118; 5,359,100; 5,124,246; and 5,681,697, each of which is hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

30 A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step

parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the ovarian cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress an ovarian cancer expression pattern leading to a normal expression pattern, or to modulate a single ovarian cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated ovarian cancer tissue reveals genes that are not expressed in normal tissue

or ovarian cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for ovarian cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced
5 proteins and used to target novel therapeutics to the treated ovarian cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of ovarian cancer cells, that have an associated ovarian cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by
10 action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if
15 desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., ovarian cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress the ovarian cancer phenotype. A change in at least one
20 gene, preferably many, of the expression profile indicates that the agent has an effect on ovarian cancer activity. By defining such a signature for the ovarian cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "ovarian cancer proteins"
30 or a "ovarian cancer modulatory protein". The ovarian cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the ovarian cancer modulatory protein is a fragment. In a preferred embodiment, the ovarian cancer amino acid sequence which is used to determine

sequence identity or similarity is encoded by a nucleic acid of the Tables. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

- 5 Preferably, the ovarian cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In another embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to
- 10 cysteine. Or, the ovarian cancer proteins are conjugated to an immunogenic agent, e.g., to BSA.

- Measurements of ovarian cancer polypeptide activity, or of ovarian cancer or the ovarian cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the ovarian cancer polypeptides can be
- 15 measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of ovarian cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone
- 20 release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian ovarian cancer polypeptide is typically used, e.g., mouse, preferably human.

- Assays to identify compounds with modulating activity can be performed in vitro.
- 25 For example, an ovarian cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the ovarian cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the ovarian cancer polypeptide
- 30 or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or

enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the ovarian cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "ovarian cancer proteins." The ovarian cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the ovarian cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining an ovarian cancer protein and a candidate compound, and determining the binding of the compound to the ovarian cancer protein. Preferred embodiments utilize the human ovarian cancer protein, although other mammalian proteins, e.g., counterparts, may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative ovarian cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the ovarian cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be

made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is non-diffusible. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the ovarian cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the ovarian cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the ovarian cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the ovarian cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one

component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophore for the compound. Proximity reagents, e.g., quenching or energy transfer reagents, are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (e.g., an ovarian cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically 4–40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hr will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the ovarian cancer protein and thus is capable of binding to, and potentially modulating, the activity of the ovarian cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the ovarian cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the ovarian cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the ovarian cancer proteins. In this embodiment, the methods comprise combining an ovarian cancer protein and a competitor in a first sample. A second sample comprises a test compound, an ovarian cancer protein, and a

WO 02/102235

PCT/US02/19297

competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the ovarian cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the ovarian cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native ovarian cancer protein, but cannot bind to modified ovarian cancer proteins. The structure of the ovarian cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of an ovarian cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of an ovarian cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising ovarian cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes an ovarian cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including

chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate ovarian cancer agents are identified.

- 5 Compounds with pharmacological activity are able to enhance or interfere with the activity of the ovarian cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

- In one embodiment, a method of inhibiting ovarian cancer cell division is provided. The method comprises administration of an ovarian cancer inhibitor. In another embodiment,
10 a method of inhibiting ovarian cancer is provided. The method comprises administration of an ovarian cancer inhibitor. In a further embodiment, methods of treating cells or individuals with ovarian cancer are provided. The method comprises administration of an ovarian cancer inhibitor.

- In one embodiment, an ovarian cancer inhibitor is an antibody as discussed above. In
15 another embodiment, the ovarian cancer inhibitor is an antisense or RNAi molecule.

A variety of cell viability, growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

- 20 Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and
25 grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of ovarian cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

- 30 Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss, herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), supra, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (^3H)-thymidine at saturation density can be used to measure density limitation of growth. See, e.g., Freshney (1994), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (^3H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with an ovarian cancer-associated sequence and are grown for 24 hr at saturation density in non-limiting medium conditions. The percentage of cells labeling with (^3H)-thymidine is determined autoradiographically. See, e.g., Freshney (1994), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts. See, e.g., Temin (1966) J. Nat'l Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879; and Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino, pp. 178-184 "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly,

tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1994), supra. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino, pp. 178-184 "Angiogenesis, tumor vascularization, and potential interference with tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer Plenum; and Freshney (1985) Anticancer Res. 5:111-130.

10 Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate ovarian cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Alternatively, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by pre-labeling the cells with ¹²⁵I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

Tumor growth in vivo

Effects of ovarian cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the ovarian cancer gene is disrupted or in which an ovarian cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous ovarian cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous ovarian cancer gene with a mutated version of the ovarian cancer gene, or by mutating the endogenous ovarian cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. By breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion. See, e.g., Capecchi, et al. (1989) *Science* 244:1288-1292. Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Nat'l. Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10⁶ cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing an ovarian cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of ovarian cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of an ovarian cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., an ovarian cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-

sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the ovarian cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

- 5 Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides.

- 10 Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for ovarian cancer molecules. A preferred antisense molecule is for an ovarian cancer sequences in Tables 1-26, or for a ligand or activator thereof. Antisense or
- 15 sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. An antisense or a sense oligonucleotide can be developed based upon a cDNA sequence encoding a given protein. See, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

- 20 RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-
- 25 498. The mechanism may be used to down-regulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

- In addition to antisense polynucleotides, ribozymes can be used to target and inhibit
- 30 transcription of ovarian cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. Pharmacol. 25: 289-

317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing them are well known to those of skill in the art. See, e.g.,
5 WO 94/26877; Ojwang, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Hum. Gene Ther. 1:39-45; Leavitt, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Hum. Gene Ther. 5:1151-120; and Yamada, et al. (1994) Virology 205:121-126.

Polynucleotide modulators of ovarian cancer may be introduced into a cell containing
10 the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its
15 corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of ovarian cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be
20 used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating ovarian cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-ovarian cancer antibody that reduces or eliminates the biological activity of an endogenous ovarian cancer protein. Alternatively, the methods comprise administering to a
25 cell or organism a recombinant nucleic acid encoding an ovarian cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the ovarian cancer sequence is down-regulated in ovarian cancer, such state may be reversed by increasing the amount of ovarian cancer gene product in the cell. This can be accomplished, e.g., by over-expressing the endogenous ovarian cancer gene or administering a gene
30 encoding the ovarian cancer sequence, using known gene-therapy techniques, e.g.. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when

the ovarian cancer sequence is up-regulated in ovarian cancer, the activity of the endogenous ovarian cancer gene is decreased, e.g., by the administration of an ovarian cancer antisense or RNAi nucleic acid.

In one embodiment, the ovarian cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to ovarian cancer proteins. Similarly, the ovarian cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify ovarian cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to an ovarian cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The ovarian cancer antibodies may be coupled to standard affinity chromatography columns and used to purify ovarian cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the ovarian cancer protein.

15 **Methods of identifying variant ovarian cancer-associated sequences**

Without being bound by theory, expression of various ovarian cancer sequences is correlated with ovarian cancer. Accordingly, disorders based on mutant or variant ovarian cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant ovarian cancer genes, e.g., determining all or part of the sequence of at least one endogenous ovarian cancer genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the ovarian cancer genotype of an individual, e.g., determining all or part of the sequence of at least one ovarian cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced ovarian cancer gene to a known ovarian cancer gene, e.g., a wild-type gene.

The sequence of all or part of the ovarian cancer gene can then be compared to the sequence of a known ovarian cancer gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the ovarian cancer gene of the patient and the known ovarian cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the ovarian cancer genes are used as probes to determine the number of copies of the ovarian cancer gene in the genome.

In another preferred embodiment, the ovarian cancer genes are used as probes to determine the chromosomal localization of the ovarian cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the ovarian cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of an ovarian cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug Delivery Systems Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceutical Assn.; and Pickar (1999) Dosage Calculations Thomson. Adjustments for ovarian cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in ovarian cancer is hereby expressly incorporated by reference.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the ovarian cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intra-nasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the ovarian cancer

proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise an ovarian cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as

5 pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid,

10 propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper,

15 manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine,

20 tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

25 The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules, and lozenges. It is recognized that ovarian cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally,

30 should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise an ovarian cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs. See, e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman and Limbird (eds. 2001) Goodman and Gillman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill. Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions are readily available.

The compositions containing modulators of ovarian cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and/or its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic

treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, e.g., in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

5 It will be appreciated that the present ovarian cancer protein-modulating compounds can be administered alone or in combination with additional ovarian cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1-26, such as RNAi, antisense
10 polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of ovarian cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for
15 expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell. See,
20 e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSII Press.

In a preferred embodiment, ovarian cancer proteins and modulators are administered
25 as therapeutic agents, and can be formulated as outlined above. Similarly, ovarian cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the ovarian cancer coding regions) can be administered in a gene therapy application. These ovarian cancer genes can include antisense applications, either as gene therapy (e.g., for incorporation into the genome) or as antisense compositions, as will be appreciated by those
30 in the art.

Ovarian cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-
82

- 349), peptide compositions encapsulated in poly(D,L-lactide-co-glycolide, "PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS; see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin. Exp. Immunol. 113:235-243), multiple antigen peptide systems (MAPs; see, e.g., Tam (1988) Proc. Nat'l Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter, Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kienny, et al. (1986) AIDS Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. (1995) Nature Med. 7:649-653), adjuvants (Warren, et al. (1986) Ann. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p. 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Cease and Berzofsky (1994) Ann. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bordetella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MD); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be

used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. See, e.g., Wolff et. al. (1990) Science 247:1465-1468; U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; and WO 98/04720. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode ovarian cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like, will be apparent. See, e.g., Shata, et al. (2000) Mol. Med. Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; and Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing an ovarian cancer gene or portion of an ovarian cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in an ovarian cancer patient. The ovarian cancer gene used for DNA vaccines can encode full-length ovarian cancer proteins, but more preferably encodes portions of the ovarian cancer proteins including peptides derived from the ovarian cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from an ovarian cancer gene. For example, ovarian cancer-associated genes or sequence encoding subfragments of an ovarian cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the ovarian cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

- 5 In another preferred embodiment ovarian cancer genes find use in generating animal models of ovarian cancer. When the ovarian cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed to the ovarian cancer gene will also diminish or repress expression of the gene. Animal models of ovarian cancer find use in screening for modulators of an ovarian cancer-associated sequence or modulators of ovarian cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the ovarian cancer protein. When desired, tissue-specific expression or knockout of the ovarian cancer protein may be necessary.

- 15 It is also possible that the ovarian cancer protein is overexpressed in ovarian cancer. As such, transgenic animals can be generated that overexpress the ovarian cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.
- 20 Animals generated by such methods find use as animal models of ovarian cancer and are additionally useful in screening for modulators to treat ovarian cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

- For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include any or all of the following: assay reagents, buffers, ovarian cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, siRNA or antisense polynucleotides, ribozymes, dominant negative ovarian cancer polypeptides or polynucleotides, small molecules inhibitors of ovarian cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

- 30 In addition, the kits may include instructional materials containing directions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any medium

capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of ovarian cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: an ovarian cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing ovarian cancer-associated activity. Optionally, the kit contains biologically active ovarian cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynn, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

TABLE 1A lists about 1119 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59000 probesets on the Affymetrix/Eos Hu03 GeneChip array such that: the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 5.0. The "average" ovarian cancer level was set to the 80th percentile value amongst various ovarian cancers. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues.

TABLE 1A: ABOUT 1119 UP-REGULATED OVARIAN CANCER GENES

Key: Primerkey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene Title

ratio: ratio tumor vs normal tissues

Key	Ex. Accn	UG ID	Title	ratio
423534	AW559009	Hs.1090	heparin-binding growth factor binding protein	65.7
423017	AW178781	Hs.227948	"oxite" (or cyclin) proteases inhibitor, class B (ovalbumin)	63.6
432938	T27013	Hs.3132	steroidogenic acute regulatory protein	58.3
445810	AW265700	Hs.155580	ESTs	35.9
431938	AA938471	Hs.115242	developmentally regulated GTP-binding protein 1	32.0
407112	AA070801	Hs.51815	"ESTs, weakly similar to ALU, HUMAN ALU SUBFAM	31.3
429550	NM_001944	Hs.1525	desmoglein 3 (pemphigus vulgaris antigen)	30.0
402075			predicted exon	27.9
400301	X03535	Hs.1657	estrogen receptor 1	26.4

WO 02/102235

PCT/US02/19297

	402639			predicted exon	25.3
	421949	I42563	Ha.111758	keratin 6A	24.7
	414540	BE379050		*gb60123655F1 NIH_MGC_44 Homo sapiens cDNA clone	24.6
	418994	AA295620	Ha.89545	selectin E (endothelial adhesion molecule 1)	24.5
5	401575			predicted exon	23.6
	451024	AA397546	Ha.119151	ESTs	23.2
	440684	AI253123	Ha.127359	*ESTs, highly similar to NEST_HUMAN NEST1 [H.sapien	23.1
	458006	AW268531	Ha.27721	hypothetical protein FLJ20063	22.8
10	406954			predicted exon	22.5
	402421			predicted exon	20.9
	437320	AA811977	Ha.291761	ESTs	20.8
	414605	BE350440		*gb60128300F1 NIH_MGC_44 Homo sapiens cDNA clone	20.7
	411004	AW813242		*gbMR3-ST0191+020200-207-g10 ST0191 Homo sapiens	20.4
	401283			predicted exon	20.3
15	442533	A140985	Ha.263320	ESTs	19.9
	455603	H03845	Ha.106234	ESTs	19.7
	403786			predicted exon	19.6
	436058	AW604361	Ha.121211	ESTs	19.2
	459393	BE355725		*gb501276347F1 NIH_MGC_20 Homo sapiens cDNA clone	19.0
20	421820	N40690	Ha.28625	ESTs	18.9
	417366	BE185289	Ha.1076	small proline-rich protein 16 (conaffin)	18.9
	422525	AA758797	Ha.192607	ESTs	18.5
	458121	SA2416	Ha.74547	Human T-cell receptor alpha-chain mRNA from JM c	18.3
	435250	NM_016190	Ha.242557	chromosome 1 open reading frame 10	18.1
25	450192	AA263143	Ha.24569	RAD51-interacting protein	18.0
	416939	H64900	Ha.17582	ESTs	17.9
	440788	AB065694	Ha.128577	ESTs	17.7
	451072	AA013451	Ha.117529	ESTs	17.3
30	402203			predicted exon	17.3
	417611	AW995963		*gbRC1-BN0035-130403-013-BN0035 Homo sapiens	17.3
	438658	AI222068	Ha.123571	ESTs	17.2
	403747			predicted exon	17.2
	444588	AW292643	Ha.167047	ESTs	17.1
35	404097			predicted exon	16.9
	456375	BE251770		*gb60112470F1 NIH_MGC_16 Homo sapiens cDNA clone	16.9
	443198	AI039813		gbwx45d05.x1 Soares_tela_telas_NB2HFS_9w Homo sapi	16.9
	441557	AW452647	Ha.270482	ESTs	16.8
	433871	W02410	Ha.205555	ESTs	16.8
40	429163	AA884765		gbam20a10.x1 Soares_NFL_T_OBC_S1 Homo sapiens cD	16.7
	434006	AI058238	Ha.143316	ESTs	16.7
	400613			predicted exon	16.6
	445372	AW445166	Ha.170802	ESTs	16.5
	410929	H47233	Ha.30643	ESTs	16.5
	445887	AI263105	Ha.145957	ESTs	16.1
45	422036	AA302647	Ha.271891	ESTs	16.0
	404767			predicted exon	15.9
	420831	AA260824	Ha.190035	ESTs	15.8
	405196			predicted exon	15.8
	452947	AW130413		*gbx5094.x1 NCL_CGAP_Gap4 Homo sapiens cDNA clo	15.8
50	429538	BE182552	Ha.136322	small proline-rich protein 3	15.6
	435113	AT69400	Ha.189729	ESTs	15.7
	449635	AI585642	Ha.232150	ESTs	15.6
	424098	AF077374	Ha.139322	small proline-rich protein 3	15.4
55	411690	AW885718		*gbRC1-CT0279-070100-021-005 CT0279 Homo sapiens c	15.4
	422653	BE282247	Ha.170226	Homo sapiens clone 23075 mRNA sequence	15.4
	443534	AI075123		glyox2a04.x1 Soares_tela_liver_spleen_TNFS_L1 Homo	15.4
	458012	AI424899	Ha.188211	ESTs	15.3
	441018	AB095857	Ha.148782	ESTs	15.1
60	423972	BE391563	Ha.165433	*ESTs, highly similar to T17342 hypothetical protein DKFZ	15.1
	418062	RA5154	Ha.108604	ESTs	15.1
	410909	AW898181	Ha.53112	*ESTs, highly similar to ALUS_HUMAN ALU SUBFAM	15.1
	458234	BE551408	Ha.127196	ESTs	15.0
	434208	T92641	Ha.127648	hypothetical protein PRO2176	15.0
65	423177			predicted exon	15.0
	423725	AI403108	Ha.132127	hypothetical protein LOC57822	14.9
	425090	AA350552		*gbEST57666 Infant brain Homo sapiens cDNA 5' end, mR	14.7
	409723	AW865757	Ha.257892	ESTs	14.6
70	423735	AA330280		*gbEST133963 Embryo, 12 week II Homo sapiens cDNA 5'	14.6
	444286	AA20484	Ha.125465	ESTs	14.5
	443341	AW531480	Ha.8668	ESTs	14.4
	457335	AW999657	Ha.291029	ESTs	14.4
	440500	AA972165	Ha.150308	ESTs	14.4
	445252	AF081497	Ha.270652	Rb type C glycoprotein	14.3
75	438006	AA336519	Ha.301167	*Homo sapiens cDNA: FLJ21645 fls, clone COL06195'	14.3
	434715	BE005345	Ha.116410	ESTs	14.2
	403987	AW364900	Ha.123526	ESTs	14.2
	405272	AB014569	Ha.52526	KIA-0069 gene product	14.2
80	454913	AW041462		*gbRC3-CN0014-000300-012-009 CN0014 Homo sapiens	14.0
	439446	T03959	Ha.228320	*Homo sapiens cDNA: FLJ23537 fls, clone LNC07690'	14.0
	406895	AA296981		*gbEST112514 Adrenal gland tumor Homo sapiens cDNA	13.9
	422897	AA679784	Ha.4290	ESTs	13.9
	404954			predicted exon	13.9
	458629	AI557388		*gb:PT2.1_6_G03.2 tumor2 Homo sapiens cDNA 3', mRNA	13.8
	407327	AA487182	Ha.269414	ESTs	13.8

WO 02/02235

PCT/US02/19297

455435	AW939445		"gb:QV1-DT0072-310100-056-b67 DT0072 Homo sapiens	13.7
455827	A1636740	Ha.224572	ESTs	13.7
411953	AW857271		"gb:CMC-DT0307-210100-158-g09 CT0307 Homo sapiens	13.7
407463	AJ272034		gb:Homo sapiens mRNA for putative capacitative calcium c	13.6
446767	A1380107	Ha.158954	ESTs	13.6
433040	H70423	Ha.300511	ESTs	13.5
435209	AW027809	Ha.151908	ESTs, Highly similar to cytomegalovirus partial fusion rece	13.5
441455	A1619142	Ha.214233	ESTs	13.5
401269			predicted exon	13.4
438663	A1195575	Ha.153070	ESTs	13.4
426598	A4384104	Ha.97485	ESTs	13.4
423537	AL137729	Ha.130187	Homo sapiens mRNA: cDNA DKFZp434C01214 (from clon	13.2
448543	AW897741	Ha.213180	Homo sapiens mRNA: cDNA DKFZp596P1124 (from clon	13.2
456714	AW897265		"gtc:CMC-NN0057-150400-335-a04 NN0057 Homo sapiens	13.2
458356	A0024855	Ha.131575	ESTs	13.2
431422	A4510049		"gb:ncs401s.1 NCL_CGAP_Lip2 Homo sapiens cDNA cto	13.1
454822	AW833793		"gb:QV4-TT0008-130100-050-a06 TT0008 Homo sapiens c	13.1
453358	A1890738	Ha.240066	ESTs	13.1
439542	AA687376	Ha.265533	ESTs	13.0
421286	AA006584	Ha.187895	ESTs	13.0
457789	A1948026	Ha.213786	ESTs	13.0
444355	BE363686	Ha.101621	ESTs	13.0
444271	AW452569	Ha.146804	ESTs	12.9
434880	AW669532		"gb:CV4-SN0024-210400-181-g04 SN0024 Homo sapiens	12.9
427119	AA366153	Ha.163126	hypothetical protein FLJ110905	12.9
418282	AA215535	Ha.98133	ESTs	12.8
437308	AA748417	Ha.292353	ESTs	12.7
400584			predicted exon	12.7
425308	AA447310	Ha.164059	"Homo sapiens cDNA FLJ13338 f5, clone CVARC100188	12.7
448465	A1522100	Ha.171066	ESTs	12.7
402738			predicted exon	12.7
451531	AA018311	Ha.114762	ESTs	12.6
435243	AW225686	Ha.261373	adenosine A2b receptor pseudogeno	12.6
431725	X65714	Ha.2639	Herpes disease (pseudogamma)	12.6
425108	A1000496	Ha.95657	ESTs	12.5
422330	D30783	Ha.115263	epigargin	12.5
432949	AA570748	Ha.298566	ESTs	12.5
417008	AA161718	Ha.171672	DEAD(H) (Asp-Glu-Ala-Asp) box polypeptide E (RNA	12.4
458573	AA453387	Ha.87279	ESTs	12.4
432966	AA650114		"gb:ncs2h09s.1 NCL_CGAP_Pc3 Homo sapiens cDNA clon	12.4
440571	AA504461	Ha.130768	ESTs	12.3
411178	AW826852		"gb:RC2-ST0301-1-20200-011-f12 ST0301 Homo sapiens c	12.3
445534	AF131137	Ha.13475	hypothetical protein	12.3
433617	A1502325	Ha.122614	Human DNA sequence from clone RP5-102B015 on chrom	12.2
402018			predicted exon	12.2
424101	AA335394		"gb:EST139787 Epithelium Homo sapiens cDNA 5' and, mR	12.2
445533	AL119710	Ha.21365	nucleosome assembly protein 1-like 3	12.1
455154	AW616379		"gb:QV4-ST0234-151199-035-g01 ST0234 Homo sapiens c	12.1
440616	AW261274	Ha.262626	ESTs	12.0
415747	AA381209		"gb:EST54257 Activated T-cells I Homo sapiens cDNA 5' o	12.0
411748	AW685920		"gb:QV1-CT0364-290100-052-g05 CT0364 Homo sapiens	12.0
428275	M8521	Ha.60469	desiccation cell protein	12.0
427276	AA400299	Ha.49598	ESTs	12.0
454315	AW373564	Ha.251928	nuclear pore complex interacting protein	12.0
450786	H89632	Ha.33654	ESTs	12.0
402576			predicted exon	11.9
468591	AL037185		gb:DKFZp44A1169_r1_554 (synonym: hfx2) Homo sapie	11.9
433440	AW772282		"gb:ha1605s.1 NCL_CGAP_xd411 Homo sapiens cDNA c	11.9
429106	AA890521	Ha.126036	ESTs	11.8
454555	AW607073		"gb:MR4-ST0062-031199-018-a06 ST0062 Homo sapiens	11.7
443613	A070266		gb:ncs39h09s.1 Soares_NNNMNP_S1 Homo sapiens cDNA c	11.7
400385	NM_020389	Ha.283104	putative capacitative calcium channel	11.6
411725	AW68396		"gb:CMC-CT0341-151290-030-c06 CT0341 Homo sapiens	11.5
455714	AW64578	Ha.147801	ESTs	11.5
412402	AW681788		"gb:RC1-HN0015-120400-021-c07 HN0015 Homo sapiens	11.5
434205	AF111861	Ha.283032	hypothetical protein PRO2015	11.5
450496	AW449251	Ha.257131	ESTs	11.5
411149	N68715	Ha.269128	ESTs	11.5
414210	BE383552		"gb:60129787 f1c 1 NH_LMC_18 Homo sapiens cDNA clon	11.4
409894	D18684	Ha.57735	acetyl LDL receptor; SREC	11.3
453845	AL151568		gb:DKFZp761F0816_r1_761 (synonym: hamy2) Homo sapi	11.3
404849			predicted exon	11.3
442824	BE178065	Ha.144081	ESTs	11.3
425618	AA430038	Ha.98649	EST	11.3
434804	AA648300		"gb:ncs4400s.1 NCL_CGAP_Alv1 Homo sapiens cDNA cto	11.3
433486	BE062109	Ha.241551	"chloride channel, calcium activated, family member 2"	11.3
400174			predicted exon	11.2
424324	AA346316		"gb:EST52440 Greater omentum tumor Homo sapiens cDN	11.2
461724	AW268375	Ha.24477	ESTs	11.2
457028	AW449838	Ha.97552	ESTs	11.2
429900	AA60421	Ha.30875	ESTs	11.2
452240	A1591147	Ha.61232	ESTs	11.2
455067	AA393903	Ha.36752	"Homo sapiens cDNA: FLJ22834 f5, clone KIAA4314"	11.1
402222			predicted exon	11.1

WO 02/102235

PCT/US02/19297

	446745	AW118189	Hs.156400	ESTs	11.1
	453060	AW294002	Hs.21594	ESTs	11.1
	443452	AW183053	Hs.250385	ESTs	11.1
5	436543	AA824588		"gtrco3d02.s1 NCL CGAP_GCB1 Homo sapiens cDNA c	11.0
	416320	H47867	Hs.34024	ESTs	11.0
	435772	AA700010	Hs.132952	"XTP-binding cassette, sub-family G (WHITE), member 5 (11.0
	451542	AA018365	Hs.32713	ESTs	11.0
	408522	AI541214	Hs.46320	"Small proline-rich protein SPRK [human, odontogenic kera	11.0
	414712	N85555.comp	Hs.77039	ribosomal protein S3A	10.9
10	411940	AW575686		"gtrCMA-PT0031-130200-507-e05 PT0031 Homo sapiens c	10.9
	406733	AW549812	Hs.254290	ESTs	10.9
	452030	AI13575	Hs.27507	Homo sapiens mRNA; cDNA DKFZp564N2464 (from clone	10.9
	458175	AW296024	Hs.150434	ESTs	10.9
	400612			predicted exon	10.9
15	440159	AI637599	Hs.126127	ESTs	10.8
	429443	AB023967	Hs.202657	"Potassium voltage-gated channel, Shal-related subfamily, m	10.8
	416319	AI515601	Hs.79197	"CD83 antigen (activated B lymphocytes, immunoglobulin s	10.8
	405783			predicted exon	10.7
	405705			predicted exon	10.7
20	433286	AI963224	Hs.286677	"Homo sapiens cDNA FLJ13572 fls, clone THYRO100132	10.6
	456900	AA355442	Hs.169054	ESTs	10.6
	432408	N39127	Hs.76391	"myxovirus (influenza) resistance 1, homolog of murine (let	10.6
	451702	AW665452	Hs.246503	ESTs	10.6
	418179	XS1630	Hs.1145	Wilms tumor 1	10.6
25	401887	H85615		gtr03T11.1 Soares retina N2bSHR Homo sapiens cDNA	10.6
	402855			predicted exon	10.5
	415276	BE165900	Hs.134682	"Homo sapiens cDNA: FLJ23161 fls, clone LNC057307	10.5
	407287	AI78812	Hs.201658	"ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	10.5
	403055			predicted exon	10.5
30	414195	BE263293		"gtr501144681F2 NIH_MGC_19 Homo sapiens cDNA don	10.4
	454255	AI457286	Hs.143679	"ESTs, Weakly similar to KIAA1276 protein (H.sapiens)"	10.4
	412951	BE018611	Hs.251946	"Homo sapiens cDNA: FLJ23107 fls, clone LNC077387	10.4
	426888	AA427010	Hs.285384	ESTs	10.4
	440234	AA907027	Hs.129306	ESTs	10.4
35	437096	AA744406		"gtrm51th02.s1 NCL CGAP_Prl18 Homo sapiens cDNA do	10.4
	400135			predicted exon	10.4
	447849	AI538147	Hs.164277	ESTs	10.3
	403593			predicted exon	10.3
40	427469	AA403084	Hs.256347	ESTs	10.3
	402794			predicted exon	10.2
	452743	AW963082	Hs.614555	ESTs	10.2
	440883	AI611654	Hs.224508	ESTs	10.2
	422896	AF741204	Hs.26323	hypothetical nuclear factor SBR22	10.2
45	402946	AA442153	Hs.104744	"ESTs, Weakly similar to AF208855 1 BM-013 (H.sapiens)	10.2
	409191	AW618390		"gtrRC1-ST0278-160200-014-c10 ST0278 Homo sapiens c	10.2
	428493	AK001745	Hs.194625	hypothetical protein FLJ10863	10.2
	405076	AL350079	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (from clone	10.2
	410626	BE407727		"gtr501296771F1 NIH_MGC_21 Homo sapiens cDNA don	10.1
	445835	AW209099	Hs.145534	chromosome 21 open reading frame 23	10.1
50	452507	AI504546		"gtrQV-8T065-020399-103 BT065 Homo sapiens cDNA, m	10.1
	433277	AW635581	Hs.252633	ESTs	10.1
	428724	AA383623	Hs.230616	ESTs	10.0
	436659	AI217900	Hs.144464	ESTs	10.0
	405675			predicted exon	10.0
55	413466	BE141737	Hs.254105	"enolase 1, (alpha)"	10.0
	447168	281523	Hs.253455	ESTs	10.0
	403306	NM_00825	Hs.74368	"transmembrane protein (53kD), endoplasmic reticulum/Go	10.0
	413544	BE147225		"gtrPK2-HT0225-031299-003-411 HT0225 Homo sapiens	9.9
	437094	AW103746	Hs.136907	ESTs	9.9
60	401497			predicted exon	9.9
	416203	H72794	Hs.269055	ESTs	9.9
	426882	AA393105	Hs.97365	ESTs	9.9
	454874	AW536407		"gtrPA3-LT0031-301299-002-b09 LT0031 Homo sapiens	9.9
	406702	Z20656	Hs.278432	"myosin, heavy polypeptide 6, cardiac muscle, alpha (cardi	9.9
65	404852			predicted exon	9.9
	430691	C11487	Hs.103536	ESTs	9.9
	444518	AI160275	Hs.146884	ESTs	9.8
	416665	H72974		gtrv25a10.s1 Soares fetal liver spleen TNF1S Homo sapie	9.8
	435691	AA906288	Hs.212184	ESTs	9.8
70	405636			predicted exon	9.8
	437242	AA747536	Hs.157942	ESTs	9.8
	425627	AF019812	Hs.297007	ESTs	9.8
	452226	AA024896	Hs.296002	ESTs	9.8
	418986	AI123355	Hs.217196	ESTs	9.8
75	441139	AAW49009	Hs.126647	ESTs	9.7
	427244	AA402400	Hs.175045	ESTs	9.7
	423756	AA528125		"gtrcd71a01.s1 NCL CGAP_Ov2 Homo sapiens cDNA do	9.7
	457940	AL360189	Hs.30445	Homo sapiens mRNA full length insert cDNA clone EURO	9.6
	443526	AW769204	Hs.134002	ESTs	9.6
80	440576	AW449775	Hs.126005	ESTs	9.6
	419098	AI538323	Hs.77496	small nuclear ribonucleoprotein polypeptide G	9.6
	464707	AW614859		"gtrNR1-ST0206-170400-024-g05 ST0206 Homo sapiens	9.6
	446252	AA203105	Hs.150009	ESTs	9.6
	434374	AA631439		"gtrmp5002.s1 NCL CGAP_Tht1 Homo sapiens cDNA cl	9.6

WO 02/102235

PCT/US02/19297

	403093		predicted exon	9.6	
	454633	AW811380	"gblc1.3 ST0143:290999-019-D05 ST0143 Homo sapiens c	9.6	
	407291	AA001464	"gblc24501.1 Soares retina N264R Homo sapiens cDNA	9.6	
5	455203	AW865450	"gblcPMA SN0020-010400-006-b09 SN0020 Homo sapiens	9.6	
	403647		predicted exon	9.6	
	401530		predicted exon	9.6	
	14281	EE269751	Hs.288996	hypothetical protein FLJ20613	9.6
	411057	AW815098		"gblcQV4-ST0212-091159-023-f10 ST0212 Homo sapiens c	9.6
	415953	H14426	Hs.27947	ESTs	9.6
10	450174	T82121	Hs.177285	ESTs	9.6
	422949	AA319435		"gblcST21657 Adrenal gland tumor Homo sapiens cDNA 5	9.6
	402112	R58624	Hs.2186	cukaryotic translation elongation factor 1 gamma	9.6
	451786	AA742279	Hs.253346	ESTs	9.6
	458145	AC29457	Hs.130794	ESTs	9.6
15	452332	AW014859	Hs.101657	ESTs	9.6
	434550	AW574892		"gblcST336957 MAGE resequences, MAGN Homo sapien	9.6
	409601	AF227621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	9.6
	415968	XG430	Hs.53513	"tristricotin 6 (interleukin, beta 2)	9.6
20	436211	AK001581	Hs.80961	"polymorase (DNA directed), gamma"	9.6
	428412	AA428240	Hs.126083	ESTs	9.6
	449441	AI656040	Hs.196532	ESTs	9.6
	458771	AW265151	Hs.163612	ESTs	9.6
	458643	AA212403	Hs.257542	ESTs	9.6
25	414257	AI828600	Hs.21124	"ESTs, Weakly similar to ALU, HUMAN ALU SUBFAM	9.6
	442826	AI018777	Hs.131241	ESTs	9.6
	445740	AI911635	Hs.192606	ESTs	9.6
	428638	AA068013	Hs.22507	ESTs	9.6
	434157	AI538316	Hs.158451	ESTs	9.6
	408774	AW270899	Hs.254509	ESTs	9.6
30	424268	AA367653	Hs.144339	Human DNA sequence from clone 45S1010 on chromosome	9.6
	415715	F30394		"gblcHSP020785 HMG Homo sapiens cDNA clone s400009	9.6
	405277			predicted exon	9.6
	412167	AW897230		"gblcCMG-NN0057-150400-335-a11 NN0057 Homo sapiens	9.6
	442771	AIW406006	Hs.101550	ESTs	9.6
35	404956			predicted exon	9.6
	401230			predicted exon	9.6
	400623			predicted exon	9.6
	418806	AI821836	Hs.10359	ESTs	9.6
	433390	AI053457	Hs.229112	"Homo sapiens cDNA FLJ114411 fs, clone HEM6A100132	9.6
40	440406	AA055871	Hs.135727	ESTs	9.6
	437568	AI554795	Hs.136135	ESTs	9.6
	405382			predicted exon	9.6
	435673	AF202951	Hs.284200	"Homo sapiens uncharacterized gastric protein ZG12P mRNA	9.6
	403848			predicted exon	9.6
45	437229	AW975005		"gblcST138114 MAGE resequences, MAGN Homo sapien	9.6
	417728	AIW138437	Hs.24790	KIAA1573 protein	9.6
	454597	AW909648		"gblcMR4-ST0124-261099-015-d01 ST0124 Homo sapiens	9.6
	427053	AA388116	Hs.57579	ESTs	9.6
50	408000	L11680	Hs.620	bulbous pemphigoid antigen 1 (230k240kD)	9.6
	446566	AW239958	Hs.125968	ESTs	9.6
	401013			predicted exon	9.6
	420120	AI048610	Hs.95243	transcription elongation factor A (SII)-like 1	9.6
	417549	AA203651		"gblc5S10.1 Soares_beta_liver_spleen_INFLS_S1 Homo	9.6
	405153			predicted exon	9.6
55	437918	AI761449	Hs.121629	ESTs	9.6
	446419	R34910	Hs.119172	ESTs	9.6
	434083	AW293724	Hs.200339	ESTs	9.6
	413432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedin C)	9.6
60	454590	AW808732	Hs.222063	"Homo sapiens cDNA FLJ11572 fs, clone HEMBA100337	9.6
	454574	AW801919		"gblcMR4-ST0117-070100-027-ab4 ST0117 Homo sapiens c	9.6
	441433	AA533809	Hs.42746	ESTs	9.6
	410586	AW976294	Hs.85534	ESTs	9.6
	421616	AA243632	Hs.110196	NICE-1 protein	9.6
	451528	AA018297	Hs.35493	ESTs	9.6
65	408751	N91553	Hs.28343	ESTs	9.6
	401662			predicted exon	9.6
	417344	AW957313		"gblcRC2-0N0046-250400-018-f12 0N0046 Homo sapiens	9.6
	454445	AW752710		"gblcSLCCT0219-281099-024-A03 CT0219 Homo sapiens c	9.6
70	456592	BE008002		"gblcQVQ-EN0147-280400-214-a04 EN0147 Homo sapiens	9.6
	417650	T05870	Hs.100540	ESTs	9.6
	456309	AA225423		"gblc24s12r1 NCL_CGAP_Pv1 Homo sapiens cDNA clone	9.6
	423030	AW80400	Hs.143789	ESTs	9.6
	421492	BE175990	Hs.104616	hypothetical protein FLJ21940	9.6
75	402576			predicted exon	9.6
	426974	N67325	Hs.247132	ESTs	9.6
	403334			predicted exon	9.6
	408562	AI436323	Hs.31141	"Homo sapiens mRNA for KIAA1566 protein, partial cds"	9.6
	439443	AF086261	Hs.127892	ESTs	9.6
	428600	AA530201	Hs.15036	"ESTs, Highly similar to AF161359 S1 HSP005 (Hs) sapiens	9.6
80	414639	BE379046		"gblc00123664F1 NIH_MGC_44 Homo sapiens cDNA clone	9.6
	432637	AW955026	Hs.102754	ESTs	9.6
	403273			predicted exon	9.6
	452077	BE144949		"gblcRC2-F10167-041099-011-d12H10167 Homo sapiens	9.6
	444698	A288830	Hs.149924	ESTs	9.6

WO 02/102235

PCT/US02/19297

5	43066	AF115649	Hs.283944	"Homo sapiens PRO0565 mRNA, complete cds"	8.6
	429643	AA458989	Hs.187548	ESTs	8.6
	432340	AA634222		gln212d2s1 NCL CGAP_AA1 Homo sapiens cDNA clone	8.6
	446142	AF54093	Hs.143968	ESTs	8.6
	417412	X16966	Hs.82112	"tridekalin 1 receptor, type I"	8.6
10	416913	AW634714		"gJRC1-DT0001-031299-011-s11 DT0001 Homo sapiens	8.5
	451318	AA029888	Hs.95071	ESTs	8.5
	405547			predicted exon	8.5
	423843	AA332652		"hbs.ES136627 Embryo, 8 week I Homo sapiens cDNA 5' on	8.5
	494145	AA046872	Hs.62798	ESTs	8.4
15	401200			predicted exon	8.4
	404166			predicted exon	8.4
	412761	AW959092		"gQVQ-BN0041-030300-145-a10 BN0041 Homo sapiens	8.4
	412333	AW627485		"gbcQVS-DT0044-221259-045-b09 DT0044 Homo sapiens	8.4
	455092	BE152426		"gbcQMG-HT0323-151299-126-b04 HT0323 Homo sapiens	8.4
20	419281	H06452	Hs.42189	ESTs	8.4
	446171	AF374627		gblat6cd4x1 Soares_Jolal_Jolal_Nb2HFB_5w Homo sapie	8.3
	437362	AL335951	Hs.16493	hypothetical protein DKF2p020d2316	8.3
	420331			predicted exon	8.3
	458573	AV653836	Hs.285131	ESTs	8.3
25	439185	AF087976	Hs.233343	ESTs	8.3
	443861	A263529	Hs.210689	ESTs	8.3
	446727	A066581	Hs.245216	ESTs	8.3
	401830	AJ004832	Hs.5038	neurotoxic target esterase	8.3
	421981	NM_014818	Hs.110488	KIAA0590 protein	8.3
30	416996	W91882	Hs.59068	ESTs	8.2
	443626	AA50464	Hs.138479	ESTs, Moderately similar to ALU7_HUMAN ALU SUBF	8.2
	427471	D55944		gH-human spleen PABL (pseudoautosomal boundary-like se	8.2
	420664			predicted exon	8.2
	417682	W95661		gblat24a0r1 Soares_Jolal_Jolal_NbH191W Homo sapiens	8.2
35	424683	AF742434	Hs.189911	ESTs	8.2
	424363	AA503863	Hs.131375	ESTs, Weakly similar to ALU8_HUMAN !!! ALU CLAS	8.2
	453448	AL036710		ESTs	8.2
	455121	BE150459		"gbcQVO-HT0369-040100-052-005 HT0369 Homo sapiens	8.2
	424270			predicted exon	8.1
40	432687	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	8.1
	418122	R42778	Hs.22217	ESTs	8.1
	419629	U90266	Hs.53810	cerebral cavernous malformations 1	8.1
	430925			predicted exon	8.1
	433350			predicted exon	8.1
45	426116	AA863726	Hs.144694	ESTs	8.1
	441518	AW161097	Hs.294150	ESTs	8.1
	421888	AA269780	Hs.121036	ESTs	8.1
	422745			predicted exon	8.1
	422071			predicted exon	8.1
50	444781	NM_014400	Hs.11859	GPI-anchored metastatic-associated protein homolog	8.0
	430372	AJ206173	Hs.211375	ESTs	8.0
	449667	AF72378	Hs.73919	"clathrin, light polypeptide (lcb)"	8.0
	422174	AL046325	Hs.112493	Homo sapiens mRNA, cDNA DKF2g564d036 (from clone	8.0
	413382	BE020659		"gbcRC1-BT0728-283000-011-b08 BT0728 Homo sapiens c	8.0
55	450502	AJ798611	Hs.157277	ESTs	8.0
	405336			predicted exon	8.0
	405917			predicted exon	8.0
	430307	AJ247716	Hs.232168	ESTs	8.0
	429152	AW970536	Hs.105413	ESTs	8.0
60	437724	AW444928	Hs.184323	ESTs	8.0
	429755	AW138537	Hs.213436	ESTs	8.0
	401781			predicted exon	7.9
	430307			predicted exon	7.9
	400789	AW068311	Hs.82582	"Integrin, beta-like 1 (with EGF-like repeat domains)"	7.9
65	421459	AB21539	Hs.57249	ESTs	7.9
	446251	BE280486	Hs.84045	"Homo sapiens cDNA FLJ11979 fs, clone HEMBB100128	7.9
	423125	AA440654	Hs.271004	ESTs	7.9
	440154	BE077129	Hs.126119	"Homo sapiens cDNA FLJ13273 fs, clone ONARC10101	7.9
	413233	AW578713	Hs.47534	"ESTs, Weakly similar to ORF YKL201c [S.cerevisiae]"	7.9
70	432626	AA782163	Hs.263502	ESTs	7.9
	424246	N64635	Hs.23904	Human DNA sequence from clone GK215 on chromosome 6	7.9
	441154	BE274581		"gbc01120270F1 NIH_MGC_20 Homo sapiens cDNA clone	7.8
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	7.9
	445093	AW206208	Hs.147263	ESTs	7.9
75	421292	AA370141	Hs.251453	Human DNA sequence from clone 967N21 on chromosome	7.9
	414266	BE261834		"gbcSC112428F1 NIH_MGC_8 Homo sapiens cDNA clone	7.8
	407639	AA045144	Hs.161566	ESTs	7.8
	466101	AA159478		gbc267406.s1 Stralagone pancreas (537208) Homo sapiens	7.8
	455863	BE147225		"gbcPM2-HIT0225-031299-003411 HIT0225 Homo sapiens	7.8
80	414955	C18200		gbcC18200 Human placenta cDNA (TF14wars) Homo sapie	7.8
	427427	AW626531	Hs.287955	"Homo sapiens cDNA FLJ13395 fs, clone HIT2P3002142	7.8
	416151	T26651		"gbcAD65C7R infant brain, LNL array of Dr. M. Soares 1	7.8
	446435	AW206737	Hs.253582	ESTs	7.8
	423698			predicted exon	7.8
	424914	AA348410	Hs.115005	ESTs	7.8
	409731	AA123985	Hs.56145	"thymosin, beta, identified in neuroblastoma cells"	7.8
	401604			predicted exon	7.8
	413025	AA603265	Hs.281646	ESTs	7.8

WO 02/102235

PCT/US02/19297

	405896		predicted exon	7.8
	454505	AW001365	"gbl5.5UM0002-240300-056-a01 UM0067 Homo sapiens	7.7
	448283	A1340462	Ribosomal protein L12	7.7
5	434098	AA625499	"gblaf59g08.r1 Soares_NHMPu_S1 Homo sapiens cDNA	7.7
	431673	AW971362	ESTs	7.7
	421029	AW057782	ESTs	7.7
	406391	AW659276	"gblMR1-CT0362-240200-105-402 CT0362 Homo sapiens	7.7
	422529	AW015128	ESTs	7.7
	454389	AW752671	"gblL3-CT0213-170100-056-F02 CT0213 Homo sapiens c	7.7
10	427821	AA470156	ESTs	7.7
	434637	AA641876	ESTs	7.7
	445628	A1341166	ESTs	7.7
	424872	AA347923	"gblEST54302 Fetal heart H1 Homo sapiens cDNA 5' end, m	7.7
	439232	N46590	ESTs	7.7
15	441417	A233267	ESTs	7.7
	453596	AA441838	ESTs	7.7
	430440	X52599	"nerve growth factor, beta polypeptide"	7.7
	413306	AW303544	ESTs	7.7
	403958		predicted exon	7.7
20	446726	AW300144	"Homo sapiens cDNA FLJ11629 fig, clone HEMBA100424	7.7
	427504	AA775743	ESTs	7.7
	405621		predicted exon	7.6
	414127	A1431863	ESTs	7.6
25	403806	AW922152	"gblSF-HF-6R0-p-ijr-4-11-QULr1 NIH_MGC_52 Homo sap	7.6
	446232	A1281848	ESTs	7.6
	403658		predicted exon	7.6
	451458	AI797558	ESTs	7.6
	439157	AA912327	ESTs	7.6
	401793		predicted exon	7.6
30	429839	AI190291	ESTs	7.6
	445572	AI807438	ESTs	7.6
	449444	AW815436	"isolate center family 16 (monocarboxylic acid transporters)	7.6
	447499	AW282650	"KAA1621 protein	7.6
	421773	W69233	ESTs	7.6
35	439706	AW872527	ESTs	7.5
	432189	AA527941	"gblmh30c04.s1 NCL_GCAP_P30 Homo sapiens cDNA clone	7.5
	402080		predicted exon	7.5
	426687	AI675749	nucleoporin 153KD	7.5
40	423193	R07829	"Homo sapiens cDNA FLJ13502 fig, clone PLACE1004836	7.5
	415548	H62963	"gblr4705.r1 Soares fetal liver spleen 1NFLS Homo sapien	7.5
	443236	AI679498	ESTs	7.5
	430653	AI677224	ESTs	7.4
	437191	NM_005846	"serine protease inhibitor, Kazal type, 5"	7.4
	451029	AW964081	ESTs	7.4
45	443161	AI827193	ESTs	7.4
	452055	AI377431	ESTs	7.4
	445286	A210256	ESTs	7.4
	401032		predicted exon	7.4
	448184	BE541240	ESTs	7.4
50	414808	T99945	"gblr42602.r1 Soares fetal liver spleen 1NFLS Homo sapien	7.4
	415540	A5211897	"ESTs, Weakly similar to ALLU1_HUMAN/ALLU SUBFAM	7.4
	410449	AW748954	Ser/Arg-related nuclear matrix protein (plenty of proteins 1	7.4
	435566	AA688048	ESTs	7.4
	459100	AA904723	"gblCMT6-102299-002 BT066 Homo sapiens cDNA,	7.4
55	419753	N42531	"gblr471c12.r1 Soares melanocyte 2NFHM Homo sapiens cD	7.4
	432383	AK006144	"Homo sapiens cDNA FLJ20137 fig, clone COL07137"	7.4
	404893		predicted exon	7.4
	425349	AA425234	ribose 5-phosphate isomerase A (ribose 5-phosphate epimer	7.3
60	413864	BE175882	"gblRCS-HT0680-100500-022-C01 HT0680 Homo sapiens	7.3
	425871	AA330441	ESTs	7.3
	415613	R20233	"gblr471b.r1 Soares infant brain 1NFH Homo sapiens cDN	7.3
	427026	AA397589	ESTs	7.3
	444683	AI378101	"ESTs, Weakly similar to ALLU1_HUMAN/ALLU SUBFAM	7.3
	447780	AA426183	"ESTs, Weakly similar to similar to perlecan/trecan-like	7.3
65	412740	AW065984	"gblRCL1-EN00035-130400-013-a05 EN00035 Homo sapiens	7.3
	416642	T96118	"ESTs, Weakly similar to ALLU1_HUMAN/ALLU SUBFAM	7.3
	416506	H59879	ESTs	7.3
	429130	AA853262	"gblNH17ECae04007.r1 Normal Human Trabecular Bone Cell	7.3
70	427392	AK002369	"gblHomo sapiens MIST mRNA, partial cds."	7.3
	423265	AK001106	hypothetical protein FLJ10244	7.3
	451221	AI949701	ESTs	7.3
	443161	AI038316	"gblr44c08.x1 Soares_fetal_fetus_N02HF8_9w Homo sapi	7.3
	418186	BE541042	"Homo sapiens cDNA FLJ10496 fig, clone PLACE1004471	7.3
75	439152	H65014	"gblr44c08.x1 Soares_fetal_fetus_N02HF8_9w Homo sapi	7.2
	459534	BE386808	ESTs	7.2
	443326	BE158494	ESTs	7.2
	417351	T90278	ESTs	7.2
	454192	AW177335	"gblCMT-CT0129-180899-006-b08 CT0129 Homo sapiens	7.2
80	422396		predicted exon	7.2
	468562	N34128	ESTs	7.2
	407021	US2077	"gblHuman malner1 transposase gene, complete consensus	7.2
	449270	AW241510	ESTs	7.2
	418251	AA832123	ESTs	7.2
	420788	AA937957	ESTs	7.2

WO 02/102235

PCT/US02/19297

401881			predicted exon	7.2
465438	AA261879	Hs.156306	ESTs	7.2
415426	F20956		"gpcHSPDQ5390 HM3 Homo sapiens cDNA clone 032-34-	7.2
448966	AK372914	Hs.267462	"Homo sapiens cDNA FLJ116175 fls, clone HEMBA100707	7.2
420340	N35038	Hs.195429	"Homo sapiens mRNA; cDNA DKFZp434M2216 (from clone	7.2
405053			predicted exon	7.2
406551			predicted exon	7.2
431009	BE149762	Hs.246213	"gap junction protein, beta 6 (connexin 30)"	7.2
426662	AA679474	Hs.122710	ESTs	7.1
408536	AW361532	Hs.135186	ESTs	7.1
455013	BC073250		"gpcMR3-CT0176-061099-002-c05 BT0551 Homo sapiens	7.1
428910	W69697	Hs.153792	ESTs	7.1
424634	NM_003613	Hs.151407	"cartilage intermediate layer protein, nucleotide pyrophosph	7.1
449794	AW444502	Hs.266962	"ESTs, highly similar to AF116665 1 hedgehog-interacting	7.1
423410	AF055969	Hs.126231	"G antigen, family B, 1 (granulose associated)"	7.1
445400	AF784743	Hs.200468	ESTs	7.1
447265	AJ371640	Hs.200696	"ATPase, Class VI, type 11C"	7.1
419750	AL079741	Hs.163114	"Homo sapiens cDNA FLJ14236 fls, clone NT2NP4000515	7.1
438966	AF065888	Hs.265307	ESTs	7.1
420767	XT6692	Hs.529915	androgen receptor (jellyroll/steroid hormone receptor, testicular	7.1
432479	AL042644	Hs.275675	katanin p60 (W040-containing) subunit B 1	7.1
449733	R74546	Hs.294336	"Homo sapiens cDNA FLJ12094 fls, clone HEMBA100260	7.1
437846	AA773896	Hs.244509	ESTs	7.1
445434	AW640080	Hs.261076	"gpcMR3-CT0176-061099-002-b09 CT0176 Homo sapiens	7.1
421929	AA300545	Hs.247360	ESTs	7.1
401780			predicted exon	7.0
448106	AB004470	Hs.171941	ESTs	7.0
448835	BE277929	Hs.11081	"ESTs, Weakly similar to S57447/HP8E-7 protein [H.sap	7.0
400642			predicted exon	7.0
429364	AA451797	Hs.201202	"ESTs, Moderately similar to Pro-Pol-dUTPase polypeptide	7.0
454963	AW647647	Hs.261076	"gpcIL3-CT0213-280100-055-A06 CT0213 Homo sapiens c	7.0
423891	AK002042	Hs.134795	"Homo sapiens cDNA FLJ11180 fls, clone PLACE1007452	7.0
407506	J71600	Hs.13802	"gpcHanc zinc finger protein zfp51 (zfp51) mRNA, partial	7.0
413802	AW64400	Hs.32241	ESTs	7.0
440051	BE556660	Hs.gpcMR3-CT0176-061099-002-b09 CT0176 Homo sapiens	7.0	
446283	AI048801	Hs.171073	ESTs	7.0
419236	AA330447	Hs.135159	"Homo sapiens cDNA FLJ11481 fls, clone HEMBA100180	7.0
405472			predicted exon	7.0
435024	AB63518	Hs.127743	"ESTs, Weakly similar to V-ATPase G-subunit like protein	7.0
453960	AW090763	Hs.301731	"Homo sapiens cDNA FLJ11738 fls, clone HEMBA100547	7.0
404992			predicted exon	7.0
426129	AI244311	Hs.26912	ESTs	7.0
414315	Z24676	Hs.50868	"gpcHSPDQ5390 STRATAGENE Human skeletal muscle cD	6.9
400491	H25530	Hs.50868	"solute carrier family 22 (organic cation transporter), memb	6.9
459275	AI080913	Hs.118321	ESTs	6.9
450653	AA473629	Hs.44243	ESTs	6.9
457460	AF143212	Hs.164004	ESTs	6.9
434168	AI024525	Hs.116156	ESTs	6.9
445153	AI214671	Hs.gpcMR3-CT0176-061099-002-b09 CT0176 Homo sapiens	6.9	
450028	AB120122	Hs.200737	ESTs	6.9
414954	CG1402	Hs.gpcHSPDQ5390 Human fetal brain (Tfujuzaki) Homo sa	6.9	
449478	AW105966	Hs.263162	ESTs	6.9
426269	H15302	Hs.168950	"Homo sapiens mRNA; cDNA DKFZp556A1046 (from clone	6.9
401050			predicted exon	6.9
447888	AI394154	Hs.279659	"ESTs, Weakly similar to unknown protein [H.sapiens]"	6.9
440002	AF020181	Hs.117461	ESTs	6.9
452759	AW500773	Hs.250996	ESTs	6.9
443220	R65304	Hs.132032	"Homo sapiens cDNA FLJ11683 fls, clone HEMBA100490	6.9
400749			predicted exon	6.8
406277			predicted exon	6.8
433765	BE044693	Hs.112704	ESTs	6.8
434129	AB007757	Hs.221041	ESTs	6.8
453369	BE551550	Hs.232630	ESTs	6.8
411722	AW675942	Hs.gpcMR3-CT0176-061099-002-b09 CT0176 Homo sapiens	6.8	
455152	AW686921	Hs.gpcMR3-CT0176-061099-002-b09 CT0176 Homo sapiens	6.8	
412670	AA115456	Hs.191510	"ESTs, Weakly similar to ORF2 [Muscutus]"	6.8
419054	N40340	Hs.191510	ESTs	6.8
421316	AA267203	Hs.251397	SNAS	6.8
432363	AA534880	Hs.gpcMR3-CT0176-061099-002-b09 CT0176 Homo sapiens	6.8	
456803	AW103346	Hs.61162	"RNA0771 protein	6.8
439527	AW298119	Hs.202536	ESTs	6.8
408920	AL120071	Hs.46959	fibronectin leucine rich transmembrane protein 2	6.8
439127	AW978465	Hs.252366	ESTs	6.8
434900	AF161345	Hs.263930	"Homo sapiens HSPC062 mRNA, partial cds"	6.8
429413	NM_014058	Hs.201677	DESC1 protein	6.7
407788	BE514962	Hs.38991	S100 calcium-binding protein A2	6.7
447262	R03916	Hs.gpcMR3-CT0176-061099-002-b09 CT0176 Homo sapiens	6.7	
455581	BE146879	Hs.gpcMR3-CT0176-061099-002-b09 CT0176 Homo sapiens	6.7	
439509	AF086332	Hs.58314	ESTs	6.7
416858	AW061605	Hs.21145	"Homo sapiens cDNA: FLJ22489 fls, clone HRC10951"	6.7
419323	AI092379	Hs.135275	ESTs	6.7
415317	Z43368	Hs.5570	hypothetical protein FLJ10006	6.7
416854	AA226334	Hs.154291	ESTs	6.7
407413	AF067801	Hs.gpcMR3-CT0176-061099-002-b09 CT0176 Homo sapiens	6.7	

WO 02/102235

PCT/US02/19297

	430694	AA843915	Hs.54707	ESTs	6.7
	451191	N67900	Hs.118446	ESTs	6.7
	454006	U12775	Hs.37036	agouti (mouse)-signaling protein	6.7
5	443957	R14973		gby4210.s1 Soares fetal liver spleen 1NF.LS Homo sapien	6.7
	456670	BE153276		"gbrFM4-HT0335-189400-006 c11 HT0335 Homo sapiens	6.7
	451358	BE242152	Hs.289417	protein sulfate fructose kinase GNA	6.7
	453509	AL040021		gbrDKFZp434N1812.1 434 (synonym: hlec3) Homo sapie	6.7
	420892	AW597076	Hs.172589	nuclear phosphoprotein similar to S. cerevisiae PWP1	6.7
10	423372	A246575	Hs.154458	ESTs	6.7
	452016	W04446	Hs.17850	ESTs	6.7
	447795	AW295151	Hs.163612	ESTs	6.7
	413252	BE074910		"gbrRCS-BT0580-170300-021-F12 BT0580 Homo sapiens	6.7
	405771			predicted exon	6.6
	411483	AW648115		gbrL3-CT0214-301259-948-C09 CT0214 Homo sapiens c	6.6
15	420271	A954365	Hs.42892	ESTs	6.6
	431948	AA917708	Hs.194616	ESTs	6.6
	408629	AW449569	Hs.279724	ESTs	6.6
	456041	W23965		gbr24d10 Human retina cDNA randomly primed sublibrary	6.6
	416585	AW000090	Hs.444970	ESTs	6.6
20	409097	AA677927	Hs.144269	ESTs	6.6
	441832	A1018249	Hs.128062	ESTs	6.6
	457285	A033658	Hs.228780	"ESTs, Highly similar to AF195957 1 A-type potassium cha	6.6
	405504			predicted exon	6.6
	414608	BE387771		"gbr001283251F1 NH_LMGC_44 Homo sapiens cDNA clone	6.6
25	452956	AW003578	Hs.231672	ESTs	6.6
	410743	AA069474	Hs.272153	ESTs	6.6
	404599			predicted exon	6.6
	423576	C18663	Hs.163443	"Homo sapiens cDNA FLJ11576 fs, clone HEMBA100354	6.6
30	443027	A1027847	Hs.253550	ESTs	6.6
	456663	AW654444	Hs.260776	"Homo sapiens cDNA FLJ13684 fs, clone PLACE2000021	6.6
	431277	AA501406	Hs.249565	ESTs	6.6
	445322	BE294357		"gbr001128287F1 NH_LMGC_37 Homo sapiens cDNA clone	6.6
	459170	AW055518		"gbrRC-BT051-210159-098 BT051 Homo sapiens cDNA, m	6.6
35	437676	AA770151	Hs.126424	ESTs	6.6
	406752	A126598	Hs.217493	anexin A2	6.6
	401245			predicted exon	6.6
	449102	AW168067	Hs.252956	ESTs	6.5
	446989	AW001858	Hs.16740	hypothetical protein FLJ11036	6.5
40	421160	AL080215	Hs.102031	"Homo sapiens mRNA cDNA DKFZp566J0323 (from clone	6.5
	456831	H71739	Hs.200227	ESTs	6.5
	402914	AW450209		gbrULH-B193-alc-g-09-0 Ula1 NCL_CGAP_Sub5 Homo sa	6.5
	411018	AW813428		"gbrMFS-ST0192-010200-210-c05 ST0192 Homo sapiens c	6.5
	436562	H71537	Hs.169756	"component component 1, s subcomponent"	6.5
	457620	AA502711		"gbrgbrCH06.s1 NCL_CGAP_Pr2 Homo sapiens cDNA clone	6.5
45	438647	AA813118	Hs.163220	ESTs	6.5
	438570	T7925	Hs.269166	ESTs	6.5
	419273	DE271130	Hs.293490	ESTs	6.5
	443745	AB039670	Hs.5728	ALEX1 protein	6.5
50	431029	BE335725	Hs.248571	"Homo sapiens PAC clone RFS-1163J12 from 7q21.2-q31.1	6.5
	456955	AW601519	Hs.282284	ESTs	6.5
	410696	AW812068		"gbrRC4-ST0173-151099-032-a07 ST0173 Homo sapiens c	6.4
	417135	AA422067	Hs.50547	ESTs	6.4
	416441	BE407197		"gbr001201552P1 NH_LMGC_21 Homo sapiens cDNA clone	6.4
55	413702	BE170313		"gbrCVA-HT0536-040306-153-g02 HT0536 Homo sapiens	6.4
	422663	AB7352		"gbrRC-BT147-120659-044 BT147 Homo sapiens cDNA, m	6.4
	408556	AW001668	Hs.295306	"ESTs, Highly similar to unnamed protein product [Hsapien	6.4
	406349			predicted exon	6.4
	425420	BE538911	Hs.234545	"ESTs, Weakly similar to AF165135 1 novel rodent pigmen	6.4
60	459430	AW662086		gbr02811.s1 Soares_JFL1_T_GRC.S1 Homo sapiens cDNA	6.4
	425733	F13287	Hs.155088	"Homo sapiens clone 23676 mRNA sequence	6.4
	458678	A306162	Hs.170938	"ESTs, Weakly similar to KIAA0075 protein [Hsapiens]"	6.4
	429695	AA835714	Hs.293556	ESTs	6.4
	426872	AW140446	Hs.112011	"ESTs, Weakly similar to unknown [Hsapiens]"	6.4
65	437152	AL050027		gbrHomo sapiens mRNA; cDNA DKFZp566C0324 (from c	6.4
	440517	AW139632	Hs.132446	ESTs	6.4
	450877	AW199808	Hs.29178	ESTs	6.4
	410654	NM_006033	Hs.65370	"lipase, endothelial"	6.4
	405763			predicted exon	6.4
70	418709	AA227394		gbrzr17c10.1 Stratagene NT2 neuronal precursor 93/2320 H	6.4
	428884	AA431792	Hs.44784	ESTs	6.4
	448516	AW898595		"gbrRC1-NN0073-260400-011-g09 NN0073 Homo sapiens	6.4
	401983			predicted exon	6.3
	422365	AQ055337	Hs.115521	"REV3 (yeast homolog)-like, catalytic subunit of DNA pol	6.3
75	425612	BE004257		"gbrCMA-EN0103-180300-296-c04 EN0103 Homo sapiens	6.3
	401521			predicted exon	6.3
	430290	AQ734110	Hs.136355	ESTs	6.3
	411631	AK000342	Hs.775946	"Homo sapiens mRNA; cDNA DKFZp751M0223 (from clone	6.3
	437539	AW258600	Hs.141840	"ESTs, Weakly similar to S55051 interferon receptor JFNA	6.3
	451842	AL820539	Hs.267087	"ESTs, Moderately similar to ALLU4_HUMAN ALLU SUBF	6.3
80	405610			predicted exon	6.3
	443747	AV648352		"gbrAV648352 GLC Homo sapiens cDNA clone G1.CAME	6.3
	427287	NM_014903	Hs.174188	KIAA0038 protein	6.3
	413521	BE145814		"gbrMRQ-HT0208-101220-202-c04 HT0208 Homo sapiens	6.3
	428090	AW820278	Hs.99066	ESTs	6.3

WO 02/102235

PCT/US02/19297

	451488	H22999	Hs.208846	ESTs	6.3
	455173	BE068891		"g3c24-BT0401-201299-054-b01-BT0401 Homo sapiens	6.3
	452161	RA3077	Hs.221747	ESTs	6.3
5	428647	AA830050	Hs.124344	ESTs	6.3
	449063	A1246275	Hs.149196	ESTs	6.3
	456671	AB011142	Hs.114293	KIA06270 gene product	6.3
	401508			predicted exon	6.3
	412677	AW029608	Hs.17384	ESTs	6.3
	441720	A1346487	Hs.28739	ESTs	6.3
10	418051	AW192635	Hs.19479	ESTs	6.3
	438014	NT1183	Hs.121906	"Homo sapiens cDNA FLJ11971 fls, clone HEMBB100120	6.3
	432101	A1918950	Hs.11082	"Homo sapiens cDNA FLJ14290 fls, clone PLACE1006795	6.3
	421032	AW293133	Hs.101340	ESTs	6.3
	436532	AA721522		"ghm54h12r1 NCL_CGAP_Ew1 Homo sapiens cDNA clo	6.3
	451316	AW502700	Hs.293147	"ghm54h12r1 NCL_CGAP_Ew1 Homo sapiens cDNA clo	6.3
15	413470	N29334		gbyr5d31.1s1 Soares melanocyte 2NRHM Homo sapiens c	6.3
	402425			predicted exon	6.3
	455993	BE179095		"g3c24-BT0401-201299-054-b01-BT0401 Homo sapiens	6.3
	400160			predicted exon	6.3
20	413795	AL049178	Hs.142003	ESTs	6.2
	405071			predicted exon	6.2
	403741			predicted exon	6.2
	432489	A1804855	Hs.207830	ESTs	6.2
	402296			predicted exon	6.2
25	448931	AW022152	Hs.200197	ESTs	6.2
	444788	AB71122	Hs.202821	ESTs	6.2
	404972			predicted exon	6.2
	404227			predicted exon	6.2
30	433954	A1836561	Hs.112740	ESTs	6.2
	446807	A1571940	Hs.7549	ESTs	6.2
	404340			predicted exon	6.2
	424632	AB014523	Hs.151406	KIA0623 gene product	6.2
	446547	H83543	Hs.117853	ESTs	6.2
35	408445	Y01383	Hs.203987	metallothionein 1A (functional)	6.2
	433663	AF081311	Hs.229535	CATX-15 protein	6.2
	407806	AW082279	Hs.244106	ESTs	6.2
	418342	BE002723	Hs.293504	"ESTs, Moderately similar to ALU1_HUMAN ALU SURF	6.2
	438007	AA113508	Hs.158975	ribosomal protein L14	6.2
	410536	N39533		gbyr2g04s1 Soares fetal liver spleen 1NFLS Homo sapie	6.2
40	448005	AW207437	Hs.170378	ESTs	6.2
	414083	AL121282	Hs.257786	ESTs	6.2
	405362			predicted exon	6.2
	418102	AW248508	Hs.278727	"Homo sapiens cDNA FLJ14035 fls, clone HEMBA100463	6.2
	457868	AW575133		"g3c24-BT0401-201299-054-b01-BT0401 Homo sapiens	6.2
45	407385	AF005082		"g3c24-BT0401-201299-054-b01-BT0401 Homo sapiens	6.2
	443603	BE302601	Hs.134289	"ESTs, Weakly similar to KIAA1063 protein [H sapiens]	6.2
	430651	AA464611	Hs.52515	transducin (beta)-like 2	6.1
	434569	A1311295	Hs.58008	ESTs	6.1
	430481	AA479678	Hs.203269	"ESTs, Moderately similar to ALU1_HUMAN ALU SURF	6.1
50	402859			predicted exon	6.1
	401280			predicted exon	6.1
	406344			predicted exon	6.1
	428446	A1024600	Hs.58612	ESTs	6.1
	412248	A160873	Hs.69233	"ESTs, Weakly similar to KIAA1064 protein [H sapiens]	6.1
55	404240	A327247	Hs.287369	interleukin 22	6.1
	455962	BE068387		"g3c24-BT0401-201299-054-b01-BT0401 Homo sapiens	6.1
	428613	AB037749	Hs.186928	KIAA1326 protein	6.1
	432687	AW450630	Hs.133651	ESTs	6.1
	433405	AW157566	Hs.156952	ESTs	6.1
60	416795	AA497778	Hs.168553	"ESTs, Highly similar to AF227948.1 HBV pX associated p	6.1
	438706	W31254	Hs.7045	GLOD4 protein	6.1
	450789	AA057418	Hs.33654	ESTs	6.1
	427174	AA398848	Hs.97541	ESTs	6.1
	425369	AW974489	Hs.152183	ESTs	6.1
65	416675	H73802	Hs.35361	ESTs	6.1
	432749	NM_014438	Hs.278909	Interleukin-1 Superfamily a	6.1
	401809			predicted exon	6.1
	403041			predicted exon	6.0
	426523	AW833259		"g3c24-BT0401-201299-054-b01-BT0401 Homo sapiens c	6.0
70	416515	N91716	Hs.154140	ESTs	6.0
	452591	BE173164	Hs.1516	Insulin-like growth factor-binding protein 4	6.0
	437146	AA730977		"g3c24-BT0401-201299-054-b01-BT0401 Homo sapiens cDNA clo	6.0
	450004	A1174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp554D1164 (from clone	6.0
	402529			predicted exon	6.0
75	450706	NM_003540	Hs.247816	"H4 histone family, member C"	6.0
	459195	AB08287		"g3c24-BT0401-201299-054-b01-BT0401 Homo sapiens cDNA, m	6.0
	452158	AB691120	Hs.61198	ESTs	6.0
	411237	AW833676		"g3c24-BT0401-201299-054-b01-BT0401 Homo sapiens	6.0
	400441	M15530	Hs.99879	B-cell growth factor 1 (Tb2f)	6.0
80	439398	AA284267	Hs.221504	ESTs	6.0
	440862	H39048	Hs.127432	ESTs	6.0
	415451	H19415	Hs.268720	"ESTs, Moderately similar to ALU1_HUMAN ALU SURF	6.0
	469507	AA031956		gbyr2g04s1 Soares pregnant_fetus_JBHFU Homo sapi	6.0
	469672	H54381		gbyr2g04s1 Soares fetal liver spleen 1NFLS Homo sapie	6.0

WO 02/102235

PCT/US02/19297

	409654	AW512770	Ha.266457	ESTs	6.0
	443468	A073495	Ha.133912	"ESTs, Weakly similar to methyl-CpG binding domain-cont	6.0
	430825	A1734186	Ha.185105	ESTs	6.0
5	454465	AA964138	Ha.279895	"Homo sapiens mRNA for KIAA1578 protein, partial cds"	6.0
	455505	AA278277	Ha.194212	ESTs	6.0
	445226	AJ403107	Ha.148590	"ESTs, Weakly similar to AF209846 [BM-004 [H.sapiens]	6.0
	457727	AW974687	Ha.146180	"gbEST1386776 MAGE resequences, MAGM Homo sapien	6.0
	442440	BE464435	Ha.146180	"ESTs, Weakly similar to non-receptor protein tyrosine kina	5.9
	455110	BE154505		"gbtMAD-BN0343-281299-003-e08 HT0343 Homo sapiens	5.9
10	422790			predicted exon	5.9
	409892	BE005839	Ha.179982	"gbtRC2-BN0120-250400-012-003 BN0120 Homo sapiens	5.9
	427635	BE397988	Ha.179982	tumor protein p53-binding protein	5.9
	408948	AW296713	Ha.221441	ESTs	5.9
15	420246			predicted exon	5.9
	415438	R89238	Ha.34262	ESTs	5.9
	403063			predicted exon	5.9
	402481			predicted exon	5.9
	409867	AW502161		gbtUH-HF-BR03p-sig-a-12-0-ULR1 NH_MGC_52 Homo sap	5.9
20	422352	U79324	Ha.57205	lunghigh interceding protein 1	5.9
	421375	AA485200	Ha.100595	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	5.9
	437630	AJ252782	Ha.153029	ESTs	5.9
	443500	AV545388	Ha.137071	ESTs	5.9
	448995	AK513278	Ha.5562	"gamma nucleotide binding protein (G protein), beta polyp	5.9
25	438214	H00076	Ha.26320	TRABID protein	5.9
	428046	AW812795	Ha.155381	"ESTs, Moderately similar to U30022 hypothetical protein [H	5.9
	431941	AK000106	Ha.272227	"Homo sapiens cDNA FLJ20099-05, clone COL04544"	5.9
	403336			predicted exon	5.9
	430331	AF075079		gbt-Homo sapiens full length insert cDNA YC60A08	5.9
30	430332	AW536136	Ha.99610	ESTs	5.9
	423457	F08206	Ha.155605	paired mesoderm homeo box 1	5.9
	422158	L10343	Ha.112341	"protease inhibitor 3, skin-derived [SKALP]"	5.9
	406592			predicted exon	5.9
	416835	AW740655		"gbtCVA-ET0534-281299-053-c35 BT0534 Homo sapiens	5.8
35	426399	AA452244	Ha.16727	ESTs	5.8
	406590	AW238162	Ha.253873	ESTs	5.8
	422158	AA588694	Ha.112408	S100 calcium-binding protein 4 [psoralein 1]	5.8
	417421	AL136201	Ha.82120	"nuclear receptor subfamily 4, group A, member 2"	5.8
	401129			predicted exon	5.8
	434745	AW974445	Ha.185155	"ESTs, Weakly similar to HuEMAP [H.sapiens]"	5.8
40	402620			predicted exon	5.8
	435165	AW753260	Ha.49753	"Homo sapiens mRNA for KIAA1561 protein, partial cds"	5.8
	419819	A1198719	Ha.175376	ESTs	5.8
	452642	AW812286		"gbtRC0-ST0174-191099-031-a07 ST0174 Homo sapiens c	5.8
45	427166	AA431576	Ha.155658	ESTs	5.8
	416168	H23687		gbt-mt2612.r1 Soares adult brain N26tHE659Y Homo sapie	5.8
	431487	NT1631	Ha.256398	Homo sapiens mRNA; cDNA DNFPz43486228 (from don	5.8
	421558	AS011125	Ha.105740	KIAA0653 protein	5.8
	458055	AW979121	Ha.131375	"ESTs, Weakly similar to ALUB_HUMAN III ALU CLAS	5.8
50	416345	AJ001695	Ha.241407	"serine (or cysteine) proteinase inhibitor, clade B (ovalbumi	5.8
	425544	AA462328		gbtST011511 NCL_CGAP_Prd Homo sapiens cDNA clone	5.8
	433544	A7783211	Ha.165372	"ESTs, Moderately similar to ALU1_HUMAN ALU SUBF	5.8
	442007	AA301116	Ha.142838	"Homo sapiens cDNA: FLJ22444 fn, clone H301343"	5.8
	443422	R10288	Ha.301529	ESTs	5.8
55	434311	BE543489	Ha.265263	"Homo sapiens cDNA FLJ14115 fn, clone MAMMA19017	5.8
	424985	AL077312	Ha.130965	"solute carrier family 7 (anionic amino acid transporter, p-	5.8
	447744	AA906622	Ha.200938	ESTs	5.8
	413101	BE055215		"gbtRC1-BT0314-310300-015-01 BT0314 Homo sapiens c	5.7
	446687	W40362	Ha.149297	ESTs	5.7
60	414389	AA031535		gbt05504s.1 NCL_CGAP_Lu5 Homo sapiens cDNA clone	5.7
	414428	BE298906	Ha.162625	VAMP (vesicle-associated membrane protein)-associated pr	5.7
	431211	M86849	Ha.5566	"gap junction protein, beta 2, 26kD [connexin 26]"	5.7
	411541	W03940	Ha.171285	gbt-a2b202.r1 Soares fetal liver spleen TNFLS Homo sapien	5.7
	448612	AA596363	Ha.171285	ESTs	5.7
65	411518	AA234223	Ha.139204	ESTs	5.7
	406322			predicted exon	5.7
	454690	AW854639		"gbtMR1-CT0258-140100-203-d10 CT0258 Homo sapiens	5.7
	450313	AJ038989	Ha.24809	hypothetical protein FLJ10626	5.7
	412292	AA178233	Ha.42390	hypothetical protein FLJ10626	5.7
70	448309	AW558623	Ha.224189	nasopharyngeal carcinoma susceptibility protein	5.7
	408418	AW963897	Ha.44743	KIAA1435 protein	5.7
	416100	H18700	Ha.266799	ESTs	5.7
	432845	AA768678	Ha.504068	ESTs	5.7
	443345	AB052908	Ha.164482	"ESTs, Weakly similar to contains similarity to TPR domain	5.7
75	418407	AL044818	Ha.84928	"nuclear transcription factor Y, beta"	5.7
	434557	AW855486	Ha.271806	"ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	5.7
	431688	AA513906		"gbtmg7c08.s1 NCL_CGAP_Lip2 Homo sapiens cDNA do	5.7
	437641	AA811452	Ha.291911	ESTs	5.7
	409319	AW752736	Ha.33565	ESTs	5.7
80	403967	AF030107	Ha.17165	regulator of G-protein signalling 13	5.7
	445189	AB36450	Ha.147482	ESTs	5.7
	414418	HB2943	Ha.154186	ESTs	5.7
	416663	BE320588	Ha.141454	ESTs	5.7
	445075	AW451457	Ha.278179	ESTs	5.7
	428068	AW016437	Ha.233462	ESTs	5.7

WO 02/102235

PCT/US02/19297

5	438425	AW292922	Hs.293170	ESTs	5.7
	415532	R14780	Hs.12825	ESTs	5.7
	441442	AL043282	Hs.131824	ESTs	5.7
	443380	AF92478	Hs.135377	ESTs	5.7
	446527	Y52694	Hs.83286	ESTs	5.7
10	414375	DE393856	Hs.66915	"ESTs, Weakly similar to 16.7Kd protein [Hsapiesm]"	5.7
	457960	AA771881	Hs.298149	ESTs	5.6
	453293	AA382267	Hs.10553	ESTs	5.6
	452503	AB000609	Hs.29735	TNF receptor-associated factor 5	5.6
	405227			predicted exon	5.6
15	442257	AW503831	gb U18F-0ND-0b-b-05-Q-ULr1 NIH_MGC_50 Homo sap	5.6	
	403403			predicted exon	5.6
	454377	AA076811	gb 7803C12 Chromosome 7 Fetal Brain cDNA Library Hom	5.6	
	438656	HBS310	ESTs, Weakly similar to NC022 [Hsapiesm]"	5.6	
	419536	AI792798	"gb u18f05.y5 NC1_CGAP_K65 Homo sapiens cDNA clo	5.6	
20	437267	AW511443	Hs.258110	ESTs	5.6
	430563	AA461239	Hs.176361	ESTs	5.6
	444835	AI198964	Hs.158479	ESTs	5.6
	444902	AJ132029	Hs.12114	varin 1	5.6
	451800	AW977435	Hs.31890	ESTs	5.6
25	405465			predicted exon	5.6
	403891			predicted exon	5.6
	425557	A1894300	Hs.46730	ESTs	5.6
	432162	AA584062	Hs.272798	hypothetical protein FLJ20413	5.6
	450162	AI138635	Hs.22966	ESTs	5.6
30	410053	AW579707	Hs.53332	ESTs	5.6
	421285	NM_000102	Hs.1353	"cytochrome P450, subfamily XVII (steroid 17-alpha-hydro	5.6
	425264	AA352923	Hs.20369	ESTs, Weakly similar to gonadotropin inducible transcript	5.6
	416844	M52982	Hs.1200	archidoxate 12-lyopogenase	5.6
	420616	A1682722	Hs.120845	ESTs	5.6
35	423528	AB011137	Hs.129740	KIA00595 gene product	5.6
	403389			predicted exon	5.6
	414373	AW162907	Hs.75959	proline-rich protein with nuclear targeting signal	5.6
	403687			predicted exon	5.6
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	5.5
40	432601	BE546532	Hs.287329	Fas binding protein 1	5.5
	403691			predicted exon	5.5
	405545	BE256182	gb 60117732.F1 NIH_MGC_17 Homo sapiens cDNA clone	5.5	
	435990	AJ015862	Hs.131793	ESTs	5.5
	444409	AF192140	Hs.45265	ESTs	5.5
45	425478	AA626822	gb 20005.a1 Soares_fetal_liver_spleen_INFLS_S1 Homo	5.5	
	430981	AI348406	Hs.124675	ESTs, Weakly similar to unnamed protein product [Hsapie	5.5
	433644	AW342028	Hs.256112	ESTs	5.5
	441541	AA538663	Hs.159828	ESTs	5.5
	400709			predicted exon	5.5
50	407615	AW753085	gb PM1-CT0247-151299-005-s03 CT0247 Homo sapiens	5.5	
	424153	AA461737	Hs.141496	MAGE4e2	5.5
	452465	AA610211	Hs.34244	ESTs	5.5
	408030			predicted exon	5.5
	431671	AA461379	gb sa6905.f1 NC1_CGAP_GC01 Homo sapiens cDNA cl	5.5	
55	418086	AA211791	Hs.263666	"Homo sapiens cDNA FLJ13415 fls, clone PLACE1001799	5.5
	453034	BE246010	Hs.184109	abnormal protein L37a	5.5
	412563	Z45794	Hs.238802	ESTs	5.5
	425351	AJ062324	Hs.15924	cAMP responsive element modulator	5.5
	408146			predicted exon	5.5
60	416533	BE244053	Hs.75362	retinoblastoma-like 2 (p130)	5.5
	458378	AJ040535	Hs.150524	ESTs	5.5
	401213			predicted exon	5.5
	405904			predicted exon	5.5
	446132	Z44811	gb HSIC29031 normalized infant brain cDNA Homo sapie	5.5	
65	406138			predicted exon	5.5
	442238	AW135374	Hs.270949	ESTs	5.5
	415852	AF283776	Hs.80325	Homo sapiens mRNA: cDNA DKFZp586C1723 (from clone	5.5
	448691	AA481119	Hs.283568	hypothetical protein PRO1655	5.5
	452242	R50966	Hs.59503	"ESTs, Weakly similar to AF157318 1 AD-D17 protein [Hs	5.5
70	456994	AA383623	Hs.233616	ESTs	5.5
	440913	AJ267491	Hs.163953	ESTs	5.5
	435380	A4970001	Hs.192221	ESTs	5.5
	450375	AA009647	Hs.8859	a disintegrin and metalloproteinase domain 12 (meltrin alph	5.5
	414035	Y00630	Hs.75716	"serine (or cysteine) proteinase inhibitor, clade B (ovalbumi	5.4
75	459084	HD1699	Hs.27289	CGI-125 protein	5.4
	405867			predicted exon	5.4
	414053	BE544667	gb 60107687.F1 NIH_MGC_12 Homo sapiens cDNA clone	5.4	
	447306	AJ373163	Hs.170333	ESTs	5.4
	413063	BE064528	gb RC4-ET0311-250200-014-h06 ET0311 Homo sapiens	5.4	
80	404828			predicted exon	5.4
	402543			predicted exon	5.4
	421988	AW460481	Hs.161333	ESTs	5.4
	413404	BE503463	Hs.297431	ESTs	5.4
	459043	AJ806444	Hs.208113	"ESTs, Weakly similar to N-WASP [Hsapiesm]"	5.4
	404410			predicted exon	5.4
	430264	AA470519	gb nc711f0.s1 NC1_CGAP_Fr1 Homo sapiens cDNA clone	5.4	
	431499	NM_001514	Hs.258561	general transcription factor IIB	5.4
	412566	AW962574		"gb-EST374647 MAGE resequences, MAGG Homo sapien	5.4

WO 02/102235

PCT/US02/19297

454228	BE176420	Hs.8177	ESTs	5.4
456163	AA684304	Hs.131163	ESTs	5.4
460206	AW172662	Hs.149478	ESTs	5.4
465276	AW977806		"gb:EST389810 MAGE resequences, MAGO Homo sapiens	5.4
415679	AA108232	Hs.222068	ESTs	5.4
422200	AA322073	Hs.289363	ESTs	5.4
440052	AE33744	Hs.195648	ESTs	5.4
424717	H03764	Hs.152213	"wilegless-type MMTV integration site family, member 5A"	5.4
420111	AA256552		gb:z21k11.1 NCL_CGAP_G031 Homo sapiens cDNA cdo	5.4
432140	AA000404	Hs.272658	hypothetical protein FLJ23037	5.4
414904	AA157881	Hs.143055	ESTs	5.4
409479	BE163800	Hs.136912	ESTs	5.4
404727			predicted exon	5.4
440011	AG23778	Hs.145606	ESTs	5.4
450083	UA6522	Hs.77252	"Eggle histidine triad gene	5.4
424834	AQ001432	Hs.153408	"Homo sapiens cDNA FLJ10570 fls, clone NT2RP2003117	5.4
426071	NM_013989	Hs.154424	"Melodine, iodothyronine, type II"	5.4
420005	N32049		gb:yg5g08.s1 Soares_placenta_8w/weeks_zh18P809W	5.4
415902	FI2520	Hs.165576	ESTs	5.4
432839	AA679465	Hs.287332	ESTs	5.4
416879	H96859	Hs.42599	ESTs	5.4
456086	BE177320	Hs.150148	"Homo sapiens cDNA: FLJ23082 fls, clone LNG06451"	5.4
423175	W27895	Hs.18563	ESTs	5.4
424555	AA464840		gb:z43h11.1 Soares_total_fetus_Mb2HF8_9w Homo sapie	5.3
452281	T33500	Hs.26752	"Homo sapiens cDNA FLJ11041 fls, clone PLACE1004405	5.3
424323	AA338791	Hs.140763	nascent polypeptide-associated complex alpha polypeptide	5.3
425701	AI98103	Hs.209461	"Homo sapiens cDNA FLJ12836 fls, clone NT2RP2003206	5.3
447545	AW897321	Hs.195959	ESTs	5.3
402974			predicted exon	5.3
436607	AW661783	Hs.211061	ESTs	5.3
428873	AI701009	Hs.58908	ESTs	5.3
406454			predicted exon	5.3
431827	AA523600	Hs.191727	ESTs	5.3
442708	AL046534	Hs.48458	"ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	5.3
424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (RDC)	5.3
435038	AF174394	Hs.177461	"Homo sapiens apoptotic-related protein PCAR mRNA, par	5.3
421284	UC245	Hs.103128	"cholinegic receptor, nicotinic, alpha polypeptide 9"	5.3
436711	AF226067	Hs.58553	CTP synthase II	5.3
405292			predicted exon	5.3
410123	T16581	Hs.21963	ESTs	5.3
435435	T85473	Hs.192328	ESTs	5.3
417071	N58820	Hs.276133	ESTs	5.3
438958	H50167	Hs.33113	ESTs	5.3
457405	AA504820		gb:ab03at1.0.1 Stratagene fetal retina 937202 Homo sapiens	5.3
413542	BE114837		"gb:PMH-IT0345-121199-001-030 HT0345 Homo sapiens	5.3
433868	AA612260		gb:ncp06.s1 NCL_CGAP_Co10 Homo sapiens cDNA cdo	5.3
444451	R63734	Hs.25978	ESTs	5.3
427088	AA398085	Hs.142390	ESTs	5.3
451307	AW293207	Hs.211516	ESTs	5.3
403831			predicted exon	5.3
402892			predicted exon	5.3
433420	AI674093	Hs.293961	ESTs	5.3
456759	BE080409		"gb:OV1-BT0630-280200-086-005 BT0630 Homo sapiens	5.3
411379	AB81344	Hs.12654	"ESTs, Weakly similar to Nucleosome Assembly Protein 1-	5.3
428463	AB90839	Hs.184592	KIA0244 gene product	5.3
429208	AA447990	Hs.190478	ESTs	5.3
447572	AE31546	Hs.159732	ESTs	5.3
434895	AW022054	Hs.136591	ESTs	5.3
417616	R07728	Hs.268606	ESTs	5.3
411805	AAW64183		gb:PM9-SNM0014-260400-002-402 SNM014 Homo sapiens	5.3
419000	T79855	Hs.288592	ESTs	5.3
413468	BE144017	Hs.164593	"transcription elongation factor B (SII), polypeptide 1 (T9	5.3
403976			predicted exon	5.3
407453	AJ132067		gb:PMH-IT0345-121199-001-030 HT0345 Homo sapiens	5.3
430757	AI458623		gb:ncp06.s1 NCL_CGAP_Co10 Homo sapiens cDNA cdo	5.3
417793	AA405434	Hs.82575	small nuclear abundant protein polypeptide B"	5.2
401617	AG011094	Hs.129592	KIA0252 protein	5.2
457122	AG026167	Hs.33128	"ESTs, Weakly similar to ZNF1_HUMAN ZINC FINGER P	5.2
410705	AT324404	Hs.65846	ESTs	5.2
435607	A033299	Hs.113614	ESTs	5.2
426398	AI243068	Hs.96565	ESTs	5.2
401088			predicted exon	5.2
414501	N43691	Hs.171584	ESTs	5.2
419083	AA79563	Hs.58613	"Homo sapiens cDNA FLJ12292 fls, clone MAMMA10018	5.2
421107	AA283322	Hs.55606	"ESTs, Weakly similar to ZNF1_HUMAN ZINC FINGER P	5.2
411489	AA584340		"gb:IL3-CT0214-150200-075-F03 CT0214 Homo sapiens c	5.2
415246	X14167	Hs.85768	"gamma-aminobutyric acid (GABA) A receptor, beta 1"	5.2
420082	AAW514083	Hs.190125	ESTs	5.2
426088	NM_010112	Hs.195241	polycystic kidney disease 2-like 1	5.2
451686	AA068246	Hs.110293	ESTs	5.2
453867	AA925353	Hs.108195	NSP287 protein	5.2
419595	H96373	Hs.18973	"ESTs, Highly similar to h3383316.3 [Hsapiens]"	5.2
426650	AA382814		"gb:EST196097 Testis 1 Homo sapiens cDNA 5' end, mRNA	5.2
424115	AA325497	Hs.293965	ESTs	5.2

WO 02/102235

PCT/US02/19297

	405576		predicted exon	5.2
	409584	AA076010	gbczm012a1 Stratagene ovarian cancer (937219) Homo sa	5.2
	454423	AW003985	Hs.179662 nucleosome assembly protein 1-like 1	5.2
	417173	U61397	Hs.81424 ubiquitin-like 1 (ubiquitin)	5.2
	409155	IB1078	Hs.263001 ESTs	5.2
	432267	AK004872	Hs.274227 "Homo sapiens cDNA FLJ100010 fls, clone HEMBA100030	5.2
	459024	AW020799	Hs.179825 KAN binding protein 2-like 1	5.2
	404088		predicted exon	5.2
	403825		predicted exon	5.2
10	445882	A3948717	Hs.226155 "ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIATE	5.2
	448257	AW772070	Hs.253145 ESTs	5.2
	410500	R09442	gby20609.1 Soares fetal liver spleen INFLS Homo sapien	5.2
	456084	AA153659	Hs.79708 ESTs	5.2
	410523	BE143630	gbcMR0-IT0154-151299-012-003-110164 Homo sapiens	5.2
15	434623	AK021633	Hs.4014 KAP45946 protein; Hunting interacting protein H	5.2
	454484	AW795196	Hs.218857 ring finger protein 14	5.2
	402131		predicted exon	5.2
	438913	AI380429	Hs.172445 ESTs	5.2
	402626		predicted exon	5.1
20	415973	R24707	Hs.260201 ESTs	5.1
	455640	BE064059	gbc:QV3-BT0296-010300-111-004 BT0296 Homo sapiens	5.1
	442780	A016803	Hs.131096 ESTs	5.1
	404638		predicted exon	5.1
25	431117	AF003322	Hs.250500 delta (Drosophila)-like 1	5.1
	428819	AL135623	Hs.193914 KIA00575 gene product	5.1
	439519	AA837118	Hs.116366 ESTs	5.1
	427335	AA448542	Hs.259677 C antigen 7B	5.1
	415440	AA180467	Hs.143556 ESTs	5.1
	440876	AW613524	Hs.279570 ESTs	5.1
30	414584	BE400565	"gbc01031836F1 NIH_MGC_21 Homo sapiens cDNA clone	5.1
	443175	N57883	gbyR6002s1 Soares fetal liver spleen INFLS Homo sapio	5.1
	403988	AB02228	Hs.49378 hypophthallic acid FLJ20644	5.1
	416554	AW963633	"gbcEST380439 MAGE sequences, MAGI Homo sapiens	5.1
	440559	AW629054	Hs.129976 "ESTs, Weakly similar to metalloproteinase/disintegrin/cyste	5.1
35	421236	AI287622	Hs.151956 ESTs	5.1
	416258	N46661	Hs.275131 ESTs	5.1
	405882		predicted exon	5.1
	406589		predicted exon	5.1
40	412458	AW953229	Hs.169142 ESTs	5.1
	435693	A033134	Hs.119887 ESTs	5.1
	449182	AW292381	Hs.224150 ESTs	5.1
	403963		predicted exon	5.1
	440830	A1733112	Hs.176101 ESTs	5.1
	415412	F08049	Hs.52132 ESTs	5.1
45	442832	AW009560	Hs.253659 ESTs	5.1
	443359	AB081726	Hs.147753 ESTs	5.1
	412068	AW69496	Hs.106932 ESTs	5.1
	428785	A015953	Hs.125265 ESTs	5.1
	430163	X06610	Hs.234748 "embryo alpha, lung-specific"	5.1
50	455441	AA941864	"gbc:QV0-ET0001-006000-228-009 ET0001 Homo sapiens c	5.1
	403004	AF005082	Hs.113281 "Homo sapiens skin-specific protein (p-33) mRNA, partial	5.1
	403944		predicted exon	5.1
	457069	BE159191	Hs.114316 "ESTs, Weakly similar to ORF1 [H.sapiens]"	5.1
	414125	BE283167	"gbc:01116804F1 NIH_MGC_16 Homo sapiens cDNA clone	5.1
55	448566	AW021319	Hs.194574 ESTs	5.1
	457946	AA98640	Hs.159354 ESTs	5.1
	438240	N92638	Hs.124004 ESTs	5.1
	404070		predicted exon	5.1
	422709		predicted exon	5.1
60	416425	BE077308	gbc:RCT-BT0506-060200-012a-12 BT0605 Homo sapiens	5.0
	407173	T64349	gbyc10408s1 Stratagene lung (937210) Homo sapiens cDN	5.0
	452502	A304298	gbc:PM-BT0405-220199-280_1 BT0406 Homo sapiens cDNA	5.0
	446657	A3338151	Hs.260702 "gbc:PM-BT0405-220199-280_1 BT0406 Homo sapiens cDNA	5.0
	459124	AW001478	Hs.299176 ESTs	5.0
65	409940	BE548143	"gbc:01070310F1 NIH_MGC_12 Homo sapiens cDNA clone	5.0
	413547	AW271273	Hs.23767 "Homo sapiens cDNA FLJ12666 fls, clone NT2HMA00225	5.0
	447452	BE161626	Hs.102480 ESTs	5.0
	414327	BE401445	Hs.185254 "ESTs, Moderately similar to NAC-1 protein [R.novaeigios]"	5.0
	416155	A1807264	Hs.205442 "ESTs, Weakly similar to AF117810 1 inner centromere pro	5.0
70	409081	AW451597	Hs.167409 ESTs	5.0
	425634	A1091533	Hs.135167 ESTs	5.0
	433388	AW577277	"gbc:MR4-PT0061-150200-001-403 PT0061 Homo sapiens	5.0
	433008	AW102693	Hs.151143 ESTs	5.0
	439721	W92142	Hs.271963 "ESTs, Weakly similar to ALUE_HUMAN ALU SURFAM	5.0
75	441818	AW30451	Hs.7976 KIA00332 protein	5.0
	459804	AL157625	gbc:DRK-Zp76 IL2016_r1 761 (synonym: hamy2) Homo sapi	5.0
	411905	BE285067	"gbc:01013383F1 NIH_MGC_7 Homo sapiens cDNA clone	5.0
	434248	AA628151	Hs.187783 ESTs	5.0
	423967	AW267956	Hs.11641 "Homo sapiens cDNA: FLJ21432 fls, clone COL04219"	5.0
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	433604	AK002185	"gbc:PM-BT0405-220199-280_1 BT0406 Homo sapiens cDNA	5.0
	442952	AW694482	Hs.263315 ESTs	5.0
	454653	AW812227	"gbc:RCT-ST0173-201099-011-g03 ST0173 Homo sapiens c	5.0

PCT/US02/19297

100

WO 02/102235

PCT/US02/19297

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WO 02/102235

PCT/US02/19297

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AW938691 AW938690 AW938689 AW938688 AW938687 AW938686 AW938685 AW938684 AW938683 AW938682 AW938681 AW938680 AW938679 AW938678 AW938677 AW938676 AW938675 AW938674 AW938673 AW938672 AW938671 AW938670 AW938669 AW938668 AW938667 AW938666 AW938665 AW938664 AW938663 AW938662 AW938661 AW938660 AW938659 AW938658 AW938657 AW938656 AW938655 AW938654 AW938653 AW938652 AW938651 AW938650 AW938649 AW938648 AW938647 AW938646 AW938645 AW938644 AW938643 AW938642 AW938641 AW938640 AW938639 AW938638 AW938637 AW938636 AW938635 AW938634 AW938633 AW938632 AW938631 AW938630 AW938629 AW938628 AW938627 AW938626 AW938625 AW938624 AW938623 AW938622 AW938621 AW938620 AW938619 AW938618 AW938617 AW938616 AW938615 AW938614 AW938613 AW938612 AW938611 AW938610 AW938609 AW938608 AW938607 AW938606 AW938605 AW938604 AW938603 AW938602 AW938601 AW938600 AW938599 AW938598 AW938597 AW938596 AW938595 AW938594 AW938593 AW938592 AW938591 AW938590 AW938589 AW938588 AW938587 AW938586 AW938585 AW938584 AW938583 AW938582 AW938581 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AW938469 AW938468 AW938467 AW938466 AW938465 AW938464 AW938463 AW938462 AW938461 AW938460 AW938459 AW938458 AW938457 AW938456 AW938455 AW938454 AW938453 AW938452 AW938451 AW938450 AW938449 AW938448 AW938447 AW938446 AW938445 AW938444 AW938443 AW938442 AW938441 AW938440 AW938439 AW938438 AW938437 AW938436 AW938435 AW938434 AW938433 AW938432 AW938431 AW938430 AW938429 AW938428 AW938427 AW938426 AW938425 AW938424 AW938423 AW938422 AW938421 AW938420 AW938419 AW938418 AW938417 AW938416 AW938415 AW938414 AW938413 AW938412 AW938411 AW938410 AW938409 AW938408 AW938407 AW938406 AW938405 AW938404 AW938403 AW938402 AW938401 AW938400 AW938399 AW938398 AW938397 AW938396 AW938395 AW938394 AW938393 AW938392 AW938391 AW938390 AW938389 AW938388 AW938387 AW938386 AW938385 AW938384 AW938383 AW938382 AW938381 AW938380 AW938379 AW938378 AW938377 AW938376 AW938375 AW938374 AW938373 AW938372 AW938371 AW938370 AW938369 AW938368 AW938367 AW938366 AW938365 AW938364 AW938363 AW938362 AW938361 AW938360 AW938359 AW938358 AW938357 AW938356 AW938355 AW938354 AW938353 AW938352 AW938351 AW938350 AW938349 AW938348 AW938347 AW938346 AW938345 AW938344 AW938343 AW938342 AW938341 AW938340 AW938339 AW938338 AW938337 AW938336 AW938335 AW938334 AW938333 AW938332 AW938331 AW938330 AW938329 AW938328 AW938327 AW938326 AW938325 AW938324 AW938323 AW938322 AW938321 AW938320 AW938319 AW938318 AW938317 AW938316 AW938315 AW938314 AW938313 AW938312 AW938311 AW938310 AW938309 AW938308 AW938307 AW938306 AW938305 AW938304 AW938303 AW938302 AW938301 AW938300 AW938299 AW938298 AW938297 AW938296 AW938295 AW938294 AW938293 AW938292 AW938291 AW938290 AW938289 AW938288 AW938287 AW938286 AW938285 AW938284 AW938283 AW938282 AW938281 AW938280 AW938279 AW938278 AW938277 AW938276 AW938275 AW938274 AW938273 AW938272 AW938271 AW938270 AW938269 AW938268 AW938267 AW938266 AW938265 AW938264 AW938263 AW938262 AW938261 AW938260 AW938259 AW938258 AW938257 AW938256 AW938255 AW938254 AW938253 AW938252 AW938251 AW938250 AW938249 AW938248 AW938247 AW938246 AW938245 AW938244 AW938243 AW938242 AW938241 AW938240 AW938239 AW938238 AW938237 AW938236 AW938235 AW938234 AW938233 AW938232 AW938231 AW938230 AW938229 AW938228 AW938227 AW938226 AW938225 AW938224 AW938223 AW938222 AW938221 AW938220 AW938219 AW938218 AW938217 AW938216 AW938215 AW938214 AW938213 AW938212 AW938211 AW938210 AW938209 AW938208 AW938207 AW938206 AW938205 AW938204 AW938203 AW938202 AW938201 AW938200 AW938199 AW938198 AW938197 AW938196 AW938195 AW938194 AW938193 AW938192 AW938191 AW938190 AW938189 AW938188 AW938187 AW938186 AW938185 AW938184 AW938183 AW938182 AW938181 AW938180 AW938179 AW93817

WO 02/102235

PCT/US02/19297

Play	Ref	Strand	Nt position
	400684	Minus	18398-18573
	400693	Minus	25013-25127
5	400612	Minus	151513-151602
	400613	Plus	32278-32472
	400623	Plus	74185-74335,74653-74827
	400709	Plus	153375-154590
	400749	Plus	9162-9293
	400842	Plus	90452-90573
10	400925	Plus	38163-38391,43900-44086
	400964	Minus	155262-155403
	400965	Plus	19338-20043
	400975	Plus	108473-108847
	400983	Plus	107903-108632
15	401032	Minus	58451-58555
	401050	Minus	78449-78455
	401058	Plus	194659-195179
	401129	Minus	62022-62422,62326-62451,62543-62710,63072-63167
20	401200	Plus	111556-111805,114791-114916,115419-115583,116351-116445,116847-116907,122653-123057,124962-125407
	401213	Plus	96243-96380,96485-96619
	401230	Plus	33635-34006,34539-34592,35461-35745,48925-49098,52604-52758
	401245	Minus	60373-60531
	401260	Minus	65008-65355
25	401269	Plus	2229-2251
	401283	Minus	47259-47466
	401457	Plus	52607-52613
	401508	Minus	110779-110983
	401521	Plus	9127-9234
30	401530	Plus	41468-42405
	401575	Minus	75253-75354
	401604	Minus	119335-120185
	401780	Minus	28397-28617,28920-29045,29135-29296,29411-29667,29705-29787,30224-30573
	401781	Minus	83215-83435,83531-83666,83740-83901,84237-84393,84958-85037,85290-86814
	401753	Minus	102345-103033
35	401809	Minus	107545-105298
	401852	Minus	55839-55923,59145-59293
	401881	Minus	154870-148551,153418-153618,154262-154438
	402018	Plus	168725-168839
	402046	Plus	165394-165556,168167-168395
40	402050	Minus	130105-130227
	402071	Plus	85924-86039
	402075	Plus	121907-122635,122604-122911,124019-124161,124455-124610,125672-126078
	402131	Minus	31114-32508,32495-32618
	402203	Minus	6124-6285
45	402222	Plus	3261-3834,3939-4209
	402296	Plus	22587-23723
	402296	Plus	36758-37953
	402421	Minus	46503-46662,46758-46811,46233-46346,48978-49029,90049-90101,102817-102924
50	402425	Minus	60224-50395
	402451	Plus	67891-68991
	402529	Minus	165-917
	402543	Minus	59564-60883
	402576	Minus	1867-2247
	402578	Plus	66350-66495
55	402628	Plus	31753-31955
	402631	Minus	115555-115580
	402639	Minus	20167-22383
	402654	Plus	70318-70846
	402709	Minus	56847-57055
60	402738	Minus	8725-8869
	402745	Minus	75516-76590
	402790	Minus	147744-147861
	402794	Minus	131034-131794
	402800	Plus	43921-44049,40181-46273
65	402829	Minus	95052-95057
	402892	Minus	194384-194645
	402974	Plus	124035-124321
	403041	Plus	70527-71019
70	403065	Minus	71615-71773,73930-74144
	403083	Plus	163701-163351
	403089	Plus	171964-172239
	403093	Plus	177063-177373,177464-177751
	403177	Minus	142560-142726
	403273	Plus	133609-134009
75	403334	Minus	137205-137350
	403350	Minus	135374-135523
	403356	Plus	92639-93036
	403403	Plus	21240-21399
	403525	Plus	152431-152443
80	403598	Minus	85509-85558
	403647	Minus	35849-36204
	403667	Plus	9009-9634
	403891	Minus	86280-86463
	403986	Plus	10464-10907

PCT/US02/19297

	403741	7630532	Minus	2833-3468
	403747	7568395	Minus	20493-20621
	403766	8082636	Minus	73028-73177
5	403831	7424249	Minus	61469-61525
	403891	7331467	Minus	19199-19320
	403944	7711864	Minus	129213-129415
	403963	8568150	Plus	149496-149665
	404070	2596642	Plus	7210-7474,10043-10195
	404088	9095257	Plus	184131-184296
	404097	7770701	Plus	55515-55718
	404176	7596822	Plus	86147-86509
	404210	9628129	Minus	3549-3750,4161-4306,5962-6040,6849-6995
	404340	7633665	Plus	10898-11509
15	404410	7342122	Plus	69632-69716,56177-56273,93384-50488
	404599	8075107	Plus	110443-110733
	404638	9796751	Plus	99439-99526,100035-100161
	404694	8797412	Minus	104257-105215
	404727	8081050	Plus	115534-115747
20	404767	7882827	Plus	23244-23759
	404828	6580415	Minus	26291-27253
	404849	7706865	Plus	144843-144964,149496-150121
	404993	8039447	Plus	650363-65292
	404998	7331420	Minus	17315-17738
25	404992	7382669	Plus	136326-136618
	404972	3213020	Plus	48711-48524
	404992	4662677	Minus	105104-105195,116159-11781
	405071	7700197	Minus	111115-11552
	405138	8576241	Plus	90303-90516
30	405196	7230083	Minus	15757-136651
	405227	8712145	Minus	22590-22802
	405277	8980473	Plus	2471-23572
	405285	9130078	Plus	587448-58903,9800-57170,61478-61560
	405292	3546240	Plus	32227-33442
	405336	6094635	Plus	33207-33563
35	405362	2337962	Minus	105008-106142,105808-106091,140445-140555,142519-142694
	405378	6453761	Plus	21623-321
	405454	7566675	Plus	133670-134063
	405465	7757904	Plus	9385-9073,1242-12367,13364-13606,14065-16438
40	405472	8439781	Plus	105287-105447,108462-103590
	405477	1054740	Plus	124561-1052,124913-125956
	405576	4001382	Plus	84000-5990
	405621	8523811	Plus	59362-60607
	405630	5123990	Plus	55384-56687
	405675	4057387	Plus	70304-70300
45	405708	4105182	Plus	55028-55804
	405771	7810949	Plus	91191-91264,91510-91589
	405783	5738434	Minus	27238-27885
	405793	1405897	Minus	89197-89463
	405800	2791346	Plus	19271-19913
	405810	4983307	Plus	84843-84986
	405848	7651909	Minus	28135-28244
	405861	6146995	Minus	26407-27181
	405957	6768231	Plus	74563-75173
55	405966	6768795	Plus	87311-87374
	405904	7705118	Minus	16375-16584
	405917	7712162	Minus	106828-107213
	405930	8026498	Minus	36028-36498
	405980	8312238	Minus	90123-92407
	406061	6756997	Plus	30592-31552
60	406057	6691254	Minus	20830-21222
	406149	7144791	Plus	44464-45164
	406363	7158901	Plus	69680-69835
	406277	5985030	Minus	4719-6490
65	406322	9212102	Minus	130230-130418
	406349	9256007	Minus	21251-21526
	406504	7711360	Minus	107068-107277
	406544	7711508	Plus	45578-46757
	406569	8224211	Plus	38066-38899
	406592	4567182	Plus	352560-352963

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WO 02/102235

PCT/US02/19297

Phy	Ex. Acn No.	UG ID	Title	PFAM domain	ratio
	423017	AW176761	serine (or cysteine) proteinase inhibitor	serpin	63.6
	431938	AA284771	Ha.115242	SCP	32.0
	425650	NM_001944	Ha.1925	cathepsin	30.0
5	418994	AA296520	Ha.89546	EGF_boln_sushi	24.5
	452947	AW130413	solacin E (endothelial adhesion molec	alpha-amylase	15.8
	418992	R45154	gbs0004.x1 NCL_CGAP_Gas4 Hom	phosphoactiv_recop	15.1
	431725	X65724	Ha.2839	Cys_Lind	12.6
	422330	D30783	Ha.115283	EGF	12.5
10	446745	AW181189	Ha.156400	vwa	10.1
	416319	A1815501	Ha.79107	ig	10.8
	432408	N39127	Ha.78391	ion_transC_Letra	10.6
	405285		predicted exon	A2MA2M_N	10.5
	405536		predicted exon	EGF3d1_recop1_sdl1_recop1_b	9.8
15	403050		predicted exon	hs3	9.5
	446740	A1811695	Ha.192605	RVDK_TPR	9.2
	405547		predicted exon	ABC_tranABC_membrane	8.5
	412333	AW374485	gbsCV3-Q10044-221299-045-509 DT	7tm_1	8.4
	404270		predicted exon	SCP	8.1
	402745		predicted exon	EGF3d1_recop1_b1lyogobulin_1	8.1
20	452755	AW138307	Ha.213436	cystatin	8.0
	412459	A1821539	Ha.97249	disintegrin/Reprolysin	7.9
	416151	T26661	gbsAB55CTR Infant brain, LUNL sera	leminin_CIEGF	7.8
	446832	A0261648	Ha.165547	7tm_3	7.8
25	411009	BE145782	Ha.245213	connexin	7.2
	424834	NM_003613	Ha.151407	igtp_1	7.1
	400749		predicted exon	hs3d1_recop1_sdl1_recop1_b	6.8
	419054	N40340	Ha.191510	igSPRY	6.8
	409170	A1802518	Ha.976709-1-210159-008 81091 Ha	ABC_tranABC_membrane	6.6
30	416441	BE407137	gbs60130155CF1 NH_MGC_21 Hom	SDC	6.4
	419664	NM_006033	Ha.65370	Ribosomal_L22	6.4
	402425		predicted exon	ion_trans	6.3
	415451	H19415	Ha.268720	Ephrin	6.0
	403083		predicted exon	hs3	5.9
35	448995	A1813276	Ha.5962	SDC	5.9
	418345	AJ001885	Ha.241407	serpin	5.8
	424946	AW077512	Ha.153595	aa_permeases	5.6
	411211	M18548	Ha.5599	connexin	5.7
	403063	AA481269	Ha.178381	ABC_tranABC_membrane	5.6
40	450152	A113635	Ha.22968	igkinase	5.6
	418844	MG2962	Ha.1200	lipoygenase/PLAT	5.6
	403389		predicted exon	hs3	5.6
	401687		predicted exon	hs3_15e/prolysin	5.6
	403691		predicted exon	hs3_1Reprolysin	5.6
45	414035	Y00303	Ha.75716	serpin	5.4
	421284	U52435	Ha.103128	neur_chan	5.3
	425435	T89473	Ha.192228	lipase/PLAT	5.3
	457122	A1026157	Ha.33728	lipoygenase/PLAT	5.2
	419249	X14767	Ha.89768	neur_chan	5.2
50	425698	NM_016112	Ha.159241	ion_trans	5.2
	421117	AF003522	Ha.250500	EGF_CSL	5.1
	427945	A469840	Ha.153354	O-alphaurl	5.1
	435174	AA667376	Ha.194624	SPRY	5.0
	408170	AW204516	Ha.31635	artras	5.0
55	434351	AW574991	Ha.191852	artras	4.9
	437026	U78308	Ha.276485	7tm_1	4.8
	422597	BE245909	Ha.119834	ABC_tranABC_membrane	4.8
	405545		predicted exon	ABC_tranABC_membrane	4.8
60	420471	V22440	Ha.170009	EGF	4.7
	423632	AY42071	Ha.55279	serpin	4.6
	420206	M1463	Ha.36568	sugar_tr	4.6
	415138	C16356	Ha.78045	Kunitz_BPT/G-gamma	4.6
	424402	M31036	Ha.1769	7tm_1	4.5
65	426450	AJ271943	Ha.67459	ASC	4.5
	430226	BE245592	Ha.2501	7tm_1	4.4
	436126	AW448757	Ha.163036	SNF	4.4
	406812	AF000575	Ha.67846	igp	4.4
	403985	AA071267	Ha.196491	TMPP	4.3
70	431914	AW296255	Ha.196491	hs3FR_c6	4.3
	410555	N29340	Ha.64311	disintegrin/Reprolysin	4.3
	422389	AF240635	Ha.115897	cathepsin	4.3
	405281		predicted exon	A2MA2M_N	4.3
	413548	BE147555	Ha.268541	EGF3d1_recop1_sdl1_recop1_b	4.3
75	440935	Y15267	Ha.23872	hs3_recop1_sdl1_recop1_b	4.3
	425984	U56420	Ha.159903	7tm_1	4.3
	410611	AW954134	Ha.20924	Peptidase_S9	4.2
	403666	NM_001942	Ha.2633	cathepsin/Cathepsin_C_lem	4.1
	416863	A1750816	Ha.67400	hw_density_lipoprotein_receptor_cst	4.0
	445924	A1264871	Ha.164166	sugar_tr	3.9
80	457148	AF091035	Ha.184627	artras	3.9
	428968	AC004755	Ha.184922	E1-E2_ATPase	3.9
	412170	D16532	Ha.73729	EGF3d1_recop1_sdl1_recop1_b	3.8
	422966	R37337	Ha.12111	acidphosphatidy_TIG	3.8
	403783		predicted exon	7tm_1	3.8

WO 02/102235

PCT/US02/19297

401657			predicted exon	/m_1	2.6
456711	A4033699	Hs.83038	ESTs, Moderately similar to MASP-2	sun1/hypsin/CUB	2.6
430042	AW971345	Hs.282715	ESTs	sugar_1r	2.6
433138	AB029486	Hs.59729	semaphorin sem2	ig_Sema	2.6
452530	AB05518	Hs.169825	gb-RC8T091-210199-036 BT091 Hs	ABC_1var/ABC_memb	2.6
426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syn	ABC_Col4	2.6
403786			predicted exon	collin	2.6
431728	NM_007351	Hs.268107	multimin	EGF-C1q	2.6
441595	AW206035	Hs.192123	ESTs	sugar_1r	2.6
445337	AJ245671	Hs.12844	EGF-like domain, multiple 6	EGF-MAM	2.6
447197	D30375	Hs.12844	glycylserine 1.1 Sema placenta NB2H	3GF	2.5
428165	Y54150	Hs.193122	Fc fragment of IgA, receptor for	ig	2.5
450245	AJ007536	Hs.271767	ESTs, Moderately similar to ALU1_H	ig	2.5
416429	H54658	Hs.268942	ESTs	E1-E2_ATPase/hydrolase	2.5
417067	AJ001417	Hs.81086	ubiquitin carboxyl family 22 (extraneuro	sugar_1r	2.5
435182	AB039820	Hs.127821	BWR1 protein	ion_1var	2.5
403092			predicted exon	fn3	2.5
406850	AB24300	Hs.172928	collagen, type I, alpha 1	vnc;Collagen/COLFI	2.5
43698	AW297855	Hs.125815	ESTs	lipoygenase/PLAT	2.5
45615	NM_013348	Hs.144011	potassium inwardly-rectifying channel	IRK	2.5

TABLE 2B:

Play: Unique Eos probe/identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Play	CAT Number	Accession
408385	112523_1	AA071267 T65940 T64515 AA071334
412333	126037_1	AA057465 AA181789 AA057358 AW037402
413605	1379792_1	BE152644 BE152712 BE152668 BE152659 BE152810 BE152811 BE152816 BE152643 BE152706 BE152656 BE152660 BE152715 BE152682 BE152669 BE152661 BE152672 BE152653 BE152716 BE152651 BE152767 BE152652 BE152714 BE152708 BE152665 BE152670 BE152771 BE152775 BE152666 BE152769 BE152813 BE152664 BE152676 BE152681 BE152709 BE152667 BE152814 BE152828 BE152771 BE152707 BE152815 BE152878 BE152873 BE152762 BE152671 BE152662 BE152760 BE152809 BE152778 BE152780 BE152762 BE152778
416151	1573826_1	T26061 Z44135 H23016
416441	159480_1	BE407187 AA182474 AA180369 BE275828 BE276131
416631	1635019_1	U09466 U09604 U09604
425573	228714_1	AA326504 AA327785 AA062370
447197	171623_1	R30075 AB06646 R36167
447420	721207_1	AJ378628 N32350 H65772
452530	920646_1	AB05518 AB05516 AB05457 AB05515 AW176013 AW176037
452847	938511_1	AW176013 AB05282
453420	956433_1	AJ033459 AB03461
459170	920646_1	AB05518 AB05516 AB05457 AB05515 AW176013 AW176037

TABLE 2C:

Play: Unique number corresponding to an Eos probe/identifier

Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham.1 et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Play	Ref	Strand	NL_position
40484	9929670	Plus	22074-22214
407074	8118964	Minus	63110-63241
407449	7331445	Minus	9162-9239
401244	4827300	Minus	55359-55376
401537	7960358	Minus	18676-187029, 190607-190779, 196218-196348
401657	9100664	Minus	7312-8163
402172	8575911	Minus	143378-143671
402425	9786347	Minus	50224-50385
402745	9212200	Minus	76516-76690
403074	8954241	Plus	143375-143561
403077	8954241	Plus	146928-147222, 147325-147628
403083	8954241	Plus	163019-163351
403089	8954241	Plus	171964-172239
403092	8954241	Plus	174720-175016, 175104-175406, 175508-175813
403093	8954241	Plus	177083-177373, 177464-177751
403411	9436635	Minus	104271-104420
403661	9706027	Minus	30265-30482
403687	7387384	Plus	9009-9534
403691	7387384	Minus	88280-88463
403763	7229888	Minus	43575-43687
403796	8959896	Minus	75073-77654
404187	4481839	Plus	7544-7991
404243	5672608	Plus	74585-75123
404270	9628129	Minus	3649-3750, 4161-4306, 5982-6049, 6849-6965
404866	4884022	Plus	30058-30086
405281	6139075	Minus	34202-34351, 35194-35336, 45412-45475, 45731-45958, 47296-47457, 49549-49658, 49790-49804, 50231-50242, 53583-53667, 54111-54279
405285	6139075	Minus	56744-56903, 57080-57170, 61478-61560
405445	1034740	Plus	110577-110807, 110891-110936, 121626-121823
405547	1034740	Plus	124361-124520, 124914-125080
405636	5123990	Plus	56384-56687

407590 1203598 Plus 136394-136609,136570-136699,136805-136941

5 TABLE 3A lists about 1543 genes up-regulated in ovarian cancer compared to normal ovaries. Those were selected as for Table 1A, except that the ratio was greater than or equal to 15, and the denominator was the arithmetic mean value for various non-malignant ovary specimens obtained.

TABLE 3A: ABOUT 1543 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Key: Primerkey

Ex. Accon: Exemplar Accession

UG ID: UniGene ID

Title: UniGene Title

PFAM domain

ratio: tumor vs. normal tissues

Key	Ex. Accon No.	UG ID	Title	ratio
420855	AW650357	Hs.100000	S100 calcium-binding protein A6 (calgranulin A)	218.9
422156	W72424	Hs.112405	S100 calcium-binding protein A9 (calgranulin B)	160.2
422158	110343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	166.0
424789	BE550723	Hs.153179	fatty acid binding protein 5 (psoriasis-associated)	151.5
424242	NM_000394	Hs.8272	prostaglandin H2 synthase (cyclooxygenase 2)	150.2
408522	AS11214	Hs.45320	Small proline-rich protein SPHK1 (pancreatic, embryonic)	146.5
431369	BE164455	Hs.251754	secretory leukocyte protease inhibitor (antileukoprotein)	144.9
430620	NM_015190	Hs.242057	chromosome 1 open reading frame 10	135.5
428471	X57348	Hs.184610	stratelin	129.5
421975	AJ243862	Hs.110139	NICE-1 proteoglycan	106.7
437191	NM_006846	Hs.5475	serine protease inhibitor, Kazal type, 5	105.2
407786	BE514982	Hs.38991	S100 calcium-binding protein A2	105.5
441555	AW953575	Hs.169902	solute carrier family 2 (facilitated glucose transporter),	103.5
431211	N65845	Hs.5555	gap junction protein, beta 2, 29kD (connexin 26)	102.1
415329	AW072220	Hs.26898	S100-type calcium-binding protein A14	95.3
430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3 (Sorsby fundus)	87.0
417079	U65590	Hs.81134	interleukin 1 receptor antagonist	85.1
412535	NM_004415	Hs.74315	desmoplakin (DP1, DP2)	85.0
417515	L24203	Hs.169139	alpha-1-macroglobulin group D-associated protein	84.6
428295	AA357283	Hs.75639	zinc finger protein 5 (CIMP1)	84.5
452589	AA216393	Hs.282556	ESTs, Weakly similar to alternatively spliced product u	84.4
435711	N25514	Hs.77365	myosin, light polypeptide 5, alkali, smooth muscle and n	83.8
435712	N31212	Hs.77365	myosin, light polypeptide 5, alkali, smooth muscle and n	81.0
432680	T47564	Hs.276113	interferon, alpha-2-inducible protein 27	81.0
415869	AW250318	Hs.50395	mat, T-cell differentiation protein	77.8
409453	AB85515	Hs.59512	ESTs	75.3
424570	W51215	Hs.115551	epithelial V-like antigen 1	57.5
417130	AW785558	Hs.81255	S100 calcium-binding protein A4 (calcium protein, calv	57.0
429334	AW655908	Hs.1590	heparin-binding growth factor binding protein	56.7
442379	NM_004513	Hs.8255	transglutaminase 2 (C-peptide, protein-glutamine-g	64.7
456985	NM_001926	Hs.155597	D component of complement (adipsin)	54.6
423017	AW178751	Hs.227946	serine (or cysteine) proteinase inhibitor, clade B (ovalbu	53.6
447930	BE048521	Hs.20144	small inducible cytokine subfamily A (Cys-Cys), memb	50.7
424392	AL137946	Hs.149001	Homo sapiens mRNA; cDNA DKFZp568F0624	50.3
414438	AB792777	Hs.75135	thioredoxin	59.9
420135	AW601090	Hs.195851	actin, alpha 2, smooth muscle, aorta	56.9
433335	AF017195	Hs.31395	ESTs, highly similar to JED174 Hicized protein-2 [Hsa	55.5
403741			predicted exon	57.0
430637	BE100081	Hs.255290	S100 calcium-binding protein A11 (calgizarin)	55.1
424096	AF073734	Hs.139322	small proline-rich protein 3	55.6
441691	AF065992	Hs.163	Duffy blood group	55.6
428521	AF181445	Hs.170219	hypothelical protein	55.5
406713	U32929	Hs.77365	myosin, light polypeptide 6, alkali, smooth muscle and n	55.3
405725	D51245	Hs.268051	actin, beta	54.1
422156	AA565554	Hs.112406	S100 calcium-binding protein A7 (psoriasis I)	54.0
456755	N60129	Hs.94309	metallothionein 1L	54.0
425553	AA278921	Hs.1906	proteoglycan 1, secretory granule	53.3
442257	AW036331		gbr11-F-BNO-ub-b-05-0-Ur1 NH_MGC_50 Homo	53.1
421957	AW069537	Hs.109557	hypothelical protein DKFZP434A0620	52.3
447525	AL045763	Hs.246	small inducible cytokine A2 (monocyte chemoattractan	51.2
405722	H27695	Hs.53395	Homo sapiens SNK73 protein (SNK73) mRNA, clone	51.0
427223	BE208189	Hs.174031	cytochrome c oxidase subunit Vb	51.0
414420	AA43424	Hs.76095	immediate early response 3	50.9
417259	AW903638	Hs.61000	chondroitin sulfate proteoglycan 2 (versican)	50.3
414191	AW263089	Hs.73607	PDZ and LIM domain 1 (olfr)	49.5
436905	H55990	Hs.181244	major histocompatibility complex, class I, A	49.0
408000	L11590	Hs.820	bullous pemphigoid antigen 1 (230/240kD)	49.0
414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibitor, clade B (ovabu	48.8
427295	NM_013220	Hs.265124	CD24 (small cell lung carcinoma cluster 4 antigen	48.8
421948	L42583	Hs.117258	keratin 5A	48.7
414652	AL036058	Hs.76807	major histocompatibility complex, class II, DR alpha	48.5
425071	NM_013969	Hs.154424	deiodinase, iodothyronine, type II	48.5
404757			predicted exon	48.4
415327	U70379	Hs.84135	paired-like homeodomain transcription factor 1	48.2
435729	BE521807	Hs.3337	transmembrane 4 superfamily member 1	47.7
414183	AW957446	Hs.301711	ESTs	47.2
400183			predicted exon	47.0
433423	BE407127	Hs.8997	heat shock 70kD protein 1A	46.9
423457	F08208	Hs.155606	paired anion channel homeo box 1	46.6

WO 02/102235

PCT/US02/19297

414085	AA114016	Hs.75746	aldehyde dehydrogenase 6	46.0
423169	MG8371	Hs.171596	EphA2	45.6
433440	NG636	Hs.124004	ESTs	45.5
417366	BE185269	Hs.1076	small proline-rich protein 1B (comitin)	45.3
412774	AA120665	Hs.23136	ESTs	45.1
407242	M16728		gh:Human nonspecific crossreacting antigen mRNA, co	44.8
431782	AA370141	Hs.251453	Human DNA sequence from clone 367N21 on chromosome	44.8
406955			predicted exon	43.5
417365	D50653	Hs.82028	transforming growth factor, beta receptor II (70-300kd)	43.4
423231	W37862	Hs.274398	Human sapiens mRNA; cDNA DKFZp6881524 (from c	43.4
424475	AF042326	Hs.145098	smoothelin	43.3
444726	NX_006147	Hs.11801	inversin/regulatory factor 6	43.2
432314	AA533447	Hs.265173	ESTs	43.2
429500	K76565	Hs.289114	hexabrachion (tenascin C, cytotoxin)	43.1
414406	Z45367	Hs.7837	Human sapiens cDNA FLJ10457 fs, clone NT29P1001	42.7
412969	A1271462	Hs.75103	lysine 3-monooxygenase/hydrolysis 5-monooxygenase	42.5
423720	AL044151	Hs.23368	Homo sapiens cDNA: FLJ21310 fs, clone COL02160	42.5
400111			predicted exon	42.4
407207	T03651	Hs.175661	tubulin, beta polypeptide	42.4
417164	AA332823	Hs.61351	heterogeneous nuclear ribonucleoprotein A/B	42.2
424971	AA479006	Hs.154036	tumor suppressing substrate/candidate 3	41.9
430394	AA142520	Hs.56105	ESTs, Weakly similar to WDNM RAT WDNM1 PROT	41.9
406957	A167644	Hs.277477	major histocompatibility complex, class I, C	41.6
451092	A207256	Hs.13766	Homo sapiens mRNA for FLJ00074 protein, partial cds	41.6
412696	A1615219	Hs.739	diphtheria toxin receptor (heparin-binding epidermal gro	41.6
422103	AA584330	Hs.111676	protein kinase H11; small stress protein-like protein HS	41.5
426765	AA015963	Hs.125265	ESTs	41.3
450386	BE818671	Hs.429	ATP synthase, H+ transporting, mitochondrial F0 comp	41.0
414522	A1752656	Hs.76669	nicotinamide N-methyltransferase	40.6
450522			predicted exon	40.6
408221	AA912183	Hs.47447	ESTs	40.8
446500	U76093	Hs.15154	sushi-repeat-containing protein, X chromosome	40.7
421416	BE302380	Hs.104126	adenyl cyclase-associated protein	40.6
412247	AF122375	Hs.73793	vascular endothelial growth factor	40.5
410541	AA065003	Hs.64719	hypothetical protein	40.5
406958	A1920965	Hs.77961	major histocompatibility complex, class I, B	40.0
420225	AW243046	Hs.54769	ESTs	40.0
406925	A1962269	Hs.94298	CD74 antigen (variant polypeptide of major histocom	39.4
436623	AA345510	Hs.5941	complement component 1, q subcomponent, alpha pol	39.4
404201	AF055656	Hs.103953	solute carrier family 5 (sodium iodide symporter), mem	39.3
405136			predicted exon	39.1
406733	AF054612	Hs.254290	ESTs	39.0
414044	BE514154	Hs.75721	profilin 1	38.9
430162	AB001325	Hs.234642	aquaporin 3	38.8
428121	AB006622	Hs.162536	Homo sapiens cDNA: FLJ21370 fs, clone COL03092	38.6
434311	BE543469	Hs.256263	Homo sapiens cDNA FLJ14115 fs, clone MAMM/410	38.7
425140			predicted exon	38.5
432516	AF077200	Hs.275613	hypothetical protein	38.4
420107	AL043580	Hs.7856	peptide (Drosophila) homolog 1	36.4
427693	BE546832	Hs.180370	cofilin 1 (non-muscle)	38.1
446035	BE277528	Hs.11061	ESTs, Weakly similar to GS7447 HPBR1-7 protein [H	36.1
423374	W69615	Hs.301855	Homo sapiens cDNA FLJ11346 fs, clone PLACE1010	37.9
428363	BE816599	Hs.184029	hypothetical protein DKFZp781A062	37.7
436236	AW667451	Hs.107125	ESTs, Weakly similar to GS7447 HPBR1-7 protein [H	37.7
430798	W93774	Hs.99930	keratin 10 (epidermolytic hyperkeratosis; keratosis palm	37.6
420327	M18579	Hs.247942	Human variant GS-rhva-like gene and ORF, complete	37.5
407151			predicted exon	37.6
448257	AW772070	Hs.263146	ESTs	37.3
428415	AA337211	Hs.184222	Down syndrome critical region gene 1	37.2
424206	NM_005734	Hs.155241	amine oxidase, copper containing 3 (vascular adhesion p	37.2
405112	AF030976	Hs.67346	leukocyte immunoglobulin-like receptor, subfamily B (37.2
425682	UB3116	Hs.161002	absent in melanoma 1	37.2
432501	BE546532	Hs.267329	Fox binding protein 1	37.1
421766	A1189653	Hs.21351	ESTs	37.1
427951	BE275968	Hs.151511	asparaginyl-tRNA synthetase	37.0
410143	AA168189	Hs.268819	Homo sapiens cDNA: FLJ21022 fs, clone CA063633	36.8
451326	AW653606	Hs.105012	ESTs	36.7
414135	NM_004419	Hs.2126	dual specificity phosphatase 5	36.7
414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (from	36.7
407765			predicted exon	36.5
411469	T09967	Hs.70327	cysteine-rich protein 2	36.2
415693	AA133745	Hs.52323	FXYD domain-containing ion transport regulator 3	36.1
417039	AA302160	Hs.80958	ATP synthase, H+ transporting, mitochondrial F0 comp	36.1
406716	AA595225	Hs.169476	glyceraledehyde 3-phosphate dehydrogenase	36.0
402543			predicted exon	36.0
406669	A163591	Hs.78146	platelet/endothelial cell adhesion molecule (CD31 anti	35.9
414987	AA524394	Hs.165544	ESTs	35.9
445810	AW265700	Hs.115660	ESTs	35.5
409553	AA574074	Hs.77961	major histocompatibility complex, class I, B	35.7
407496	U26131		gh:Human H1A/G-C chimera transcript mRNA, partial	35.6
412624	AA417813	Hs.111177	ESTs	35.5
401521			predicted exon	35.4
401948	AW296713	Hs.221441	ESTs	35.1
406726	AE66345	Hs.163704	ubiquitin C	34.9

[illegible]

WO 02/102235

PCT/US02/19297

	416511	NM_006762	Hs.79356	Lysosomal-associated multipassspanning membrane protein	29.9
	431093	BE149762	Hs.248213	gag junction protein, beta 6 (connexin 30)	29.7
	436651	BE046962	Hs.275958	ESTs	29.6
5	419766	BE243101	Hs.22291	chromosome 20open reading frame 3	29.5
	420747	BE294407	Hs.59910	phosphofructokinase, platelet	29.5
	436895	AF037335	Hs.5338	carboxylic anhydrase XII	29.5
	412765	AK006020	Hs.74571	ADP-ribosylation factor 1	29.4
	419223	X60111	Hs.1244	CD5 antigen (p24)	29.4
10	413796	AW408094	Hs.75545	interleukin 4 receptor	29.4
	417795	AW265151	Hs.163612	ESTs	29.4
	413103	M57399	Hs.44	phlebotomy (heparin binding growth factor 8, neurite g	29.4
	415314	N88802	Hs.5422	glycoprotein M58	29.3
	428411	AW291464	Hs.10338	ESTs	29.3
15	430380	AA806105	Hs.140	immunoglobulin heavy constant gamma 3 (3m marker)	29.3
	433451	AA833472	Hs.246982	calcipapin B	29.2
	453949	AU071146	Hs.36327	heat shock 105MD	29.2
	413859	AW592336	Hs.8364	pyruvate dehydrogenase kinase, isoform 4	29.2
	407845	AL036518	Hs.118598	ESTs	29.1
20	453500	A418427	Hs.43125	ESTs	29.1
	456954	BE13241	gb00151545F1 NIH_MGC_19 Homo sapiens cDNA	29.0	
	453457	AI535997	Hs.30089	ESTs	29.0
	411794	AL118577	Hs.75658	phosphorylase, glycogen; brain	28.9
	421773	W69233	Hs.112457	ESTs	28.9
25	423621	BE02304	gbtCIV-00090-07040-163-c07 EN0090 Homo sapi	28.8	
	408935	BE530106	Hs.28533	ESTs	28.8
	450847	NM_003155	Hs.25590	stannocalbin 1	28.8
	431243	U48455	Hs.252189	syndecan 4 (amphipycan, ryudocan)	28.7
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	28.7
30	433469	F12741	gbcSCC0201 normalized infant brain cDNA Homo sapi	28.7	
	405783		predicted exon	28.7	
	417308	H60720	Hs.81892	gAA0101 gene product	28.7
	407049		predicted exon	28.7	
	413442	BE140643	gbtCIV-00090-07040-163-c07 EN0090 Homo sapiens c	28.6	
35	404828		predicted exon	28.6	
	407453	AJ132087	gbtCIV-00090-07040-163-c07 EN0090 Homo sapiens mRN	28.6	
	418529	AW005695	Hs.250897	TRK-fused gene (NOTE: non-standard symbol and nam	28.6
	417387	A032558	Hs.75844	lysine 3-monooxygenase/tryptophan 5-monooxygenas	28.5
	450690	AA295596	Hs.25334	FXR1 domain-containing ion transport regulator 5	28.5
40	402430		predicted exon	28.4	
	413929	BE501889	Hs.75817	collagen, type IV, alpha 2	28.2
	423803	NM_005709	Hs.132945	PDZ-73 protein	28.2
	405086		predicted exon	28.2	
45	416586	X54162	Hs.79385	elastin (smooth muscle)	28.2
	417055	N39469	Hs.7256	Homo sapiens cDNA: FLJ22021 fa, clone HEP08253	28.1
	449184	AW296235	Hs.194941	ESTs	28.1
	445542	NM_004281	Hs.15259	BCL2-associated athanogene 3	28.1
	412793	AW597986	gbtCIV-00090-07040-163-c07 EN0090 Homo sapi	28.0	
	452818	W21908	Hs.8372	ubiquitin-cytochrome c reductase (5.4kD) subunit	28.0
50	402869		predicted exon	27.9	
	438810	AA353044	Hs.5321	ARP3 (actin-related protein 3, yeast) homolog	27.9
	402075		predicted exon	27.9	
	410480	R97457	Hs.63984	cathepsin 13, H-cathepsin (heav)	27.8
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell adhesion molecu	27.8
55	439786	AE033492	Hs.301241	Homo sapiens mRNA; cDNA DKFZp566A0424 (from	27.7
	424482	BE266821	Hs.149155	voltage-dependent anion channel 1	27.6
	423737	L0608	Hs.99899	tumor necrosis factor (ligand) superfamily, member 7	27.6
	414663	BE360326	gbtCIV-00090-07040-163-c07 EN0090 Homo sapiens cDNA c	27.6	
	409703	NM_005187	Hs.56009	2-oxoglutarate synthetase 3	27.6
60	448108	AL036596	Hs.102773	ESTs	27.5
	428144	BE265943	Hs.182625	VAMP (vesicle-associated membrane protein)-associate	27.5
	445688	N248205	Hs.153244	ESTs	27.5
	405411		predicted exon	27.5	
	410275	U86668	Hs.61796	transcription factor AP-2 gamma (activating enhancer-b	27.5
65	424675	NM_005512	Hs.151641	glycoprotein A repetitions predominant	27.3
	463455	AL117424	Hs.26535	chloride intracellular channel 4	27.2
	414855	AA156586	Hs.104540	HIV-1 inducer of short transcript binding protein	27.2
	433578	BE336886	Hs.3416	adipose differentiation-related protein	27.2
	401994		predicted exon	27.2	
	445933	AV652402	Hs.155145	ESTs	27.2
70	402277		predicted exon	27.1	
	428106	BE620016	Hs.182470	PTD101 protein	27.1
	448625	AW370786	Hs.178470	Homo sapiens cDNA: FLJ22662 fa, clone HSD08080	27.1
	427587	AI979352	Hs.118625	heparinase 1	27.0
	427204	BE264152	Hs.221994	ESTs	27.0
75	444094	AN695764	Hs.202394	ESTs	27.0
	414053	BE318635	Hs.76725	keratogen 2	26.9
	430511	BE018196	Hs.2675	calpain 1, (mu1) large subunit	26.9
	424039	L32877	Hs.37112	ubiquitin-cytochrome c reductase, Rhesus-like-sulfur po	26.9
	424939	AK000059	Hs.153881	Homo sapiens: NY-REN-62 antigen mRNA, partial cds	26.9
80	414639	BE379046	Hs.153881	gbtCIV-00090-07040-163-c07 EN0090 Homo sapiens cDNA	26.9
	404675		predicted exon	26.8	
	401597	AA172106	Hs.110950	Rag C protein	26.8
	401405		predicted exon	26.8	
	411641	W03940	gbc262602.1 Soares total liver spleen TNF-LS Homo sa	26.8	

WO 02/102235

PCT/US02/19297

	412025	AB27451	Hs.24143	ESTs	26.7
	414276	BE297862		gb501174763F1 NH MIGC 17 Homo sapiens cDNA	26.7
	440865	AW404815	Hs.10260	Homo sapiens cDNA: FLJ13141 f1s, clone PLACE1010	26.7
5	447681	RS3772	Hs.6929	hypothetical protein FLJ11362	26.7
	410677	NM_003278	Hs.65424	letracrin (plasmalogen-binding protein)	26.5
	400982			predicted exon	26.5
	452933	AW391423	Hs.286555	Homo sapiens cDNA: FLJ22425 f1s, clone HFC08665	26.5
	407233	X16354	Hs.50964	carcinoembryonic antigen-related cell adhesion molecule	26.4
	430127	AA219498	Hs.233952	proteasome (prosome, macropain) subunit, alpha type, 7	26.3
10	448218	A1184469		gb050512x1 Soares, placenta, 8/week, 2/nt/1P60	26.3
	413511	AB271178	Hs.75412	Arginase-rich protein	26.2
	459511	AI142379		gb0614d1.1 Soares, testis, NHT Homo sapiens cDNA	26.2
	410988	BE379794	Hs.65403	hypothetical protein	26.2
	458652	AB23410	Hs.169149	karyopherin alpha 1 (importin alpha 5)	26.2
15	451219	AA054209	Hs.187954	ESTs	26.2
	449839	BE267795	Hs.22595	hypothetical protein FLJ10637	26.2
	400800	Y10262	Hs.46925	eyes absent (Drosophila) homolog 3	26.2
	44342	BE268655	Hs.14846	Homo sapiens mRNA: cDNA DKF2p554D016 (from c	26.2
20	421177	AW070211	Hs.102415	Homo sapiens mRNA: cDNA DKF2p558N0121 (from	26.1
	433846	AF036719	Hs.53764	carboxypeptidase A3	26.1
	449457	BE513286	Hs.21693	ESTs, Weakly similar to glycyl 3-phosphate permease	26.1
	415279	F04237	Hs.1447	glial fibrillary acidic protein	26.0
	419323	AI062376	Hs.132575	ESTs	26.0
	432465	L38033	Hs.273356	stromal cell-derived factor 1	25.9
25	437679	NM_014214	Hs.57563	histidinylmethyl-lysine C-mannosyltransferase 2	25.9
	425635	AB007637	Hs.158287	KIAA0458 gene product	25.8
	412523	AA179522	Hs.70506	adaptor-related protein complex 3, delta 1 subunit	25.8
	447980	AF033367	Hs.202355	ESTs	25.8
	415118	AA234223	Hs.135204	ESTs	25.8
30	421224	AW402164	Hs.125812	ESTs	25.8
	414890	BE281095	Hs.77573	uridine phosphorylase	25.8
	447330	BE279848	Hs.18141	ladinin 1	25.7
	403610			predicted exon	25.7
35	447804	AW069833	Hs.203674	ESTs	25.7
	449677	H96577	Hs.8638	ras homolog gene family, member E	25.7
	450088	BE177320	Hs.166148	Homo sapiens cDNA: FLJ23082 f1s, clone LING0451	25.7
	417120	N76687	Hs.48616	ESTs	25.6
	425154			predicted exon	25.6
40	410687	U24386	Hs.65436	lysyl oxidase-like 1	25.6
	421888	AA299780	Hs.121036	ESTs	25.6
	420459	AF016045	Hs.57905	ova (Drosophila) homolog-like 1	25.5
	416323	N72630	Hs.33661	Homo sapiens genomic DNA, chromosome 21q, section	25.5
	446252	AF051467	Hs.27656	Rh type C glycoprotein	25.5
45	416274	AW160404	Hs.78126	guanine nucleotide binding protein 10	25.5
	430028	BE564110	Hs.227760	NADH dehydrogenase (ubiquinone) 1 beta subcomplex	25.5
	438450	AI050895	Hs.55853	notal, mouse, homolog	25.5
	423215			predicted exon	25.4
	430014	H59354	Hs.182485	actinin, alpha 4	25.4
50	453682	AW854339	Hs.33476	hypothetical protein FLJ11537	25.4
	405867			predicted exon	25.4
	459170	AI905518		gbRC-CT081-210199-098 BT091 Homo sapiens cDNA	25.4
	407944	R34008	Hs.236727	desmoglein 2	25.4
	415748	D60086	Hs.679	pyruvate dehydrogenase (liponamide) beta	25.3
55	423287	H38340		gbyp70K07.1 Soares adult brain N26-H555Y Homo s	25.3
	450644	AA554989	Hs.209061	zwd (suppressor of bimD, Aspergillus nidulans) homo	25.3
	423505	BE265498	Hs.3123	kbat gnt1a1a (Drosophila) homolog 2	25.3
	401014			predicted exon	25.3
	449019	AB64695	Hs.67776	ESTs, Weakly similar to ALL7_HUMAN ALU SUBFA	25.3
60	403687	MS7417		gbHomo sapiens mucin (mucin) mRNA, partial cds.	25.3
	402639			predicted exon	25.3
	447147	AA510383	Hs.262815	ESTs	25.3
	453379	AA035261	Hs.81753	ESTs	25.3
	414217	A1309298	Hs.279898	Homo sapiens cDNA: FLJ23165 f1s, clone LING00946	25.3
65	430223	NM_025214	Hs.239535	nephroblastoma overexpressed gene	25.3
	406865	M19726	Hs.276652	gb-Human non-specific cross-reacting antigen mRNA, co	25.3
	444747	AW450407	Hs.257291	ESTs, Weakly similar to P558_HUMAN PROSTATIN	25.2
	417883	R22519	Hs.23388	ESTs	25.2
	430235	BE266049	Hs.236494	RAB10, member RAS oncogene family	25.2
70	459061	AI761313	Hs.264265	ESTs	25.2
	434368	AW515020	Hs.212640	Homo sapiens cDNA FLJ13265 f1s, clone OVARC1000	25.2
	415917	Z43912		gbHSC10A111 normalized infant brain cDNA Homo	25.2
	444409	AI792140	Hs.49265	ESTs	25.2
	426876	BE391797	Hs.62146	hypothetical protein	25.1
75	433417	AA587773	Hs.135404	ESTs	25.1
	426372	BE304680	Hs.169531	DEAD(H) (Asp-Glu-Ala-AspHis) box polypeptide 21	25.1
	402131			predicted exon	25.1
	450545	AW135582	Hs.201767	ESTs	25.0
80	434162	AI221214	Hs.116136	ESTs	25.0
	406971			predicted exon	24.9
	427600	AW630916	Hs.179774	proteasome (prosome, macropain) activator subunit 2 (P	24.9
	405402	AF208234	Hs.695	cystatin B (stein II)	24.9
	430135			predicted exon	24.9
	428403	AI3933048	Hs.239894	lecithin-rich repeat (in FLJ) interacting protein 1	24.9
	430223			predicted exon	24.8

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WO 02/102235

PCT/US02/19297

5	128362	AA426655	Hs.169333	ESTs	23.3
	128349	AA425234	Hs.79868	ribose 5-phosphate isomerase A (fructose 5-phosphate ep	23.3
	122440	NM_004912	Hs.116724	aldol-keto isomerase family 1, member E11 (aldose red	23.3
	110962	BC273749	Hs.752	FKBP6-binding protein 1A (12kD)	23.2
	111796	AA807197	Hs.8918	ESTs	23.2
	458954	AW379375	Hs.141742	Homo sapiens cDNA FLJ12211 fls, clone MAMMA10	23.2
	438805	AB103477	Hs.48778	ribon protein	23.2
	457024	AA397545	Hs.119151	ESTs	23.2
	414591	AB88490	Hs.55902	ESTs	23.2
10	437846	AA773866	Hs.244569	ESTs	23.2
	401220			predicted exon	23.1
	421747	AB16224	Hs.107747	DKFZ266C243 protein	23.1
	452950	AA428123	Hs.7745	17kD fetal brain protein	23.1
15	414327	BE408145	Hs.185254	ESTs, Moderately similar to NAC-1 protein (JLNorvegic	23.1
	402526			predicted exon	23.1
	452415	AJ026115	Hs.114777	ESTs	23.1
	440684	AG231323	Hs.127356	ESTs, Highly similar to NEST_HUMAN NEST1 [Lsasp	23.1
	446603	H03845	Hs.108234	ESTs	23.1
20	456306	AA805939	Hs.117927	ESTs	23.1
	434687	AF159442	Hs.103362	phosphatidyl seramblase 3	23.0
	404727			predicted exon	23.0
	407317	AJ204033	Hs.271461	ESTs, Weakly similar to ALUS_HUMAN ALU SUBFA	23.0
	405580			predicted exon	23.0
25	437898	W61260	Hs.43410	ESTs	22.9
	445781	AW284319	Hs.251048	ESTs	22.9
	457297	AW068188	Hs.290599	ESTs	22.9
	405545			predicted exon	22.9
	431562	AB843334	Hs.11637	ESTs	22.9
30	440703	AL137653	Hs.7378	Homo sapiens mRNA: cDNA DKFZp434G227 (from c	22.9
	439845	AW070249	Hs.9357591359	MAGE: resequenced, MAGP Homo sap	22.9
	418149	AA811473	Hs.291677	ESTs	22.9
	439332	AW842747	Hs.293314	ESTs, Highly similar to unnamed protein product [Hsa	22.8
	401166			predicted exon	22.8
35	425578	NM_002599	Hs.15437	phosphodiesterase 2A, cGMP-stimulated	22.8
	405684	X16354	Hs.50964	carcinoembryonic antigen-related cell adhesion molecu	22.8
	421651	AW860512	Hs.283586	ESTs	22.8
	421064	A245432	Hs.101352	tumor necrosis factor, alpha-induced protein 2	22.8
	411269	AA811586	Hs.166250	ESTs	22.8
40	457624	AA809159	Hs.267581	Homo sapiens cDNA FLJ13544 fls, clone PLACE1006	22.8
	437380	AFJ05082		gcb1-homo sapiens skin-specific protein (gp33) mRNA, p	22.8
	469006	AW296631	Hs.27721	hypothetical protein FLJ20353	22.8
	436827	H72167	Hs.5322	guanine nucleotide binding protein (G protein), gamma	22.7
	418174	L20648	Hs.83565	Rho GDP dissociation inhibitor (GDI) beta	22.7
45	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin transporter), mem	22.7
	456035	N54958	Hs.271726	ESTs	22.7
	457687	AA0456767	Hs.5300	bladder cancer associated protein	22.7
	440401	A126341	Hs.143687	ESTs	22.7
	400126			predicted exon	22.7
50	414931	AK003042	Hs.77646	Homo sapiens mRNA: cDNA DKFZp761M0223 (from	22.7
	406719	AB32982	Hs.169478	glyceraldhyde-3-phosphate dehydrogenase	22.6
	439575	W06357	Hs.138680	Rho GTPase activating protein 1	22.6
	459508	N04567	Hs.55093	ESTs	22.6
	441926	AB15051	Hs.130953	ESTs	22.6
	428423	AJ076517	Hs.184278	solute carrier family 9 (sodium/hydrogen exchanger), is	22.6
55	438518	BE561958	Hs.285823	immunoglobulin heavy constant mu	22.6
	429674	NL_000055	Hs.1327	hydroxymethyltransferase	22.6
	422150	AW582858		glc3d7604.y1 Homo Panotrace: Ikabts Homo sapiens c	22.5
	412408	DE1103	Hs.73851	ATP synthase, H+-transporting, mitochondrial F0 comp	22.5
	400964			predicted exon	22.5
60	434350	AW015415	Hs.127790	ESTs	22.5
	427977	AW630727	Hs.161307	H3 histone, family 3A	22.4
	450339	AB93281	Hs.54547	ESTs	22.4
	424059	AW451266	Hs.107418	ESTs	22.4
65	414026	BE410589		phs501303306F1 NH_MGC_21 Homo sapiens cDNA	22.4
	401991			predicted exon	22.4
	419741	NM_007019	Hs.93002	oligulic carrier protein E2-C	22.3
	457952	U25750	Hs.210783	Human chromosome 17q21 mRNA clone 1046:1-1	22.3
	422597	BE246909	Hs.116834	ATP-binding cassette, sub-family B (MDR/TAP), mem	22.3
70	428504	X09133	Hs.204235	tpostacin 2 (oncogene 24p3)	22.3
	441306	AB73163	Hs.171333	ESTs	22.3
	424966	AU077312	Hs.153585	solute carrier family 7 (cations/ amino acid transporter,	22.3
	422739	H20106	Hs.119591	adaptor-related protein complex 2, sigma 1 subunit	22.2
	432504	AL121015	Hs.277704	oxygen regulated protein (150kD)	22.2
75	423304	AW403416	Hs.17026	interferon-stimulated transcription factor 3, gamma (46k	22.2
	404683	AB94204	Hs.173259	uncharacterized bone marrow protein BM033	22.2
	441624	AF220191	Hs.179666	uncharacterized hypothalamus protein HSMNP1	22.2
	425751	T19239	Hs.19140	crystallin, alpha B	22.2
	452376	RA4214	Hs.101189	ESTs	22.2
80	414542	AL150130		gcb3d3001.y1 Soares_pregnaad_uterus_NbHPU Homo	22.2
	437452	AL390127	Hs.7104	Homo sapiens mRNA: cDNA DKFZp761P06121 (from	22.2
	417426	NM_002291	Hs.82124	tannin, beta 1	22.2
	414774	X02419	Hs.77274	plasmalogen activator, unknown	22.1
	424631	AA658021	Hs.170818	ESTs	22.1
	413957	AW204431	Hs.117853	ESTs	22.1

WO 02/102235

PCT/US02/19297

	400174		predicted exon	22.1
	431837	T79326	ESTs, Weakly similar to dJ808.1 [Hsapiens]	22.1
5	431828		predicted exon	22.1
	418374	AJ011916	Hs.84359	22.0
	429297	X82464	Hs.198862	22.0
	433588		predicted exon	22.0
	428338	AJ017717	Hs.126525	22.0
10	407382	AA603620	chromosome 21 open reading frame 15	22.0
	411492	T46848	Hs.70337	22.0
	428186	ALJ04066	Hs.158047	22.0
	409646	BC206148	immunoglobulin superfamily, member 4	22.0
	429662	AAT078474	ESTs	22.0
	424247	X14308	Hs.234734	22.0
15	433062	N7999	Hs.8963	21.9
	427447	AA310711	Hs.124340	21.9
	421514	AJ001152	Hs.105924	21.9
	435302	AJ076259	Hs.190337	21.9
	414527	BC241739	Hs.76359	21.9
20	414336	AW137772	Hs.185980	21.9
	454178	AW177274	gb:CM2-CT0128-230899-005-002 CT0128 Homo sapie	21.8
	448838	BE514761	gb:G1281335F.1 NIH_MGC_39 Homo sapiens cDNA	21.8
	427889	AA00968	Hs.181046	21.8
	441114	AA917466	Hs.126600	21.8
25	451851	NM_001674	Hs.460	21.8
	426600		activating transcription factor 3	21.8
	449981	AF652743	Hs.197497	21.8
	432639	AA679465	Hs.287332	21.8
	435208		predicted exon	21.8
30	433525	T6990	Hs.4742	21.7
	413976	AB295452	Hs.75655	21.7
	423615	AA327017	Hs.162204	21.7
	453229	N36626	Hs.29106	21.7
	433350	AA320946	Hs.13679	21.7
35	413679	BE156785	Hs.147066	21.6
	442166	AAW45280	Hs.204723	21.6
	445585	AJ243836	Hs.147066	21.6
	435160		predicted exon	21.6
40	433325	AA374749	Hs.279920	21.6
	445598	AW250546	Hs.292774	21.6
	434493	AA635305	Hs.121574	21.6
	429582	AF69068	Hs.22247	21.6
	433796		predicted exon	21.6
	433208		predicted exon	21.6
45	426997	AA382250	Hs.145601	21.6
	437308	AA749417	Hs.292353	21.6
	447384	AJ377221	Hs.40528	21.6
	430600	AA139155	Hs.194995	21.6
	437068	AA743643	Hs.291427	21.6
50	418509	AB028624	Hs.85539	21.5
	432999	BC284029	Hs.279903	21.5
	407663	NM_016429	Hs.37482	21.5
	446627	AJ273016	Hs.16725	21.5
	413605	BE152644	Hs.16725	21.5
55	427786	AW732802	Hs.21332	21.5
	456226		predicted exon	21.4
	422570		predicted exon	21.4
	457960	AA771881	Hs.298149	21.4
	400684		predicted exon	21.4
60	429943	H46986	Hs.31861	21.4
	442440	AF119912	Hs.258119	21.4
	446376	AA043332	Hs.196963	21.4
	400899	H59799	Hs.47644	21.4
	400304	AF060082	Hs.113261	21.4
65	412652	AJ071777	Hs.6774	21.4
	428373	AJ051656	Hs.183986	21.3
	416138	C18946	Hs.79026	21.3
	425184	BE778288	Hs.155048	21.3
	411028	AW813703	Hs.82741	21.3
70	417438	Z45969	Hs.82751	21.3
	417634	NM_004998	Hs.180714	21.2
	427767	AJ079283	Hs.180714	21.2
	433300	AA682307	Hs.469	21.2
	463061	AJ074259	Hs.146246	21.2
75	411939	AJ050585	Hs.233349	21.2
	435060	AA422719	Hs.162201	21.2
	432412	AA705049	Hs.162201	21.2
	407491	S82769	Hs.89526	21.1
	416980	NM_034494	Hs.188541	21.1
80	428254	BE101103	Hs.137840	21.1
	468188	AW297226	Hs.137840	21.1
	406215		predicted exon	21.1
	426461	AK000602	Hs.157938	21.1
	448296	BC522158	Hs.10940	21.1
	409415	AA579258	Hs.6083	21.1

5	408546	W49512	Ha.46348	bradykinin receptor B1	21.1
	450308	H52570	Ha.36888	WAP four-disulfide core domain 1	21.1
	439996	AF128347	Ha.204308	indolethyl-lysine N-methyltransferase	21.1
	438901	AF086834	Ha.29036	ESTs	21.1
	440500	AA72185	Ha.150308	ESTs	21.1
10	413101	BE062515	glc:RC1-ET03 14-310300-015-01 ET0314 Homo sapien	21.1	
	447452	BE119268	Ha.103480	ESTs	21.1
	412448	AI0768015	Ha.52127	ESTs	21.1
	418975	T75495	Ha.299890	ESTs	21.0
	454961	AW847807	glc:IL3-CT0213-19C020-040-E12 CT0213 Homo sapien	21.0	
15	401072			predicted exon	21.0
	401204			predicted exon	21.0
	433526	AF078859	Ha.86347	hypothetical protein	21.0
	418047	R37633	Ha.4847	ESTs	21.0
	443380	AI075478	Ha.135377	ESTs	21.0
20	427424	AA402463	Ha.113011	ESTs	21.0
	433412	AV853729	Ha.8185	CSG-44 protein; sulfide dehydrogenase like (yeast)	21.0
	422599	BE387202	Ha.118538	non-metastatic cells 1, protein (NM23A) expressed in	20.9
	433555	R93409	Ha.120759	ESTs	20.9
	413745	AW472592	Ha.75514	nucleoside phosphorylase	20.9
25	418674	T68672	glc:ly7.2h11.51 Stratogene ovary (337217) Homo sapien	20.9	
	452574	AF127461	Ha.35093	lymphoid blast crisis oncogene	20.9
	400332	S66407	Ha.248032	FLT4	20.9
	402421			predicted exon	20.9
	427138	N17624	Ha.173717	phosphatidic acid phosphatase type 2B	20.9
30	432038	AA524746	Ha.162210	ESTs	20.8
	423711	AF069194	Ha.131953	v-maf musculoaponeurotic fibrosarcoma (avian) oncoge	20.8
	402227			predicted exon	20.8
	405133			predicted exon	20.8
	436661	AI128270	Ha.128089	ESTs, Weakly similar to similar to collagen [C.olegana]	20.8
35	437836	BE269291	Ha.292458	ESTs	20.8
	437329	AA811977	Ha.291761	ESTs	20.8
	445830	R110451	Ha.42656	Homo sapiens cDNA FLJ12967 f1s, clone NT29M4002	20.8
	408234	AW615981	Ha.84398	CD74 antigen (Invariant polypeptide of major histocom	20.7
	421271	AW170057	Ha.133179	ESTs	20.7
40	400256			predicted exon	20.7
	414026	AA792576	Ha.4944	Homo sapiens cDNA FLJ12763 f1s, clone NT2RP2001	20.7
	456726	AL120077	Ha.122367	hsc70 (Drosophila) Ho 2 (Mayen)	20.7
	417707	AL036786	Ha.82425	actin related protein 2/3 complex, subunit 5 (16 kD)	20.7
	438713	H18902	Ha.6749	ESTs	20.7
45	460306	AL080080	Ha.24766	DKFZP564E1962 protein	20.7
	436956	AB199663	Ha.106249	ESTs	20.7
	433270			predicted exon	20.7
	414605	BE390440	glc:80128301F1 NH_MGC_44 Homo sapiens cDNA	20.7	
	401283			predicted exon	20.7
50	403703			predicted exon	20.6
	416969	AB15443	Ha.283404	organic cation transporter	20.6
	443400	AW391148	Ha.3593	ESTs	20.6
	447563	BE536115	Ha.160983	ESTs	20.6
	419784	H52299	Ha.75243	bromodomain-containing 2	20.6
55	405204	AA454801	Ha.43695	protein tyrosine phosphatase type IVA, member 3	20.6
	456507	AV095503	Ha.250991	ESTs	20.6
	429612	AF062649	Ha.262587	pituitary tumor-transforming 1	20.6
	413788	BE162391	Ha.272698	glc:PM2-HT0461-090100-002-04 HT0461 Homo sapie	20.6
	432140	AK000044		hypothetical protein FLJ20367	20.6
60	405842			predicted exon	20.4
	431582	F07136	Ha.261826	G protein-coupled receptor kinase 7	20.4
	442724	AA355526	Ha.159604	cysteinyl-IFNA synthetase	20.4
	417881	AA334561	Ha.82767	sperm specific antigen 2	20.4
	402946			predicted exon	20.4
65	411004	AW813242	glc:M3-STD191-402000-207-g10 ST0191 Homo sapie	20.4	
	436478	AA682622	glc:Z2009.s1 Sources_fetal_liver_spleen_INFLS_S1 Ho	20.4	
	447965	BE344271	Ha.288390	Homo sapiens cDNA: FLJ22795 f1s, clone KIAA2543	20.3
	433692	NM_004542	Ha.3436	deleted in oral cancer (mouse, homolog 1)	20.3
	423855	N73241	Ha.100001	soluble carrier family 17 (iodine phosphatidyl), member 1	20.3
70	449482	AI784288	Ha.28774	ESTs	20.3
	403007			predicted exon	20.3
	419942	U25138	Ha.33841	potassium large conductance calcium-activated channel	20.3
	426783	AB559308	Ha.39923	lectin, galactoside-binding, soluble, 7 (galactin 7)	20.3
	402986	BE234588	Ha.8456	chaperonin containing TCP1, subunit 2 (beta)	20.3
75	451375	AI792055	Ha.283902	Homo sapiens BAC clone RP11-481U13 from 2	20.3
	453566	AA246089	Ha.50841	ESTs, Weakly similar to trypsin [M.musculus]	20.3
	433090	AF700500	Ha.143552	immunization-uptake protein	20.3
	425553	AF045024	Ha.154320	ubiquitin-activating enzyme E1C (homologue to yeast	20.3
	412802	UA1518	Ha.74602	aquaporin 1 (channel-forming integral protein, 28kD)	20.3
80	409738	BE222975	Ha.55205	insulin induced gene 1	20.3
	428245	AF151048	Ha.183180	hypothetical protein	20.2
	412582	BE270631	Ha.74077	proteasome (prosome, macropain) subunit, alpha type, 6	20.2
	405207			predicted exon	20.2
	400931	AL122109	Ha.65735	Homo sapiens mRNA; cDNA DKFpZ344M1827 (from	20.2
	428436	NM_001955	Ha.2271	endothelin 1	20.2
	445918	AL135125	Ha.13913	KIAA1577 protein	20.2
	417821	BE245149	Ha.82643	protein tyrosine kinase 9	20.2

WO 02/102235

PCT/US02/19297

	429113	D28235	Ha.196384	prostaglandin-endoperoxide synthase 2 (prostaglandin G
	414811	AA148725	Ha.12969	hypothetical protein
	451546	AF051782	Ha.26584	Homo sapiens clone CDABP0036 mRNA sequence
	441999	A0372588	Ha.8022	TUS3A protein
	428811	AL039104	Ha.155557	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)
	411014	AW816072	gb:AF03-ST0226-070100-021-467 ST0226 Homo sapi	
	451400	BE150479	gb:U71-HT0413-210200-081-g05 HT0413 Homo sapi	
	458247	HA6243	Ha.110373	ESTs
	441633	AW555444	Ha.112242	ESTs
	427466	AA523543	Ha.7578	cellular retinoic acid-binding protein 1
	408593	M22406	gb:Human Intestinal mucin mRNA, partial cds, clone SM	
	402618			predicted exon
	403348			predicted exon
	400970			predicted exon
	414045	NM_002951	Ha.75722	rhodopsin II
	427169	AA358523	Ha.97549	EST
	405986			predicted exon
	445834	AI913290	Ha.145532	ESTs, Weakly similar to Gag polyprotein [Mus musculus
	425256	AA768797	Ha.152607	ESTs
	425383	DC8407	Ha.150507	Down syndrome critical region gene 1-like 1
	454590	AW097162	Ha.222095	Homo sapiens cDNA FLJ11572 fls, clone HEMBA100
	411529	AA034038	Ha.268537	Homo sapiens cDNA FLJ12527 fls, clone NTZRP2004
	425397	JA0408	Ha.155346	topoisomerase (DNA) II alpha (170KD)
	403234			predicted exon
	427257	AI201185	Ha.119164	ESTs
	402023			predicted exon
	449296	AL137257	Ha.23455	Homo sapiens mRNA; cDNA DKFZp434C1613 (from
	408704	M21565	Ha.529	myosin, heavy polypeptide 7, cardiac muscle, beta
	425083	AJ221774	Ha.142418	ESTs, Weakly similar to IFFL_HUMAN PROTEIN PH
	422112	BE040540	Ha.111783	Lamin protein
	413262	BE081659		gb:CMO-BT0915-140200-175-e06 BT0915 Homo sapi
	453702	AA037637	Ha.421128	ESTs
	403065			predicted exon
	446333	AI140956	Ha.263320	ESTs
	456994	AA383623	Ha.293916	ESTs
	458260	RA1782	Ha.22279	ESTs
	452386	BI001969	Ha.25267	retinoblastoma-binding protein 8
	422276	AF072873	Ha.142418	klizad (Drosophila) homolog 5
	441655	AA382307	Ha.255241	Homo sapiens cDNA: FLJ22898 fls, clone HS112044
	416786	AW565311	Ha.87016	ESTs
	406846	K33600	Ha.180255	major histocompatibility complex, class II, DR beta 1
	433053	BE401509	Ha.279552	glutathione S-transferase albumin 13 homolog
	414154	BE175454	Ha.75511	H-asparaginase amidohydrolase (acid cismidase)
	452321	AW544498	Ha.289052	Homo sapiens LENG8 mRNA, variant C, partial sequen
	445713	AW022025	Ha.232622	ESTs
	458827	AW670786	Ha.176470	Homo sapiens cDNA: FLJ22662 fls, clone HS08080
	414092	Z14244	Ha.175752	cytochrome c oxidase subunit VIII
	441730	AI243276	Ha.145017	ESTs
	420701	NA2919	Ha.88630	ESTs, Weakly similar to AC007226 1 R31665 2 [H.sapi
	403642			predicted exon
	408987	H55615		gb:y0311.1 Soares retina N2b5HR Homo sapiens cD
	445712	AW204789	Ha.209823	ESTs
	403266			predicted exon
	434439	AI022360	Ha.190583	ESTs
	404087			predicted exon
	455684	BE367300		gb:PM2-BT0348-161299-001-h10 BT0349 Homo sapi
	402387			predicted exon
	434633	AI189687	Ha.120915	ESTs
	408189	AA132637	Ha.15396	ESTs
	420080	M54055	Ha.54925	thymidylate dehydrogenase
	408682	AW291435	Ha.254591	ESTs
	403786			predicted exon
	416839	H64900	Ha.17882	ESTs
	434385	AA531546	Ha.259550	ESTs
	446845	AA343645	Ha.155103	ESTs
	425612	BE034257		gb:CMO-BN0103-180300-296-c04 BN0103 Homo sapi
	402620			predicted exon
	436098	R20597	Ha.5739	ESTs
	428974	AF368516	Ha.5454	chromosome 19 open reading frame 3
	447751	AA339041	Ha.24195	hypothetical protein FLJ22056
	451310	AW250651	Ha.26213	ESTs, Moderately similar to d4H47F3.3 [H.sapiens]
	438961	BE263127	Ha.283722	GTT1 protein
	452937	BE410390	Ha.289490	five-span transmembrane protein: MB3
	404850			predicted exon
	438360	H74145	Ha.268153	hypothetical protein FLJ10375
	436508	AW604381	Ha.121211	ESTs
	403486	BE062109	Ha.241551	ESTs
	407824	AA147894	Ha.9812	chloride channel, calcium activated, family member 2
	406388			predicted exon
	430204	AA618336	Ha.146137	ESTs, Weakly similar to putative [Colobus]
	457560	AB019304	Ha.163090	ESTs
	429521	BE348708	Ha.53949	ESTs
	429788	AW137722	Ha.246804	ESTs
	441473	AA834995	Ha.184846	ESTs, Weakly similar to R28930 1 [H.sapiens]

	411724	AAJ70689	Hs.71618	polyesterase (RNAI) [DNA directed] polyisoprene L7.	19.5
	450143	AU000593	Hs.50189	ESTs	19.5
	419687	AB388589	Hs.227699	ESTs. Weakly similar to Yhr2173 (Sc.cerevisiae)	19.5
5	421761	AN034966	Hs.5470	glycolipase M5B	19.5
	435055	AA002337	Hs.5422	glycoprotein M5B	19.5
	417412	U16896	Hs.82112	interleukin 1 receptor, type 1	19.4
	413826	BE299181	Hs.75864	CD151 antigen	19.4
	422387	AA1685823	Hs.115028	insulin-like growth factor binding protein 7	19.4
	427135	AF171265	Hs.8470	LT-R1 receptor	19.4
	404069	BE17892	Hs.6895	acid related protein 23 complex, subunit 3 (21 kD)	19.4
	432277	AB98790	Hs.181828	ESTs	19.4
	428044	AA043322	Hs.158455	RNA binding motif protein 3	19.4
	426044	AA256213	Hs.72010	ESTs	19.4
15	424897	DC32126	Hs.135364	frizzled-related protein	19.4
	424673	AA345051	Hs.294092	predicted exon	19.4
	403952			predicted exon	19.3
	403958			predicted exon	19.3
	433096	AU076803	Hs.282975	carboxylesterase 2 (intestinal, liver)	19.3
	400445	NM_012368	Hs.282874	oxytocin receptor, family 1, subfamily C, member 1	19.3
	417101	AA.041429	Hs.859222	family domain, immunoglobulin domain (Ig), short basic	19.3
	400445			predicted exon	19.3
	435801	LA134751	Hs.23450	mRNA for FLJ0022 protein	19.3
	435849	BE305242	Hs.112442	ESTs. Weakly similar to CLODE_HUMAN CLAUDIN-	19.3
	454181	AF177377		ghbCMA CT102-105899-0079 CT0126 Homo sap	19.3
	414807	AT379516	Hs.77348	human chondrocyte desmosomal desmoglein 16 (hMD)	19.3
	403525			predicted exon	19.3
	412921	H83393	Hs.109571	translocase of inner mitochondrial membrane 10 (yeast)	19.2
	419604	AA149588	Hs.79572	cathepsin D (lysosomal aspartic protease)	19.2
30	435857	AB27342	Hs.224601	predicted exon	19.2
	405951			predicted exon	19.2
	418901	RO8652	Hs.20205	hemoglobin, beta pseudogene 1	19.2
	423500	NM_003378	Hs.171014	VGF nerve growth factor inducible	19.2
	425590	AJ95468	Hs.155321	desmod filament structural protein 2, phakion	19.2
	425115	AA422028		phakion-like protein 1 (ScnMLP-51) Homo sapiens cDNA	19.2
	423420	BE382808	Hs.198629	KIAM119-1 Associated	19.2
	414428	BE299905	Hs.182625	VAMP (vesicle-associated membrane protein)-associate	19.2
	404501			predicted exon	19.2
	403951			predicted exon	19.2
	438363	BE74595	Hs.336	6-guananylatecyclase synthase	19.2
	405855	M21633	Hs.181244	major histocompatibility complex, class I, A	19.1
	438374	AA059591	Hs.101465	ESTs. Highly similar to CRIS1_HUMAN VOLTAGE-G	19.1
	411154	BE307870	Hs.75103	CRIS1-CT1052-021295-031-066 CT0552 Homo sap	19.1
	403221	AA355546	Hs.8904	lysofatty protein	19.1
45	412975	T70959	Hs.75795	clatrin (component 1) lys inhibitor, SP-40, 40, sulfate	19.1
	412633	AF001891	Hs.74304	predicted exon	19.1
	402071			predicted exon	19.1
	410387	AZ177367	Hs.47094	ESTs	19.1
	423981	D13958	Hs.133348	osteoblast specific factor 2 (osteocalcin I-like)	19.1
	470332	U73799		human glycine transferase (NAC, paraf. ctn)	19.1
	404034			predicted exon	19.1
	455534	XJ1195	Hs.100623	phospholipase C, beta 3, neighbor pseudogene	19.0
	405599	297332	Hs.16475	differentially expressed in FDCP (mouse) homing 6	19.0
	428410	BE266446	Hs.180372	CD24-like 1	19.0
	419811	AA323295		CD24-like 1 (homo sapiens) cDNA	19.0
	457352	AA292161	Hs.112589	homo sapiens CD24-like 1 NCL_CGAP_031 Homo sapiens cDNA-E	19.0
	417134	AA193348	Hs.55771	thymosin alpha chromosome 19, BAC C17-HSPC_204F	19.0
	417933	XJ3038	Hs.82962	thymosin alpha synthetase	19.0
	458588	AAU134832	Hs.242635	ESTs	19.0
	419604	DS051	Hs.7819	diacylglycerol binding inhibitor (GABA receptor modulator	19.0
	404919	AA291274	Hs.252825	predicted exon	18.9
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	18.9
	401747			predicted exon	18.9
	454209	AF179083		glutathione S-transferase 2 (HSP90-006-047 ST0065 Homo sap	18.9
	4264			predicted exon	18.9
65	426461	784155	Hs.15454	Homo sapiens cDNA: FLJ21351 fls, clone COL02762	18.8
	426499	A14937	Hs.11169	Gene 33A36-g	18.8
	404240			predicted exon	18.8
	439718	AA307634	Hs.5650	vascular protein binding 45B (zebra fish homolog)	18.8
	401789			predicted exon	18.8
	459592	AA54081	Hs.301469	ESTs	18.8
70	439739	AI195891	Hs.124454	ESTs	18.8
	427813	T74445		Homo sapiens clone 24415 mRNA sequence	18.8
	427940	295152	Hs.178595	mitogen-activated protein kinase 13	18.8
	434842	AF180893	Hs.250385	predicted exon	18.8
	411420	BE390852		predicted exon	18.8
75	419604	F39575	Hs.188128	ESTs. Moderately similar to ALUS_HUMAN 931 ALLU	18.8
	417022	NM_014737	Hs.80905	ras associated (RASGAP/GAP-5) domain family 2	18.8
	413531	AL039959	Hs.75415	DNA associated protein 2	18.7
	426861	BE131077	Hs.93135	ESTs	18.7
	421596	AF650342	Hs.100621	hTb RNA binding protein	18.7
80	434801	AA074748	Hs.9953	TYRO protein tyrosine kinase binding protein	18.7
	406754	AA477223	Hs.75922	brain protein 13	18.7
	400951			predicted exon	18.7
	426338	AB06742	Hs.134713	ESTs	18.7
	434169	AA883150	Hs.179724	ESTs	18.7

WO 02/102235

PCT/US02/19297

	424126	AA335635	Hs.99917	ESTs	18.7
	408473	BE259039	Hs.129593	Ewing sarcoma breakpoint region 1	18.7
	401962			predicted exon	18.7
5	447326	AW002262	Hs.201396	ESTs	18.7
	459053	A1807062	Hs.210361	ESTs	18.7
	403362			predicted exon	18.7
	4217897	T18997	Hs.180372	BCI 2.3a-1	18.7
	402061	H83363	Hs.109571	translocase of inner mitochondrial membrane 10 (yeast)	18.7
10	433785	BE044593	Hs.112704	ESTs	18.7
	404623			predicted exon	18.6
	422959	AA420450	Hs.202911	ESTs	18.6
	444071	AB27808	Hs.110524	ESTs	18.6
	410512	AA085603	Hs.260570	ESTs	18.6
15	440376	A024452	Hs.235816	ESTs	18.6
	457353	XS6633	Hs.245144	melanocortin 2 receptor (adrenocorticotrophic hormone)	18.6
	432749	NM_014438	Hs.278909	lactileukin-1 Superfamily e	18.6
	415602	F12920	Hs.185575	ESTs	18.6
	407891	AA486620	Hs.41135	endomucin-2	18.6
20	455910	Z47112		gbH5G1A.121 normalized infant brain cDNA Homo s	18.6
	428716	NM_006379	Hs.171921	sera domain, immunoglobulin domain (Ig), short basic	18.6
	444246	H63281	Hs.10710	hypothetical protein FLJ20417	18.6
	428125	AA393071	Hs.182579	leucine aminopeptidase	18.6
	406457			predicted exon	18.5
	446025	A1333070	Hs.156141	ESTs	18.5
25	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	18.5
	423103	AA322029		gb:EST24685 Corobolium II Homo sapiens cDNA 5' en	18.5
	443649	T89608	Hs.16691	ESTs	18.5
	419229	AJ311085	Hs.62406	Homo sapiens cDNA: FLJ22573 (a, clone H502387	18.5
30	411942	AW877515		gb:CD2-PT0010-250300-096-012 PT0010 Homo sapie	18.5
	442440	BE464435	Hs.146190	ESTs, Weakly similar to non-receptor protein tyrosine k	18.5
	454574	AW805109		gb:MR4-ST0117-070100-027-a04 ST0117 Homo sapie	18.5
	454377	AA078811		gb:7800C12 Chromosome 7 Fetal Brain cDNA Library	18.5
	422386	AF035337	Hs.115521	REY3 (yeast homolog), catalytic subunit of DNA p	18.5
35	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondroplasia, the	18.5
	420603	A8042636	Hs.4775	janetophlin 3	18.4
	401373			predicted exon	18.4
	402282			predicted exon	18.4
40	444118	AA458542	Hs.10326	coatamer protein complex, subunit epsilon	18.4
	421300	AW179023		gb:PMG-ST0035-170899-001-e06 ST0036 Homo sapie	18.4
	411236	AW833752		gb:QV4-TT0008-130101-077-b07 TT0008 Homo sapie	18.4
	431405	AJ470895	Hs.262574	ribosomal protein L10e	18.4
	441468	AT733249	Hs.126897	ESTs	18.4
	453994	BE180964	Hs.165590	ribosomal protein S13	18.4
45	444518	AI160278	Hs.146884	ESTs	18.4
	402407			predicted exon	18.4
	404270			predicted exon	18.4
	409103	AF261237	Hs.112208	XAGE-1 protein	18.4
50	415198	AW009400	Hs.943	natural killer cell transcript 4	18.3
	430771	BE387244	Hs.2684	flavin containing monooxygenase 4	18.3
	432636	AA340864	Hs.278582	ctadin 7	18.3
	433524	NM_014874	Hs.3363	KU402214 gene product	18.3
	415906	W70022		gb:GDS1610.1 Soares fetal_hear1 NBH19W Homo sa	18.3
55	401401	BE47878	Hs.99093	Homo sapiens chromosome 19, cosmid R28379	18.3
	420758	AW297536	Hs.33053	ESTs	18.3
	457520	AA553495	Hs.162264	ESTs	18.3
	432323	AK001409	Hs.274356	hypothetical protein FLJ10547	18.3
	404750			predicted exon	18.3
	450645	AI117441	Hs.25264	DKFZP44N126 protein	18.3
60	445180	AI299144	Hs.150787	ESTs	18.3
	419451	BE242781	Hs.288037	Homo sapiens cDNA FLJ12999 (a, clone NT2P3000	18.3
	401809			predicted exon	18.3
	458121	S42416	Hs.74647	Human T-cell receptor active alpha chain mRNA from	18.3
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174000 1 F-box protein Flx	18.3
65	448398	AA444555	Hs.170838	ESTs	18.3
	428145	BE243327	Hs.162656	chromosome 22 open reading frame 5	18.2
	445302	AK001537	Hs.12488	hypothetical protein FLJ10675	18.2
	407352	H47860		gb:gp70h12.1 Soares fetal liver spleen INFLS Homo s	18.2
	413190	AA151802	Hs.40388	adaptor-related protein complex 1, sigma 2 subunit	18.2
70	436371	AB271912	Hs.113912	ESTs	18.2
	400965			predicted exon	18.2
	433427	AB16449	Hs.171889	cholinephosphotransferase 1	18.2
	427604	AA776743	Hs.191589	ESTs	18.2
	426759	AE590401	Hs.121213	ESTs	18.2
75	423782	AW133866	Hs.746564	ESTs	18.1
	406826	AW1516005	Hs.84298	CD14 antigen (invariant polypeptide of major histocom	18.1
	406859	AA663985	Hs.277477	major histocompatibility complex, class I, C	18.1
	437453	AI761350	Hs.181391	hypothetical protein DKFZ-p761G2113	18.1
	409276	AW272097	Hs.778429	hepatocellular carcinoma-associated antigen 59	18.1
	449628	AW697676	Hs.197713	ESTs	18.1
80	421043	BE376455	Hs.89072	ESTs	18.1
	442344	AO22925	Hs.301212	ESTs	18.1
	440744	AL135424	Hs.3498	phosphatidylcholine 3-phosphate binding protein-1	18.1
	410682	AA724511	Hs.74427	p53-induced protein	18.1
	414500	W24087	Hs.76285	DKFZP564B167 protein	18.1

WO 02/102235

PCT/US02/19297

427272	NM_001096	Hs.174140	ATP citrate lyase	18.1
403664			predicted exon	18.1
433217	AB040914	Hs.278628	KIAA1481 protein	18.1
427902	A0809202	Hs.208343	ESTs, Weakly similar to cerebroside sulfotransferase (H	18.1
449586	A863918	Hs.193078	ESTs	18.1
430826	U10061	Hs.246019	POU domain, class 4, transcription factor 3	18.1
414195	BE263283	Hs.6501144581F2 NH ₂ MG_C, 19 Homo sapiens cDNA	18.1	
416305	AU076628	Hs.79187	glycoside virus and adenovirus receptor	18.1
411086	BC247593	Hs.124573	ESTs	18.1
419407	AW103577	Hs.41502	Homo sapiens cDNA: FLJ21276 fls, clone COL01629	18.1
407636	A0805087	Hs.68260	phospholamban	18.1
449560	A640623	Hs.252720	ESTs	18.1
417286	AA122237	Hs.81874	microsomal glutathione S-transferase 2	18.0
455515			predicted exon	18.0
433319	AW016401	Hs.233476	ESTs	18.0
419387	BE279396	Hs.90107	cell membrane glycoprotein, 110000Da (surface antiq	18.0
414015	AA340987	Hs.75993	prolylcarboxypeptidase (angiotensinase C)	18.0
447778	BE260692	Hs.71190	ESTs	18.0
435523	T52645	Hs.11393	high affinity immunoglobulin epsilon receptor beta sub	18.0
429230	AF088091	Hs.198274	NAOH dehydrogenase (xanthine) 1 beta subcomplex	18.0
457822	AA870001	Hs.150319	ESTs	18.0
442424	A342715	Hs.129569	ESTs, Moderately similar to U34057 hypothetical prote	18.0
418394	AF 132818	Hs.84728	Kruppel-like factor 5 (retictrial)	18.0
413477	AB15825	Hs.48756	ESTs, Moderately similar to neuronal-STOP protein (M	18.0
450277			predicted exon	18.0
450192	AA283143	Hs.24595	RAD51-interacting protein	18.0
442191	W95186	Hs.8136	endothelial PAS domain protein 1	18.0
429460	A1971311	Hs.253694	ESTs, Weakly similar to alternatively spliced product v	18.0
403744	AA554942	Hs.279860	hypothetical protein FLJ20000	17.9
425205	NM_005854	Hs.155106	receptor (calcitonin) activity modifying protein 2	17.9
414387	AL043146	Hs.188257	ESTs	17.9
411811	AW695470		gb:PMAS00016-106500-004409 SN0016 Homo sapie	17.9
433882	J90441	Hs.3622	procollagen-proline, 2-oxoglutarate 4-oxoglutarate (pro	17.9
414333	BE274897		gb:U01122559F1 NH ₂ MG_C, 20 Homo sapiens cDNA	17.9
433542	AA687376	Hs.269533	ESTs	17.9
433263			predicted exon	17.9
412088	A1689498	Hs.108932	ESTs	17.9
450506	NM_004460	Hs.418	fibroblast activation protein, alpha	17.9
404763			predicted exon	17.9
454633	AW611380		gb:3-ST0143-290999-019-050 ST0143 Homo sapien	17.9
440788	AB066984	Hs.128577	ESTs	17.9
411800	N39042	Hs.5184	TH1 dirosophila homolog	17.9
441361	BE263308	Hs.7797	TERF1 (TRF)-interacting nuclear factor 2	17.9
422033	AW245905	Hs.110903	claudin 5 (transmembrane protein deleted in velocardiof	17.8
465333			predicted exon	17.8
408297	R17710	Hs.113314	ESTs	17.8
403036			predicted exon	17.8
417924	AU077231	Hs.82932	cyclin D1 (PRAD1; parathyroid adenomatosis 1)	17.8
417091	AA193283	Hs.291990	ESTs	17.8
447879	AB207857	Hs.74161	KIAA0097 gene product	17.8
438397	AA306478	Hs.123206	ESTs	17.8
439948	AA702675	Hs.114135	ESTs	17.8
450273	AW299454	Hs.24743	hypothetical protein FLJ20171	17.8
435989	W85773	Hs.191386	ESTs	17.8
427031	AA397601	Hs.126147	ESTs	17.8
454505	AW801355		gb:U15-UM0057-240300-050-a01 UM0067 Homo sapit	17.8
403447			predicted exon	17.8
433297	AV588581	Hs.826533	ESTs	17.8
443326	BE156494	Hs.188478	ESTs	17.8
448283	A1304062	Hs.182799	ribosomal protein L12	17.8
468067	AA389603	Hs.36752	Homo sapiens cDNA: FLJ22834 fls, clone KIAA4314	17.8
452359	BE187229	Hs.29206	Homo sapiens clone 24659 mRNA sequence	17.8
424086	AA254929		gb:U559106.f1 Soares_NhlhMPV_S1 Homo sapiens cDN	17.7
450811	AA011586	Hs.272097	ESTs	17.7
410342	R31350	Hs.743	Fc fragment of IgE, high affinity I ₁ receptor for gamma	17.7
407082	247056		gb:Human perid cDNA sequence, farnesyl pyrophosph	17.7
415271	Y84232	Hs.78335	microtubule-associated protein, RPIED family, member	17.7
417415	AA197072	Hs.86992	Human DNA sequence from clone RP11-243J16 on chr	17.7
408937	AA210734	Hs.291386	ESTs	17.7
433489	AA593498		gb:nc27b06.s1 NCL_GCAP_Gas1 Homo sapiens cDNA	17.7
469536	A1254723	Hs.145496	ESTs	17.7
428500	A3115396	Hs.194541	delta-6 fatty acid desaturase	17.7
433463	R41963	Hs.4197	ESTs	17.7
406637			predicted exon	17.7
410003	AA079487		gb:nc27b06.s1 Stratagene colon 1IT29 (93/221) Homo	17.7
440857	AA307608	Hs.135565	ESTs	17.7
451072	AA013451	Hs.117029	ESTs	17.7
419693	A1750878	Hs.87409	thrombospondin 1	17.7
443624	BE616129	Hs.9651	related RAS viral (p-ras) oncogene homolog	17.6
422626	AA344832	Hs.118786	modiolobionin 2A	17.6
410756	A0307320	Hs.62169	KIAA1399 protein	17.6
436521	A0266254	Hs.132929	ESTs	17.6
453317	NM_002277	Hs.41696	keratin, hair, acidic,1	17.6

WO 02/102235

PCT/US02/19297

458628	AF156888	Hs.104827	LIM homeobox protein 3	17.8
421486	AW088800	Hs.104869	hypothetical protein DKFZp762E1312	17.6
428834	AW899713	Hs.103338	ESTs	17.6
451419	R38309	Hs.174389	EST	17.6
448413	AT745379	Hs.42911	ESTs	17.6
424233	AA338791	Hs.146763	nucleon polypeptide associated complex alpha polypept	17.6
429343	AF153570	Hs.135758	polymerase (DNA-directed) kappa	17.5
439423	BE536678	Hs.147099	ESTs	17.5
434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	17.6
408248	MS5859	Hs.43945	L13 protein	17.5
441579	AW468847	Hs.127194	ESTs	17.5
420867	NM_014183	Hs.100002	HSPC162 protein	17.5
435380	AL079547	Hs.14485	ESTs	17.5
400202			predicted exon	17.5
410168	AF038185	Hs.65187	Homo sapiens clone 23700 mRNA sequence	17.5
409532	AJ375750	Hs.57000	adaptor-related protein complex 1, sigma 1 subunit	17.5
425563	AF084199	Hs.299837	ESTs	17.5
404075	AB078711	Hs.128343	ESTs	17.5
452767	AW014195	Hs.61472	ESTs, weakly similar to unknown [S.cerevisiae]	17.5
410870	AI133096	Hs.84593	ATP synthase, F1-transporting, mitochondrial F1F0, su	17.4
419800	AA448958	Hs.91481	NEU1 protein	17.4
419588	AI347205	Hs.91375	Human clone Z3614 mRNA sequence	17.4
428975	NM_004672	Hs.194694	mitogen-activated protein kinase kinase kinase 6	17.4
448028	AJ59280	Hs.5394	Homo sapiens cDNA FLJ11743 flt, clone HEMBA100	17.4
403924			predicted exon	17.4
419889	AF251600		gbac10412.rTNCI_GCAP_GCB1 Homo sapiens cDNA	17.4
405023	AW088800	Hs.104859	hypothetical protein DKFZp762E1312	17.4
426055	AK2049		gtyr55g01.01 Scarsa, placenta, 2h9hweh2c_2h9h9p0	17.4
453109	AI333288	Hs.301854	Homo sapiens PTC0412 mRNA, complete cds	17.4
455132	AW857955		gbtPMO-CT0325-151299-002-A12 CT0325 Homo sapi	17.4
442932	AA457211	Hs.8858	transmembrane adjacent to zinc finger domain, 1A	17.4
432035	AA401039	Hs.2393	protein phosphatase 4 (formerly X), catalytic subunit	17.3
444602	BE213613	Hs.11538	actin related protein 2/3 complex, subunit 1A (41 kD)	17.3
417935	FS3387	Hs.170044	ESTs	17.3
430050	AA400993	Hs.227913	AP5-like 1	17.3
442772	BE288912	Hs.14501	hematopoietic cell-specific Lyn substrate 1	17.3
425995	Y87330	Hs.81255	G100 calcium-binding protein A4 [calcium protein, cdy	17.3
419564	DE1467	Hs.80520	guanine nucleotide exchange factor for Rap1, R-Mas-re	17.3
437418	AA478954	Hs.59459	ESTs	17.3
447255	AB84908	Hs.158907	ESTs	17.3
402203			predicted exon	17.3
417811	AW953983		gbtRC1-EN0035-130400-013-a04 EN0035 Homo sapie	17.3
426590	AA381861	Hs.119878	ESTs	17.3
445183	AA020880	Hs.25282	Homo sapiens cDNA FLJ13603 flt, clone PLACE1010	17.3
445017	AJ205483	Hs.178580	ESTs	17.3
438558	AJ222058	Hs.125571	ESTs	17.3
442238	AW135374	Hs.270945	ESTs	17.3
443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 flt, clone NT2RP3002	17.3
442809	AL020995	Hs.8518	selenoprotein N	17.2
415591	AA091976	Hs.79387	proteasome (prosome, macropain) 26S subunit, ATPase	17.2
403874			predicted exon	17.2
430514	AA318501	Hs.241587	megakaryocyte-enhanced gene transcript 1 protein	17.2
445850	AW857404		gbtCMG-CT0313-291199-046-c11 CT0313 Homo sapie	17.2
434850	R13052	Hs.3994	Homo sapiens clone 24877 mRNA sequence	17.2
422527	BE338657	Hs.118787	transforming growth factor, beta-induced, 68kD	17.2
414364	D38521	Hs.75935	KIAA0077 protein	17.2
409119	AA531133	Hs.4253	G protein-coupled receptor 44	17.2
425840	U34051	Hs.295204	ESTs, highly similar to CDG8_HUMAN CYCLIN-DE	17.2
430444	BE247571	Hs.115827	nit protein 2	17.2
401657			predicted exon	17.2
448763	AB221212	Hs.118241	ESTs	17.2
409601	AF237821	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	17.2
449838	AB585058	Hs.281328	ESTs	17.2
444958	AW252643	Hs.157047	ESTs	17.2
429678	AA249027	Hs.241507	ribosomal protein S6	17.2
453043	AW135440	Hs.224277	ESTs	17.2
458640	AJ284935		gbtgs55g09.x1 NCI_LGAP_Cc8 Homo sapiens cDNA	17.1
455329	T41418		gbtgs fls_1b11TV Outward Alu-primered hncDNA flaser	17.1
414635	BS3892	Hs.77462	DNA (cytosine-5)-methyltransferase 1	17.1
403962			predicted exon	17.1
411651	AW855392		gbtCMG-CT0275-191099-024-e12 CT0275 Homo sapie	17.1
404097			predicted exon	17.1
447253	R09016		gbyr610.01 Scarsa adult brain N2B4H55Y Homo s	17.1
430024	AB08780	Hs.227730	integrin, alpha 6	17.1
412828	AI133396	Hs.74621	prion protein (p27-30) (Creutzfeldt-Jakob disease, Gerst	17.1
444658	AW181915	Hs.165892	ESTs	17.1
420680	X38964	Hs.123538	regulatory factor X, 1 (influences HLA class II expressi	17.1
448912	X30775	Hs.22140	DMB8 antigen	17.0
431777	AA570296	Hs.105470	found in inflammatory zone 1	17.0
422007	AJ739435	Hs.391958	ESTs	17.0
4043051			predicted exon	17.0
422427			predicted exon	17.0
417408	F17211	Hs.86092	Human DNA sequence from clone RP11-243J16 on chr	17.0
450598	AF151076	Hs.25199	hypothetical protein	17.0

WO 02/102235

PCT/US02/19297

5	421121	AA459028	Ha.86228	TRAD3 protein	17.0
	458488	AJ005955	Ha.208564	ESTs	17.0
	471758	AW865223	Ha.110062	ESTs, Weakly similar to AC/R3_HUMAN 30 KD ADIP	17.0
	493318	AW837046	Ha.6527	G-protein-coupled receptor 56	17.0
10	426758	AA433988	Ha.38502	Homo sapiens cDNA FLJ14303 fa, clone PLACE2000	17.0
	447572	AJ531546	Ha.159732	ESTs	17.0
	434424	AA633516	Ha.157201	ESTs	17.0
	400994	U66964	Ha.57735	cosyl LDL receptor; SREC	17.0
15	408927	AW299580	Ha.255453	ESTs	17.0
	433903	AA534163	Ha.5478	serine protease inhibitor, Kazal type, 5	17.0
	454466	AB864138	Ha.278856	Homo sapiens mRNA for KIAA1576 protein, partial cd	17.0
	429996	AW958304	Ha.173108	Homo sapiens cDNA: FLJ21897 fa, clone HEP30447,	17.0
20	436659	AJ217900	Ha.144464	ESTs	17.0
	422731	AL138411		gb:DKFZp434A1129_r1 434 (synonym: hies-5) Homo s	17.0
	425294	AJ485971	Ha.196793	KIAA0750 gene product	17.0
	429847	BE766941	Ha.279554	prolactinase (prolactin, macropain) 26S subunit, non-AT	16.9
25	416977	AW130242	Ha.263476	ESTs	16.9
	406827	AA871409	Ha.84296	CD74 antigen (invariant polypeptide of major histocom	16.9
	453756	U63527		gb:HSU83527 Human testis brain (M.Lovett) Homo sap	16.9
	431314	AJ732204	Ha.105423	ESTs	16.9
30	423185	BE299590	Ha.125078	omithine decarboxylase antizyme 1	16.9
	435086	AW975243	Ha.122596	ESTs	16.9
	447383	N24231		gb:yr22a11.1r1 Soares melanocytes 2N6HM Homo sapie	16.9
	455281	RI1525	Ha.21330	ESTs	16.9
35	456327	U68741	Ha.38774	ESTs	16.9
	450594	K10336		gb:yr51g04.1r1 Soares melanocytes 2N6HM Homo sapie	16.9
	428177	AA423957	Ha.178113	ESTs, Moderately similar to kinesin like protein 9 [Mun	16.9
	453260	AJ466520	Ha.127619	chromosome 11 open reading frame 15	16.9
40	419294	AF061730	Ha.83354	protein associated with PRK1	16.9
	445646	BE157587	Ha.159528	ESTs	16.9
	421100	AW351639	Ha.124650	Homo sapiens cDNA: FLJ21783 fa, clone COLF6967	16.9
	458993	BE179095		gb:RCD-H10615-140000-021-006 HT0613 Homo sapie	16.9
45	453375	BE251770		gb:SI0112470F1 NH_MGC_15 Homo sapiens cDNA	16.9
	454803	AW960148		gb:RCD-CT0375-290100-032-b10 CT0375 Homo sapie	16.9
	445474	AJ240014		ESTs	16.9
	443196	AJ039813	Ha.259558	ESTs	16.9
50	441557	AW462947	Ha.275482	ESTs	16.9
	420266	AF1453	Ha.39398	soluble carrier family 2 (facilitated glucose transporter),	16.9
	442202	BE272962	Ha.106534	Homo sapiens cDNA: FLJ23625 fa, clone HS06009	16.9
	415913	AW934714		gb:RCD-CT0001-031259-011-a11 DT0001 Homo sapie	16.9
55	419355	AA428520	Ha.30051	progestagen binding protein	16.9
	452975	U65521	Ha.59469	desferrioxamine cell protein	16.9
	422625	AJ760095	Ha.109414	ESTs	16.8
	453718	AL119317	Ha.120330	phospholipase A2, group VI (cytosolic, calcium-indepe	16.8
60	437270	RI8067	Ha.111282	ESTs, Weakly similar to cleft lip and palate transmemb	16.8
	403607	AW135955	Ha.245783	ESTs	16.8
	403954	AJ304740	Ha.25991	receptor (calcitonin) activity modifying protein 3	16.8
	402968			predicted exon	16.6
65	445555	VZ2050	Ha.21299	ESTs, Weakly similar to AF151840 1 CQ-82 protein [H	16.8
	410584	AJ081600	Ha.170298	ESTs	16.8
	427669	AJ355105	Ha.123164	ESTs, Weakly similar to match to ESTs AA667999.H.	16.8
	447659	AW139113	Ha.154307	ESTs	16.8
70	458025	AJ275405		gb:gl33c10.x1 Soares_NIHMHp_S1 Homo sapiens cDN	16.8
	445614	AW607653	Ha.110675	apolipoprotein C-VI	16.8
	454610	AW610224		gb:MR4-ST0125-021199-017-e07 ST0125 Homo sapie	16.8
	445933	AJ074146	Ha.23467	hypothetical protein FLJ10633	16.8
75	422105	AJ929700	Ha.111680	endosulfine alpha	16.8
	444788	AJ871122	Ha.202821	ESTs	16.8
	414057	AJ915559	Ha.75730	signal recognition particle receptor (docking protein)	16.8
	403622	AW609718	Ha.57079	Homo sapiens cDNA FLJ13267 fa, clone CVARC1900	16.8
80	433379	AA568398	Ha.159022	ESTs	16.8
	441552	AA937975		glucoc08e12a1 NCL_GCAP_G0B1 Homo sapiens cDN	16.8
	403582			predicted exon	16.8
	433671	WZ2410	Ha.205555	ESTs	16.8
85	435009	AF065332	Ha.58314	ESTs	16.8
	431639	AK000680	Ha.266175	phosphoprotein associated with GEMs	16.8
	430129	BE301708	Ha.233955	hypothetical protein FLJ20401	16.8
	401465			predicted exon	16.8
90	446915	AA194422	Ha.23564	myosin VI	16.8
	410251	AF145713	Ha.51490	schwannomin interacting protein 1	16.8
	427199	BE244219	Ha.102457	padilin	16.7
	400489	AJ897990	Ha.224375	ESTs	16.7
95	401085	AW002628		gb:RCS-RT0552-266100-011-402 B10552 Homo sapie	16.7
	447274	BE171725		gb:RI0441950F1 NH_MGC_65 Homo sapiens cDNA	16.7
	404881			predicted exon	16.7
	440572	AJ243445	Ha.189554	ESTs	16.7
100	415440	AJ020693	Ha.30415	KIAA0882 protein	16.7
	443406	AJ056238	Ha.143315	ESTs	16.7
	457901	AW207023	Ha.250497	ESTs, Highly similar to dJ74522.1 [Hsapiens]	16.7
	443634	T0856	Ha.16561	HSPC141 protein	16.6
105	407229	AJ076350	Ha.57845	leucocyte immunoglobulin-like receptor, subfamily B (16.6
	419147			predicted exon	16.6
	429523	AK000788	Ha.205280	Homo sapiens cDNA FLJ20781 fa, clone COL04235	16.6

WO 02/102235

PCT/US02/19297

	432645	AI089751	Hs.150378	ESTs	16.6
	430245			predicted exon	16.6
	404971			predicted exon	16.6
5	422954	AW598605	Hs.32399	ESTs, Weakly similar to Ena-VASP like prot	16.6
	415042	NM_006759	Hs.77837	UDP-glucose pyrophosphorylase 2	16.6
	432201	AJ353613	Hs.135657	ESTs	16.6
	466993	AL134377	Hs.200307	ESTs	16.6
	456525	AW468393	Hs.100000	S100 calcium-binding protein A8 (calgranulin A)	16.6
10	444000	AA340277	Hs.10248	Homo sapiens cDNA FLJ20467 fs, clone COL09512	16.6
	428928	BE466838	Hs.194657	cachectin 1, type 1, E-cadherin (epithelial)	16.6
	448199	AJ933278	Hs.170557	ESTs	16.6
	443422	R10288	Hs.301529	ESTs	16.6
	401117			predicted exon	16.6
	400513			predicted exon	16.6
15	431214	AA294921	Hs.263811	ret-1 similar leukemia viral oncogene homolog B (ras re	16.6
	431849	AL133077	Hs.266746	Homo sapiens cDNA FLJ22615 fs, clone HS05118	16.5
	421335	X98977	Hs.103505	ARF component B	16.5
	427154	AL137262	Hs.288991	Homo sapiens cDNA FLJ22523 fs, clone HRC12507	16.5
20	401010			predicted exon	16.5
	433578	BE512828	Hs.5273	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (Dk	16.5
	401589			predicted exon	16.5
	402538			predicted exon	16.5
	430478	NM_014349	Hs.241535	TNF-inducible protein CG12-1	16.5
25	431623	DK3880	Hs.5719	chromosome condensation-related SMC-associated pro	16.5
	401244			predicted exon	16.5
	416167	AA180764	Hs.26410	ESTs	16.5
	438291	BE514605	Hs.289092	Homo sapiens cDNA FLJ22380 fs, clone HRC07453,	16.5
	426183			predicted exon	16.5
30	433480	AJ271643	Hs.67469	putative acid-sensing ion channel	16.5
	456691	AJ023428	Hs.206696	ESTs	16.5
	418332	R34978	Hs.78293	ESTs	16.5
	444052	AA356760		gbc:EST57699 Fetal lung II Homo sapiens cDNA 5' end	16.5
	444659	AW449137	Hs.157487	ESTs	16.5
35	437152	AW975786	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous to yse	16.5
	400891			predicted exon	16.5
	448372	AW445166	Hs.170802	ESTs	16.5
	425798	AA364032		gbc:EST74529 Pituitary gland II Homo sapiens cDNA 5' en	16.5
	425233	AL157476	Hs.32913	Homo sapiens mRNA; cDNA DKFP151082 (non c	16.5
40	420746	AW195932	Hs.197488	ESTs	16.4
	414717	BE271039	Hs.77060	proteasome (prosome, macropain) subunit, beta type, 6	16.4
	407277			predicted exon	16.4
	422691	NM_003385	Hs.119251	ubiquitin-cytochrome c reductase core protein I	16.4
	406539			predicted exon	16.4
45	414444	BE298594		gbc:591119754F1 NIH_MGC_17 Homo sapiens cDNA	16.4
	456146	AL034349	Hs.73005	protein tyrosine phosphatase, receptor type, K	16.4
	414610	BE388044		gbc:591253747F1 NIH_MGC_44 Homo sapiens cDNA	16.4
	414387	AL078459	Hs.289109	dimethylarginine dimethylaminohydrolase 1	16.4
	401268			predicted exon	16.4
	403613			predicted exon	16.4
50	414203	BE265170		gbc:591150419F1 NIH_MGC_19 Homo sapiens cDNA	16.4
	454315	AW373564	Hs.751928	nuclear pore complex interacting protein	16.4
	452114	N22857	Hs.8236	ESTs	16.4
	404638			predicted exon	16.4
	404600			predicted exon	16.3
55	448855	AF373814	Hs.22316	Homo sapiens clone 24619 mRNA sequence	16.3
	406829	AW277078	Hs.161165	catenylase transition elongation factor 1 alpha 1	16.3
	459597	BE516202	Hs.21497	Homo sapiens mRNA for FLJ00042 protein, partial cds	16.3
	449966	H03642	Hs.37845	ESTs	16.3
60	402585			predicted exon	16.3
	436038	AJ078428	Hs.58785	ESTs	16.3
	401492			predicted exon	16.3
	412288	NM_003005	Hs.73800	selectin P (granule membrane protein 140kD, antigen C	16.3
	405088			predicted exon	16.3
65	437345	BE269622	Hs.55556	NADH dehydrogenase (ubiquinone) 1, alpha/beta subco	16.3
	432300	BE440142	Hs.2943	signal recognition protein 15kD	16.3
	419596	BE379320	Hs.31448	MKP-1 like protein tyrosine phosphatase	16.3
	428801	AW277121	Hs.254881	ESTs	16.3
	431394	AK020032	Hs.252361	HERV41 LTR-associated 2	16.3
70	412998	BE119681	Hs.5019	Homo sapiens cDNA FLJ12288 fs, clone COL01927	16.3
	439538	AL147392	Hs.124607	ESTs	16.3
	418844	M52982	Hs.1200	arachidonate 12-lipoxygenase	16.3
	4446081	AA972412	Hs.13755	E-box and WD-40 domain protein 2	16.3
	443534	AW75123		gbc:AV0604x1 Soares_Atlas_Avnc_ajlconc_1NFLS_S1 H	16.3
	459510	AA074706		gbc:7570102 Chromosome 7 Fetal Brain cDNA Library	16.3
75	450517	AJ523755	Hs.59236	ESTs, Weakly similar to E3504B ankyrin 1, erythrocyte	16.3
	451938	AJ364365	Hs.16697	down-regulator of transcription 1, TBP-binding (negativ	16.3
	454478	AW080749		gbc:DV1-UM0105-IR0400-162-110 UM0105 Homo sap	16.2
	427214	AA412048	Hs.279574	CD3-30 protein cell death-regulatory protein GRIM19	16.2
	405880			predicted exon	16.2
80	409452	BE336714	Hs.289271	cytochrome c-1	16.2
	415841	N33878	Hs.245456	heterogeneous nuclear ribonucleoprotein A1	16.2
	456710	AW608556		gbc:AV060855 GLC Homo sapiens cDNA clone GLCG	16.2
	402657	AJ001670	Hs.25277	hypothetical protein FLJ27055	16.2
	404230			predicted exon	16.2

WO 02/102235

PCT/US02/19297

5	436471	W08639	Hs.58033	ESTs	16.2
	400646			predicted exon	16.2
	426797	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKF-Zp586032.4 (from c	16.2
	416272	AA178882		gibzp36b09.1 Stratagene muscle 937209 Homo sapiens	16.2
	444465	A200592	Hs.143643	ESTs	16.2
10	437257	AF030987		gibHomo sapiens K048 autoantigen related protein 1 (K	16.2
	447775	BE179318		gibJRC1-HT0615-250300-021-g05 HT0615 Homo sapie	16.2
	400383			predicted exon	16.2
	444140	AV548089	Hs.262383	ESTs	16.2
	446102	AY168067	Hs.252996	ESTs	16.2
15	116475	T0226		gibY2902.s1 Soares fetal liver spleen INFLS Homo s	16.2
	430763	AW971246	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	16.2
	414070	AW963783		gibEST1375855 MAGE resequences, MAGI Homo sap	16.2
	444263	A115891	Hs.154036	ESTs	16.2
	406559	X32715	Hs.3057	zinc finger protein 74 (Cux5)	16.2
20	409427	AW386668		gibJRC2-ST0103-071259-013-06 ST01068 Homo sapie	16.2
	409417	AA156247	Hs.299806	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFA	16.2
	435380	AA479001	Hs.192221	ESTs	16.2
	406752	A1255596	Hs.217453	anemia A2	16.2
	409506	F12200	Hs.5511	chromosome 21 open reading frame 59	16.2
25	417551	A1816201	Hs.82273	hypothetical protein	16.2
	441252	AW350001	Hs.163047	ESTs, Weakly similar to unnamed protein product (Hs	16.2
	419508	ALJ37237	Hs.91556	transmembrane 9 superfamily member 1	16.1
	435894	A1520819	Hs.300431	ESTs	16.1
	451257	AK002165	Hs.25194	hypothetical protein FLJ11296	16.1
30	412459	AW956516	Hs.11238	KIAA0622 protein; Drosophila 'multigene esters' (Mest)	16.1
	433355	A1808235		gibw44e01.x1 Soares_NFL_T_GG_C_S1 Homo sapie	16.1
	4158116	A186408	Hs.204756	ESTs, Weakly similar to B49013 proline-rich proteoly	16.1
	438765	A031868	Hs.132554	ESTs	16.1
	424470	BE244251	Hs.5515	nuclear RNA export factor 1	16.1
35	416154	H27114	Hs.301212	ESTs	16.1
	445702	R44518	Hs.143456	ESTs	16.1
	414222	AL135173	Hs.575	corbillo dehydrogenase	16.1
	434122	A006656	Hs.206022	ESTs, Weakly similar to Pro-Pol-4UTPase polyprotein	16.1
	448848	BE614345	Hs.159089	ESTs	16.1
40	459394	W28506		gb491 Human retina cDNA randomly primed sub libra	16.1
	445867	A263105	Hs.146657	ESTs	16.1
	412332	AW937651	Hs.286324	Homo sapiens cDNA FLJ13283 fs, clone C/ARC1901	16.1
	403912			predicted exon	16.1
	441446	RS6269	Hs.28714	ESTs	16.1
45	403163			predicted exon	16.0
	444507	AW772550	Hs.148585	ESTs	16.0
	421546	RS6629	Hs.105773	hypothetical protein FLJ20625	16.0
	437513	AW410681	Hs.5548	proteasome (prosome, macropain) 26S subunit, non-AT	16.0
	407762	AA673581	Hs.13328	ESTs	16.0
50	447353	A004215	Hs.205614	Homo sapiens cDNA: FLJ22343 fs, clone HRC05043	16.0
	357598	AJ001342	Hs.14570	Homo sapiens cDNA: FLJ22635 fs, clone HRC12856	16.0
	421449	AA713451	Hs.291501	ESTs	16.0
	418323	NM_002118	Hs.11162	major histocompatibility complex, class II, DM beta	16.0
	447787	BE520108		gib501453015F1 NH_MGC_59 Homo sapiens cDNA	16.0
55	422716	A1702835	Hs.124475	ESTs	16.0
	433568	BE241880	Hs.10025	cathelin C	16.0
	417908	AA207221		gibzq5904.s1 Stratagene neuroepithelium (537231) Ho	16.0
	438842	AA810131	Hs.123317	ESTs	16.0
	403268	X06265	Hs.149539	integrin, alpha 5 (betaonectin receptor, alpha polypep	16.0
60	458825	H57220	Hs.146406	niflamine 1	16.0
	431360	NM_000427	Hs.251680	lorotidin	16.0
	414295	BE257834		gib501124428F1 NH_MGC_8 Homo sapiens cDNA c	16.0
	440371	A0040481	Hs.130798	ESTs	16.0
	420375	AW513651	Hs.270446	ESTs	16.0
70	413468	BE144017	Hs.184993	transcription elongation factor B (SII), polypeptide 1 (16.0
	445757	A1380107	Hs.158954	ESTs	16.0
	418008	W56044	Hs.211596	Homo sapiens cDNA: FLJ23378 fs, clone HEP16248	16.0
	442429			predicted exon	16.0
	458401	AW236635	Hs.172154	ESTs	16.0
75	412955	BE241849	Hs.75082	ras homolog gene family, member G (rho G)	15.9
	423072	A1792946	Hs.123116	solute carrier family 12 (sodium/potassium/chloride tran	15.9
	444954	A1924975	Hs.121553	eukaryotic translation initiation factor 2, subunit 2 (beta	15.9
	449203	AE22351	Hs.248675	ESTs	15.9
	435729	BE246866	Hs.275017	EST	15.9
80	438575	BE304709	Hs.145550	myosin, heavy polypeptide 5, non-muscle	15.9
	413047	HO2209		gibY38C09.1 Soares placenta Nb2HP Homo sapiens cD	15.9
	425957	AW000096	Hs.164946	hypothetical protein FLJ20079	15.9
	446853	AW514370	Hs.254520	ESTs	15.9
	449554	AL044952	Hs.21453	Homo sapiens mRNA for inositol 1,4,5-trisphosphate 3	15.9
	455540	BE064069		gibQV3 BT0296 010300-111-c04 BT0296 Homo sapie	15.9
	4434545	AA730407	Hs.159156	prolactinogen 11	15.9
	418512	AW498174	Hs.599561	claycollyerol human, zeta (104K)	15.9
	411551	AW851309		gibJL3-C10220-170200-057-C11 C10220 Homo sapie	15.9
	446725	AW300144	Hs.209209	Homo sapiens cDNA FLJ11629 fs, clone HEMBA100	15.9
	410748	BE383816	Hs.135005	ESTs, Highly similar to HG115G20.2 (H sapiens)	15.9
	449618	A1074459	Hs.143365	Homo sapiens cDNA FLJ12815 fs, clone N729F2002	15.9
	429637	AW295451	Hs.24035	ESTs	15.9
	424012	AW368377	Hs.137599	tumor protein G3 kDa with strong homology to p53	15.9

WO 02/102235

PCT/US02/19297

	403151			predicted exon	15.8
	452383	A1582743	His.94353	ESTs, highly similar to C1QC_HUMAN COMPLEME	15.8
	425971	AF135024	His.16296	kalirin 15	15.8
	432828	X75363	His.25070	kalirin 15	15.8
5	431972	A805145	His.191711	ESTs	15.8
	430265			predicted exon	15.8
	404703	A904493	His.99690	polymerase (DNA directed), delta 1, catalytic subunit (1	15.8
	448335	AW150717	His.296178	STAT induced STAT inhibitor 3	15.8
10	419443	NM_005235	His.85146	v-ets avian erythroblastosis virus E26 oncogene homolog	15.8
	445773	H73458	His.13299	Human sapiens mRNA, cDNA DKFZp761M0111 from	15.8
	433763	AF080945		gbl-Homo sapiens clone H-08670	15.8
	409473			predicted exon	15.8
	420831	AA280824	His.190035	ESTs	15.8
15	402939			predicted exon	15.8
	402195			predicted exon	15.8
	452947	AW130413		gbl-H2908.s1 NCL_CGAP_Gas4 Homo sapiens cDNA	15.8
	414170	AA335996	His.3743	matrix metalloproteinase 24 (membrane-inserted)	15.8
	437133	AB018319	His.5400	KIAA0776 protein	15.8
20	458368	A024855	His.131575	ESTs	15.8
	401857	A928445	His.92254	hypothetical protein FLJ29153	15.8
	405687			predicted exon	15.8
	415189	L34857	His.78146	platelet/endothelial cell adhesion molecule (CD31 antigen)	15.8
	408602	AW247699	His.105897	ESTs	15.7
	445338	A492857		gbl-H2908.s1 Soares_NHMPu_S1 Homo sapiens cDN	15.7
25	402694			predicted exon	15.7
	430224	AW675175	His.235975	hypothetical protein DKFZp434D0412	15.7
	458762	N56966		gbl-yw75e02.r1 Soares_placenta_8to9weeks_ZNH18Pbto	15.7
	402444			predicted exon	15.7
30	422573	BE018517	His.119140	eukaryotic translation initiation factor 5A	15.7
	408061	AW247625		gbl-Z520094.Sprime_NHG_C7 Homo sapiens cDNA	15.7
	423238	AA223659	His.280482	ESTs	15.7
	421517	AB018362	His.105399	KIAA0809 protein	15.7
	422655	AB023217	His.223688	KIAA1030 protein	15.7
35	448915	AW071545	His.7436	putative acyltransferase	15.7
	400634			predicted exon	15.7
	451034	AL050341	His.25546	zinc metalloproteinase, STE24 (yeast, homolog)	15.7
	451571	A1375725	His.279518	hypothetical protein	15.7
	450105	BE281124	His.298013	similar to yeast SET3 (S. cerevisiae)	15.7
40	407464	AJ276396		gbl-Homo sapiens mRNA for matrix extracellular phosph	15.7
	438465	AF086285		gbl-Homo sapiens full length insert cDNA clone ZD478	15.7
	451837	T92157	His.10970	ESTs	15.7
	435313	A789400	His.193723	ESTs	15.7
	402738			predicted exon	15.7
45	432960	AA650114		gbl-zs2909.s1 NCL_CGAP_P3 Homo sapiens cDNA c	15.7
	407268	AW470302	His.129663	ESTs	15.7
	401268			predicted exon	15.7
	427630	M62505	His.2161	complement component 5 receptor 1 (C5a1lgand)	15.7
	418846	AJ521602	His.118127	ESTs	15.6
50	448851	AJ587332	His.209115	ESTs	15.6
	445930	AF055009	His.13456	Homo sapiens clone 24747 mRNA sequence	15.6
	421264	AK001724	His.102650	cool protein gamma-cop	15.6
	447073	AW204521	His.157726	ESTs	15.6
	445438	AB014578	His.12707	KIAA0678 protein	15.6
55	432126	AA865239	His.55144	ESTs	15.6
	424051	AF235057	His.135263	calcium channel, voltage-dependent, alpha 1F subunit	15.6
	448832	A087648	His.128622	ESTs	15.6
	445228	AJ403107	His.145590	ESTs, Weakly similar to AF208846 1 EM-004 [Hsapie	15.6
	434283	AJ393345	His.116215	ESTs	15.6
60	459270	AL039604		gbl-DKFZp434E2211.r1_434 (synonym: Hs23) Homo s	15.6
	454425	AW020927	His.27192	hypothetical protein d1057E20.2	15.6
	412055	AA099907	His.271806	ESTs	15.6
	400837			predicted exon	15.6
	458860	BE186884	His.268402	Homo sapiens cDNA FLJ14999 fs, clone PLACE1010	15.6
65	417124	BE122762	His.25338	ESTs	15.6
	414376	BC383886	His.65915	ESTs, Weakly similar to 16.7kD protein [Hsapie]	15.6
	418836	AW748655		gbl-QV4-BT0534-261299-053-c05 BT0534 Homo sapie	15.6
	454128	AL031289	His.41630	programmed cell death 2	15.6
	441074	AW500001	His.4783	Homo sapiens cDNA FLJ23035 fs, clone HEP06638	15.6
70	451742	T71809	His.117970	erythrin 2, neuronal	15.6
	403687			predicted exon	15.6
	431838	A087229	His.214644	ESTs	15.6
	402855			predicted exon	15.6
	445635	AJ889442	His.232150	ESTs	15.6
75	434392	AW563709	His.268051	ESTs	15.6
	444301	AK000136	His.10760	hypothetical protein FLJ20129	15.6
	414973	C19089		gbl-C19089 Human placenta cDNA (TFUwara) Homo	15.5
	428374	AW405156	His.163994	protein phosphatase 1, catalytic subunit, alpha isoform	15.5
	415745	A301107	His.150700	ESTs	15.5
80	432532	AW056459	His.162246	ESTs	15.5
	417112	AA193439		gbl-z41809.s1 Soares_NHMPu_S1 Homo sapiens cDN	15.5
	418101	AL047476	His.98485	gap junction protein, beta 4 (connexin 30.3)	15.5
	453110	AW354928	His.225160	Homo sapiens cDNA FLJ13102 fs, clone NT2672002	15.5
	458006	AJ238397		gbl-AJ238397 Uua-ZAP XCL renal pigment epithelium H	15.5
	430989	AA741028	His.256155	ESTs	15.5

WO 02/102235

PCT/US02/19297

	440617	AA84980	Hs.181181	ESTs	15.2
	449718	AA498480	Hs.23956	hypothetical protein FLJ20502	15.2
	405227			predicted exon	15.2
5	431006	BE152871		gc:CM-H10333-101259-064-d12 HT0333 Homo sapi	15.2
	443476	AW068594	Hs.133878	ESTs, Weakly similar to AF151859 1 CG1-131 protein	15.2
	438529	AL134275	Hs.6434	hypothetical protein DKFZp751P2014	15.2
	407634	AW016569	Hs.301280	ESTs, Highly similar to AF241831 1 Intracellular hyalu	15.2
	430857	AW732647		gtrc89b01.s1 NCI CGAP_G081 Homo sapiens cDN	15.2
10	431526	Y10129	Hs.258742	myosin-binding protein C, cardiac	15.1
	447365	NM_036289	Hs.18420	KIAA0277 protein	15.1
	435673	AA723257	Hs.127138	ESTs	15.1
	432858	BE118609	Hs.278591	Homo sapiens clone 25595 mRNA sequence	15.1
	437352	AL353967	Hs.284181	hypothetical protein DKFZp434P0631	15.1
15	413209	AW063791	Hs.21263	Homo sapiens cDNA FLJ13152 lit, clone NT26P3003	15.1
	437375	AA981138	Hs.142789	ESTs, Weakly similar to ALUUF_HUMAN III: ALU OL	15.1
	430476	BE387420	Hs.241531	pefin	15.1
	446764	AW729172	Hs.285532	ESTs	15.1
20	428658	AB017548	Hs.160100	Homo sapiens gene for Septaplerin Reductase, partial c	15.1
	453464	A384911	Hs.32889	receptor (calcitonin) activity modifying protein 1	15.1
	447246	AW493032	Hs.170529	ESTs	15.1
	401780			predicted exon	15.1
	434063	AA018893	Hs.3727	uvr-interacting protein	15.1
	416114	AB095549	Hs.163658	glucuronidase, beta	15.1
25	441018	AB005687	Hs.148782	ESTs	15.1
	425972	BE391563	Hs.165433	ESTs, Highly similar to T17342 hypothetical protein D	15.1
	426062	NS7014	Hs.44013	ESTs	15.1
	451234	AB14501	Hs.24062	ESTs	15.1
	425956	AB220719	Hs.207802	KIAA912 protein	15.1
30	418052	RA5154	Hs.106604	ESTs	15.1
	424550	AB050641	Hs.115288	ESTs	15.1
	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipid G-protein-cou	15.1
	445215	AW204514	Hs.170784	ESTs	15.1
	415102	RS0569	Hs.25608	ESTs	15.0
35	450082	AB068894	Hs.245953	ESTs	15.0
	446748	NM_016069	Hs.16085	CG1-135 protein	15.0
	406124			predicted exon	15.0
	457408	AL137507	Hs.253548	Homo sapiens mRNA: cDNA DKFZp751P211 (from c	15.0
40	410051	U25773	Hs.218182	ESTs, Weakly similar to J1042K10.2 [H.sapiens]	15.0
	440965	AB236146	Hs.106859	ESTs	15.0
	414950	AW752597		gbl3L3-CT0214-161299-045 B05 CT0214 Homo sapien	15.0
	447377	U53682	Hs.82132	interferon regulatory factor 4	15.0
	404249	AW446008		g1-2821045.Sprtnr NHJM3C_7 Homo sapiens cDNA	15.0
	432276	AF163302	Hs.274256	somatostatin receptor-interacting protein	15.0
	401116			predicted exon	15.0
45	423960	AA164516	Hs.136359	CGI-61 protein	15.0
	451681	AB030650	Hs.28777	KIAA0843 protein	15.0
	450983	AA303584	Hs.25740	ERO1 (S. cerevisiae)-like	15.0
	446187	AK001241	Hs.144229	hypothetical protein FLJ10379	15.0
50	404122			predicted exon	15.0
	411239	BE409587	Hs.89469	hypothetical protein	15.0
	403077			predicted exon	15.0
	438000	AB25880	Hs.5585	non-kinase Cdc42 effector protein SPEC2	15.0
55	447118	AB014599	Hs.17411	KIAA0699 protein	15.0
	417878	U05916	Hs.82845	Human clone 23615 mRNA sequence	15.0
	444075	U02048	Hs.23306	ESTs	15.0
	458234	BE551408	Hs.127196	ESTs	15.0
	434208	T92541	Hs.127548	hypothetical protein PRO2176	15.0
	423136	AW375506	Hs.124147	ESTs	15.0
60	403177			predicted exon	15.0
	448559	AB57269	Hs.227351	ESTs	15.0
	425248	AW957442	Hs.252786	ESTs	15.0
	429430	A381637	Hs.156335	ESTs	15.0

TABLE 3B:

Key: Unique Eot probe/identifer number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

	Key	CAT Number	Accession
70	408310	105101_1	AW179023 AW179010
	408647	1071855_1	AW245831 AW273207
	406651	1073036_1	AW247625 AW246214
	403887	108306_1	HS6615 H86300 H86293 H86282 AA069278 H86304
	409427	1129657_1	AW389658 AW389657 AW389198 AW389549
75	409545	1138822_1	BE296102 AW629821
	409828	1156571_1	AW501137 AW501265 AW501212
	409865	1156516_1	AW502208 AW502396 AW502148
	409885	1157385_1	AW503058 AW503789
	410003	116761_1	AA079487 AA128547 AA128291 AA079587 AA079600
80	410186	1182096_1	AW602528 BE073859 Z36412
	410626	1212521_1	BE407222
	411004	1228076_1	AW813242 BE146089 AW813105 AW813173 AW813205 BE145953 BE146212 AW813196 AW813452 AW813241 BE051582
	411014	1229091_1	AW815072 AW813375 AW813365 AW813302 AW813436 AW813475 AW813475 AW813475 AW813475 AW813475 AW813377
	411028	1229404_1	AW813703 AW813839

WO 02/102235

PCT/US02/19297

	411236	1263374_1	AW633762 AW533633 AW533776 AW533719 AW633362 AW633749
	411420	1245222_-1	BE390552
	411541	1249044_1	WD940 TS8335 AW850705
5	411561	1261196_1	AW651309 AW550898 AW651419 AW651412 AW651299
	411651	1252835_-1	AW555392 AW555559 AW555423
	411660	1253076_1	AW555518 AW555740 AW555748
	411696	1254393_1	AW557404 AW557401 BE144856
	411811	1259427_1	AW646370 AW554319 AW646504
	411930	1266070_1	F36465 AW678454
10	411940	1266262_1	AW679658 AW679717 AW677215 AW676891 AW67722 AW677216 AW676894 AW676725
	411942	1266448_1	AW677015 AW677133 AW677016 AW677017 AW676998 AW677069 AW677063 AW677013
	412793	1327636_-1	AW697956
	413047	1346806_1	H02208 AW062154 BE062032
15	413101	1349154_1	BE062512 BE155544 BE155541 BE155540 BE155542 BE155543
	413154	1349177_1	BE067070 BE067066 BE165193 BE165334 BE165329 BE165352
	413262	1356147_-1	BE070159 BE078276 BE078163 BE078277 BE078279 BE078158
	413442	1370508_-1	BE140643 BE140645 BE140644 BE140657 BE140660 BE140659 BE140661
	413544	1375671_-1	BE147226 BE147205 BE147204
20	413605	1375752_1	BE152644 BE152712 BE152686 BE152688 BE152610 BE152611 BE152616 BE152643 BE152706 BE152696 BE152660 BE152716 BE152682
			BE152669 BE152661 BE152672 BE152653 BE152716 BE152651 BE152767 BE152677 BE152652 BE152714 BE152706 BE152665 BE152679
			BE152771 BE152776 BE152666 BE152768 BE152813 BE152664 BE152676 BE152681 BE152708 BE152667 BE152614 BE152698 BE152711
			BE152707 BE152616 BE152678 BE152673 BE152782 BE152671 BE152682 BE152760 BE152805 BE152778 BE152790 BE152762 BE152776
			BE152781 BE152774 BE152763 BE152769
			BE152754 BE152770 BE152769 BE152768 BE152769 BE152769 BE152769 BE152769 BE152769 BE152769 BE152769 BE152769
25	413679	1392784_1	BE156739 BE156633 BE156644 BE156631 BE156849 BE156799 BE156784 BE156601 BE156843 BE156793 BE156792 BE156634 BE156779
			BE156798
	413758	1395900_-1	BE162391
	414070	141442_1	AW693783 F36521 F30657 AW753177 AW753195 AW653065 AA136150 AA375028
	414195	1424854_-3	BE263293
30	414293	1426610_2	BE261170 BE342553 BE261026 BE273627
	414266	1430684_1	BE267834 BE154190 BE154095
	414276	1432115_-1	BE297962
	414333	1436482_1	BE274897 BE408199 BE274723
	414444	1446527_-1	BE295594
35	414539	1460320_1	BE379048 BE395459
	414540	1460324_-1	BE379050
	414605	1465750_-1	BE390440
	414610	1469927_-1	BE389044 BE391117 BE381530
	414626	1467132_1	BE406939 BE390549 BE408297 BE396529
	414642	146960_1	AA150350 AA361174 AW699038
40	414663	1472628_-1	BE396326
	414973	1510756_1	C19089 C19314 C10621
	415160	1531785_1	T23290 D19670 R08605
	415606	1540410_1	W70022 R36201 F12763 T74725 H63465 Z45782 H81126
	415817	1561676_1	Z43612 H09194
45	416272	1584047_-1	AA178882 AA178888 AA178887
	416476	1595363_-1	T02839 H60072 R02760
	416913	163001_1	AW634714 BE161007 BE162000 AW749502 AW749864 BE162498 BE161005 AA190449 AA6513465 BE161006 BE162499
	417112	165066_-1	AA193439 AA193637 AW614126
	417611	168800_-1	AW653983 AW64798 AW953990 AW933999 AW933989 AA204755
50	417908	170784_-1	AA307221 BE538271
	418636	177402_1	AW749565 AA223996 AW752208 AW752005
	418874	1795616_1	T50672 T69306
	419618	196533_1	AA528295 AW971284 AA247945
55	419889	188768_-1	AA361900 AA279607
	420092	197625_1	AA742277 AW679463 AA281585
	422160	172412_1	AW652656 AA305114
	422731	220607_1	AL138411 AL138412 AA315860
	422831	221879_-1	R02694 AA317715 AW951465 AF12172
60	423080	224288_-1	AA320546 H82114 BE144449 BE144438
	423163	225019_1	AA322028 BE318227
	423297	226793_1	H06340 H35061 AA324112
	423621	230314_-1	BE002904 H64800 AA328579
	424585	241161_1	AA484840 AA343628
	424995	245754_1	Z45023 AA345144
65	426132	247069_-1	AW250114 Z43124 AA31421 AB79054 AA361616 AA361036 AL048899
	426612	253609_1	BE004267 AW611190 AA360576 BE172402 BE181703
	425798	256666_-1	AA364002 AI522307
	426065	260276_-1	N32646 R34621 F08237
	426396	263811_1	BE536836 AA376153
70	426383	266126_1	BE537380 BE255215
	428161	287669_-1	AA422028 W79191
	431006	326833_1	BE152671 BE152670 AA490552
	431267	33944_1	AF036997 BE243636
75	431614	335668_1	AI195327 AW680554 AW680552 AA650543
	431822	338062_1	AA516049 AW004922
	432065	366839_-1	AA650114 AW574148 AW572946
	433300	362452_1	AA552307 BE373016
	433365	364004_1	AB002353 AW042896 AA584528
	433459	366899_-1	AA583458 AW745847 AW746630
80	433469	367263_1	F12741 T75155 AA594014
	433762	37414_1	AF009545 AW996754 AW648970
	434059	390006_1	AA525495 AA525208 AA525184
	435138	401169_1	BE314734 AA606393
	435478	406683_1	AA682622 BE141696

PCT/US02/19297

NT_{position}: Indicates nucleotide positions of predicted exons

129

WO 02/102235

PCT/US02/19297

	400931	7651921	Minus	142145-142353,144311-144721
	400964	7139719	Minus	155282-155403
	402965	7773076	Minus	173943-173554
	400970	7960492	Minus	92744-92895
5	400982	8078794	Minus	119245-119471
	401010	8117391	Minus	83967-84180
	401072	3657273	Plus	84370-84524
	401058	8482704	Plus	194659-195179
	401116	9966559	Plus	123579-124447
10	401117	8570083	Minus	26948-29204
	401167	9430381	Plus	16544-16776
	401204	9743308	Minus	33694-33872
	401220	9629324	Minus	48079-48279
	401244	4827300	Minus	55359-56376
15	401245	4827300	Minus	89373-99331
	401268	9781154	Plus	152772-152653,157312-157418,158025-158206,158838-158974,160716-160952
	401269	8954206	Plus	2259-2591
	401283	9800093	Minus	47256-47456
	401373	7248205	Minus	84211-84336
20	401405	7768126	Minus	69276-69452,69548-69958
	401465	6982292	Plus	25676-25800
	401492	7341778	Plus	171020-171262,171859-172241
	401521	7705251	Plus	9127-9234
25	401566	8469990	Minus	95277-96400,96979-97160
	401575	7228044	Minus	76253-76394
	401589	9966292	Plus	138585-138263
	401626	8676954	Minus	210517-210796
	401657	9100684	Minus	7312-8163
	401747	9795672	Minus	116596-118616,191119-119244,119626-119761,120422-120990,130161-130381,130468-130653,131097-131258,131866-131932,132451-132575,133580-134011
30	401757	7236630	Plus	68641-68751
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30024-30573
	401781	7249190	Minus	63219-63436,63631-63696,63740-63961,64237-64393,64950-65037,65290-65814
	401785	7249190	Minus	165776-165996,166189-166314,166408-166563,167112-167296,167357-167463,168634-168942
35	401789	7249213	Minus	70399-70529,70941-71055
	401809	7342191	Minus	107548-108296
	401847	7139731	Plus	85447-85593
40	401887	7229861	Plus	50373-50420
	401913	9389820	Minus	33763-33864
	401962	3176726	Minus	7143371648,767117-76833,76677-76845,76966-79763,82349-82485
	401991	4156128	Plus	2398-2513
	401994	4153808	Minus	42904-43124,43211-43336,44607-44763,45199-45261,46337-46732
	402022	7528158	Minus	132872-133540
	402056	6549209	Plus	135543-135031
45	402071	8117361	Plus	55804-96039
	402076	8117407	Plus	121907-122036,122804-122921,124019-124161,124455-124610,125672-126076
	402131	7704361	Minus	33114-33203,33496-33678
	402144	7242326	Plus	115426-115977
	402203	8576119	Minus	8124-8285
50	402277	2894631	Plus	16960-17152,17933-18018,18170-18306
	402292	2447220	Plus	33680-34029,34176-34336,34953-35103
	402297	6590624	Plus	36279-36456,36573-36969
	402407	3862498	Minus	115812-116167
	402421	9796341	Minus	46609-46662,46758-46811,46293-46346,89776-89829,90048-90101,102817-102924
55	402427	9796372	Plus	16266-16431
	402430	9796372	Plus	62383-62562
	402520	7896099	Minus	93171-93196
	402536	9601137	Minus	96314-96539
	402543	9838066	Minus	89694-90983
60	402570	9684747	Minus	12649-12696
	402585	9938590	Minus	174693-175000,183210-183435
	402639	9958129	Minus	20167-22383
	402694	8589687	Plus	2218-2440
	402699	8570304	Minus	182773-182653,184651-184732
65	402738	7331637	Minus	5725-8659
	402855	8602963	Minus	559763-69900
	402869	6434643	Minus	836639-139335
	402939	9187334	Minus	18329-18535
	402944	5368423	Plus	115411-116716,111173-111640
70	402946	9368498	Minus	143148-143626,143806-143935
	402956	9368493	Plus	13324-13507
	403010	3132346	Plus	76385-79052
	403036	3132360	Plus	66545-66712
	403051	4827080	Minus	5269-5411
75	403065	8954197	Minus	71615-71773,73930-74144
	403077	8954241	Plus	146523-147222,147326-147628
	403083	8954241	Plus	177083-177373,177464-177751
	403151	7407965	Minus	14555-14264
	403163	9799671	Minus	42232-43389
80	403177	9638213	Minus	142560-142726
	403223	7630989	Plus	81529-81692
	403234	7637801	Plus	18264-186822
	403273	6018056	Plus	133009-134069
	403296	8080320	Plus	118369-118872

WO 02/102235

PCT/US02/19297

	403287	8060320	Minus	126097-126411
	403348	7238527	Plus	13093-13968
	403359	8570207	Minus	106538-106229
5	403362	8571772	Plus	64069-64260
	403447	9837821	Minus	150072-159387
	403508	7630896	Plus	3570-3719
	403582	8101186	Plus	18338-18458
	403613	8493504	Plus	81290-81465
10	403642	8699671	Plus	7062-7311
	403662	5823349	Plus	58627-59062,59222-59548
	403674	7321542	Plus	164988-106573,107394-107590
	403687	7387384	Plus	9009-9534
	403695	3048276	Plus	168272-168514
	403703	4966380	Plus	83081-84042
15	403741	7633832	Minus	2833-3468
	403747	7658396	Minus	20493-20621
	403766	7229888	Plus	130203-136630
	403786	8083636	Minus	73028-73217
	403796	8099896	Minus	75073-77664
20	403833	887461	Plus	13323-13664
	403852	7708872	Minus	124037-124262
	403861	7708966	Plus	68363-58649
	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
	403924	7711686	Minus	89369-89582
25	403964	7596576	Plus	173174-178300
	404034	8567760	Minus	44636-47070
	404067	3282162	Plus	1415-2071
	404097	7770707	Plus	55512-55781
	404122	9796270	Plus	90540-92977
30	404230	7981448	Minus	92934-93093
	404239	5002624	Plus	94641-95095
	404240	5002624	Minus	116132-116407,116653-116922
	404270	9528129	Minus	3545-3763,4151-4306,6962-6049,6949-6966
	404395	7630896	Minus	126433-126623
35	404600	8705107	Plus	118364-118444,118649-118792
	404601	8705107	Plus	128449-128693,129085-129242,130525-130733
	404638	9796751	Minus	99433-99626,100035-100161
	404666	7272179	Minus	18971-18983
	404675	9797204	Minus	48532-48646,49008-49075,51088-61369,54944-55063
40	404727	8081050	Plus	116534-115747
	404750	7596836	Plus	181879-182198
	404763	7862612	Plus	60891-51562
	404787	7862627	Plus	23344-23799
	404828	6590415	Minus	26291-27253
45	404850	5420148	Minus	35145-35413,40535-41062
	404881	5931510	Minus	36366-36608
	404890	7328390	Plus	107280-101408
	404971	3212339	Minus	74695-75532
	405022	7330304	Plus	217163-217439
50	405028	7533974	Minus	110688-110847,110933-111115
	405071	7708797	Minus	11115-11552
	405088	8072516	Minus	118696-117621
	405133	8516055	Minus	28127-28288
55	405138	8576241	Plus	90303-90516
	405163	7209940	Plus	12335-12553
	405194	7234072	Plus	199465-199465,193346-193610
	405196	7230083	Minus	135716-135851
	405208	7230142	Plus	8068-8214
	405226	7248966	Plus	53547-54168
60	405227	6731245	Minus	22506-22892
	405256	7325310	Plus	26076-26309
	405277	3980473	Plus	23471-23572
	405307	3638954	Plus	39195-39429
	405311	3638954	Plus	46313-46496
65	405333	3165389	Plus	149895-150215
	405411	3451396	Minus	17503-17778,18021-18290
	405423	4753276	Plus	6162-6993
	405491	5801545	Plus	81857-82045
	405501	9211311	Minus	49365-49400,49565-49679,50117-50262
70	405515	5454624	Plus	37328-37469
	405545	1054740	Plus	118677-118807,119091-119296,121626-121823
	405680	4512267	Plus	168232-169647
	405686	5002511	Plus	38618-39017
	405690	5928240	Plus	29865-27225
75	405610	5757553	Minus	71907-72090
	405639	5091650	Plus	211184-211350
	405687	6249668	Minus	54787-54891,55844-55917
	405699	4166331	Plus	130772-103099
	405783	5738434	Minus	27238-27885
80	405867	6758731	Minus	74553-75173
	406036	7107817	Plus	9418-9573
	406124	9148714	Minus	1331-1774
	406130	9151404	Minus	3294-35088
	406140	9168231	Minus	49887-50219

WO 02/102235

PCT/US02/19297

406160	7144945	Plus	55498-65266
406207	5923650	Minus	162607-162800
406215	7342161	Plus	310-432
406268	6662695	Minus	6605-7072
406277	5686030	Minus	4759-5490
406326	9212365	Plus	84508-84655
406366	9236205	Plus	65153-85277
406457	9755793	Plus	44366-45406
406473	9795566	Minus	106669-109931
406537	7711476	Plus	32904-33017
406571	7711622	Minus	55534-55917,56116-66596
406580	7711638	Minus	36634-37640

15 TABLE 4A lists about 131 genes up-regulated in ovarian cancer compared to normal ovaries that are likely to be extracellular or cell-surface proteins. These were selected as for Table 3A, except that the ratio was greater than or equal to 10, and the predicted protein contained a PFAM domain that is indicative of extracellular localization.

20 TABLE 4A: ABOUT131 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL OVARY

Key: Primley
Ex. Accn: EMBL/Genbank Accession
UG ID: UniGene ID
Title: UniGene Title
PFAM domains
ratio: tumor vs. normal ovary

Key	Ex. Accn	UG ID	Title	PFAM	ratio
403077			predicted exon	fn3	15.0
426535	AU077012	Hs.288582	ESTs, weakly similar to ubiquitous TP	Kunitz_BPTI	14.9
433089			predicted exon	fn3	14.9
457148	AF081035	Hs.184627	KIAA0118 protein	amras	14.8
431176	AK26994	Hs.253662	ESTs	laminin_EGF_laminin_B	14.8
434293	NM_004445	Hs.3796	EphB6	ephrase_EPH_Bd	14.8
459452	NM_000576	Hs.45743	adenosine A2b receptor	7tm_1	14.6
428955	AU55547	Hs.185859	purinergic receptor (family A group 5)	7tm_1	14.5
426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) ho	EGF	14.4
423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxy	sugar_inMCT	14.3
421225	NM_003459	Hs.111967	solute carrier family 30 (zinc transport	Calton_efflux	14.2
427453	NM_012368		(NCKX)	7tm_1	14.2
449589	AWS04695	Hs.167046	ESTs	7tm_1	14.1
410184	AWS03667	Hs.59545	ring finger protein 15	zf-CHC4/SPRY2/zy-B_box	14.0
423217	NM_000054	Hs.1640	collagen, type VII, alpha 1 (epitome)	fn3-vwa	14.0
405448	AU015705	Hs.172089	Homo sapiens mRNA cDNA DRF2p5	typsin/azustic/CUB	14.0
459584	AA572605	Hs.25333	interleukin 1 receptor, type II		14.0
406692	L36607		glyco-homo sapiens (clone 22) pregnancy	ig	13.9
45	425649	U54863	programmed cell death 1	ig	13.8
425755	AFY138937	Hs.213456	ESTs	cystatin	13.8
427637	AF000816	Hs.179996	follin 1	Band_7	13.7
445691	R55704	Hs.150968	hyocortin (prokin) receptor 1	7tm_1	13.7
405024			predicted exon	TGF-beta1/TGFb_propeptide	13.7
405285			predicted exon	A2M/A2M_N	13.7
121116	U1402166	Hs.784	Epstein-Barr virus induced gene 2 (ym	7tm_1	13.7
402556	UB4722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascu	cadherin/Cadherin_C_term	13.6
420511	AF052892	Hs.98468	gap junction protein, beta 4 (connexin 3	connexin	13.5
448638	R17122	Hs.21639	nuclear protein, marker for differential	ig	13.4
431117	AF003822	Hs.250500	ozt6 (Drosophila)-like 1	EGF_DSL	13.4
439285	AL153916	Hs.286988	ESTs	ig	13.4
442823	AA333824	Hs.301678	ESTs	E1-E2_ATase/Hydrolase	13.3
436233	A1742878	Hs.124116	ESTs	ig	13.3
434359	NM_013409	Hs.9914	folistatin	kazal	13.2
140016	AS379377	Hs.75707	small inducible cytokine subfamily A (il8	13.2
414020	NM_002984	Hs.75703	small inducible cytokine A4 (homolog)	il8	13.2
40242			predicted exon	Ephrin	13.0
429057	AF156557	Hs.194816	stomatin-like protein 1	Band_7/SP2	12.9
438294	A093750	Hs.143004	ESTs	E1-E2_ATase/Hydrolase	12.9
458403	AF043408	Hs.252416	ESTs	RYOP/ITPR	12.8
444181	AB033063	Hs.10491	KIAA1237 protein	fn3/ig/PP4/RhoGEF	12.8
422357	AF016272	Hs.115418	cadherin 16, KSP-cadherin	cadherin	12.7
49632	V74001	Hs.55279	serine (or cysteine) proteinase inhibitor	serpin	12.7
407030	U12139		glycine human alpha1(I) collagen (COL1	TSPN/Collagen/COLR	12.7
417064	W02093	Hs.15440	ESTs	lectin_c	12.6
439389	AF314940	Hs.56004	ESTs	hemopexin/Peptidase_M10	12.6
407786	AA587538	Hs.38972	telazepan 1	transmembran4	12.5
410496	AA355749		glt-EST16459 Juxtal T-cells VI Homo	aa_gomessases	12.5
42467	AU010901	Hs.198257	mucin 4, tracheobronchial	wnt	12.5
423330	C30783	Hs.115263	epiregulin	EGF	12.5
402425			predicted exon	lov_transt	12.4
414875	H42679	Hs.77522	major histocompatibility complex, class	ig	12.2
424239	A67439	Hs.143526	adenosine receptor D5	7tm_1	12.2
442522	NM_004335	Hs.6546	Notch (Drosophila) homolog 3	EGF_fank/notch	12.2
405368			predicted exon	7tm_1	12.2
402406			predicted exon	Gal-bind_lectin	12.1
426514	BE516633	Hs.301122	bone morphogenetic protein 7 (osteog	TGF-beta1/TGFb_propeptide	12.1
408811	U82979	Hs.67846	selectin immunoglobulin-like recepto	ig	12.0
416441	BE407197		glt-601301552F1 NIH_MGC_21 Homo	SDF	12.0

WO 02/102235

PCT/US02/19297

433221	AB040917	Hs.37850	KIAA1484 protein	h33g1.LRRCT	11.9
442915	AA852875	Hs.8850	a disintegrin and metalloproteinase domain	disintegrin-like metalloproteinase	11.9
429613	AF036335	Hs.125910	lysine-specific aminopeptidase 3	lysine-specific aminopeptidase	11.9
411213	AA675939	Hs.59285	neuropilin 1	CUB&MAMF5_FB_type_C	11.9
425483	AF231022	Hs.301273	Homo sapiens protocadherin Fat 2 (FA)	EGF/cadherin/interleukin_G	11.8
421258	AA286731		glucosyltransferase NCL_GCAP_G081 Hom	7m_3	11.8
423795	AB049789		glut-3-CTD215-40200-07-004 CTD	arfas	11.7
422424	AI186431	Hs.116577	prostate differentiation factor	TGF-beta1	11.7
443296	AF165286		glut-3/305x1 NCL_GCAP_K612	ig	11.7
448999	AF179274	Hs.22791	transmembrane protein with EGF-like	kazal	11.7
414878	AA341040	Hs.77541	ADP-ribosylation factor 5	arfas	11.5
423444	R94038	Hs.139538	inhibin, beta C	TGF-beta1	11.5
402114			predicted exon	laminin_EGF, laminin_G	11.5
419216	AU076718	Hs.164021	small inducible cytokine subfamily B (IL8	11.5
433263	D12614	Hs.35	lymphoblast alpha (TNF superfamily, m	TNF	11.4
403464			predicted exon	Prokinase_S9	11.4
456841	AA875853	Hs.152345	poleovirus receptor-related 1 (heparin	ig	11.4
409420	T21508	Hs.54451	laminin, gamma 2 (nicotin (100kD), kal	laminin_EGF, laminin_B	11.4
418043	AK037752	Hs.83341	H.sapiens mRNA for tyrosine kinase re	h33g1kinase	11.3
425523	S69510	Hs.170222	sodium carrier family 1 (sodium/hydrog	Na_1L_exchanger	11.3
446051	BE440601	Hs.153315	ESTs	Receptor-like tyrosine kinase	11.2
439710	AF086543		gibbonia sapiens full length insert cDN	Xlink	11.3
415502	NM_006159	Hs.79389	nel (chicken)-like 2	wvcTSPN	11.3
418299	AA275930	Hs.83968	integrin, beta 2 (antigen CD18) (p95), ly	integrin_B	11.3
435721	AC022115	Hs.183039	uncoupling 1A	transmembrane4;COX8B;Ets	11.2
409757	NM_001598	Hs.123114	cystatin SN	ig	11.2
433630	AW269920	Hs.2621	cystatin A (stefin A)	7m_3ANF_receptor	11.2
429630	M85289	Hs.211573	heparan sulfate proteoglycan 2 (perleca	laminin_EGF, ig_M1_recep_La	11.1
427289	AK037345	Hs.174203	solute carrier family 1 (glutamate/seri	SDF	11.1
401248	AB028889	Hs.85501	mitogen-activated protein kinase 8 like	wvcwvcTIL	11.1
412627	BE391969	Hs.74275	chloride intracellular channel 1	G-palch/ig_MutB_C	11.1
420104	U03825	Hs.1287	zinc finger protein 173	zf-CHC4;SPRY2;S-B_box	11.1
426275	AG028989	Hs.88500	mitogen-activated protein kinase 5 like	wvcwvcTIL	11.1
425864	US5420	Hs.129103	olfactory receptor, family 5, subfamily	7m_1	11.1
445745	AW118189	Hs.156400	ESTs	wva	11.1
441834	AL138034	Hs.7979	KIAA0736 gene product	sugar_1r	11.0
450986	BE241845	Hs.26744	Novel human gene mapping to chromo	PHRhoGAP;GAP-bind_Jectin	11.0
451518	NE2773	Hs.157721	ESTs	heparinase;FapI;ase_M10	11.0
443301	AL080221	Hs.8985	complement component 1, q subcompo	C1P;Collagen	10.9
431247	AL021578	Hs.278489	matrilin 4	EGF-wva	10.9
431449	M69594	Hs.265278	tumor necrosis factor receptor superfam	TNFR_p6	10.9
467044	S73899	Hs.2131	arginine vasopressin receptor 1A	7m_1	10.9
416319	AB15501	Hs.79197	CD35 antigen (activated B lymphocyte	ig	10.8
402172			predicted exon	ig	10.7
424218	AF031824	Hs.143212	cystatin F (leukocystatin)	cystatin	10.5
409208	Y00093	Hs.51077	integrin, alpha X (antigen CD11C) (p15	wva	10.5
426330	M77235	Hs.153331	sodium channel, voltage-gated, type V,	loc. transIQ	10.5
439758	AA845235	Hs.154470	ESTs	transmembrane4	10.5
412429	AV660262	Hs.75765	GRO2 oncogene	IL8	10.6
449887	AW079749	Hs.184719	ESTs. Weakly similar to AF116721 11	ABC_tran;ABC_membrane	10.6
432408	N03127	Hs.75391	myxovirus (influenza) resistance 1, hom	loc. transIQ_intra	10.6
406872	U02041	Hs.195283	major histocompatibility complex, class	ig;HMG_IL_alpha	10.5
419749	X73608	Hs.93029	sparc/osteonectin, cwv and kazal-like	kazal;Myoglobin_1	10.5
419085	NM_000216	Hs.85591	Kallmann syndrome 1 sequence	h33wap	10.5
426009	X56288	Hs.154151	protein tyrosine phosphatase, receptor t	h33g1_T_phosphataseMAM	10.5
423889	BE453001	Hs.134012	alpha-related factor 1	EGF_FETTERFG_C	10.4
433009	AF177941	Hs.235358	Pro-(alpha1(V) collagen	Collagen;COLR;TSPN	10.4
400834			predicted exon	IRK	10.4
442941	AL076728	Hs.8857	cysteine-rich, angiogenic inducer, 61	Cys_knotbsp_1;wvcGFBP	10.4
403591			predicted exon	bp_1;Repsolrin	10.4
430775	AI011021	Hs.247905	potassium voltage-gated channel, subfa	ig;trans	10.3
432342	AL0335128	Hs.274404	plasminogen activator, tissue	EGF;1r;tk;angiotensin	10.3
417331	BE243845	Hs.75511	connective tissue growth factor	Cys_knotbsp_1;wvc	10.3
423309	BE006775	Hs.126782	sushi-repeat protein	subd1YR	10.3
431728	NHL_A007351	Hs.268107	actin, alpha 1	EGF;Ctq	10.3
450545	AA007635	Hs.271767	ESTs. Moderately similar to ALU1_HU	ig	10.2
446983	AA157484	Hs.97199	complement component C1q receptor	EGF;Xlink	10.2
414320	U13615	Hs.75893	angiotensin 3, node of Ranvier (ankyrin G)	death;ak;ZL5	10.1
402253			predicted exon	7m_1	10.1
406994	M84891	Hs.226932	pregnancy specific beta-1-glycoprotein	ig	10.0
418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1	EGF	10.0
410564	NM_005033	Hs.65370	lipase, endothelial	Ribosomal_L22	10.0
427274	NM_005211	Hs.171412	colony stimulating factor 1 receptor, fo	pkinaseg	10.0

TABLE 4b:

Key: Unique Eos probest identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Key	CAT Number	Accession
410498	120611_1	AA355749 AA085520 AW090333 AA340319 BE170935
416441	158480_1	BE047197 AA182474 AA183689 BE276628 BE276311
421258	200725_1	AA206711 AA201621 AW186828 AW137774
423795	232093_1	AW049759 AW049758 T09549 AA331089

WO 02/102235

PCT/US02/19297

439710 47650_1 AF086643 W96291 W96225
443296 66539_2 AT062286 AW257086 BE658958

TABLE 4C:

Play: Unique number corresponding to an Eos probe

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:48-55

Strand: Indicates DNA strand from which exons were predicted

NI_positon: Indicates nucleotide positions of predicted exons

Play	Ref	Strand	NI_positon
400464	992670	Plus	22074-22214
400834	8705192	Plus	121963-122288
402114	8318886	Plus	71578-71715
402172	8579511	Minus	143378-143871
402406	3970829	Plus	10572-11123,12932-13045
402425	9796347	Minus	50224-50355
403077	8954241	Plus	146923-147222,147326-147628
403089	8954241	Plus	171954-172229
403911	7387384	Minus	86266-86463
405024	7107727	Plus	85606-85697
405286	6139075	Minus	55744-55903,57080-57170,61478-61560
405368	2104517	Plus	40555-47188

TABLE 5A lists about 685 genes down-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 3A, except that the numerator and denominator were switched, and the ratio was greater than or equal to 3.0 (i.e., 3-fold down-regulated in tumor vs. normal ovary).

TABLE 5A: 685 DOWN-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Play: Primerkey

Ex_Accn: Exon Accession

UG_ID: UniGene ID

Title: UniGene Title

ratio: ratio normal ovary vs tumor

Play	Ex_Accn	UG_ID	Title	ratio
421013	M62287	Hs.1345	mutated in colorectal cancers	14.8
435000	A444848	Hs.55346	ESTs, Weakly similar to Z141_HUMAN ZINC FINGER	12.8
407644	D16815	Hs.37288	nuclear receptor subfamily 1, group D, member 2	12.6
424851	AA678441	Hs.119059	ESTs	11.6
465066	AW853057	gb:RCT-CT0249-170200-025-H04 CT0249 Homo sapie	11.5	
420727	H75701	Hs.59888	complement component 4-binding protein, beta	11.3
451617	CD1056	Hs.106500	ESTs	10.9
401308			predicted exon	9.9
440987	AA511705	Hs.130229	ESTs	5.7
409725	T60760	Hs.59459	EST	5.7
415752	BC514624	Hs.78778	putative transmembrane protein	5.7
437690	AA804362	Hs.180544	ESTs	5.6
437787	A1908263	Hs.261625	ESTs	5.5
465064	AW798406	Hs.82396	Z'-d-glucosyltransferase 1	5.2
435330	R16769	Hs.185089	ESTs	5.2
43642	AA724430	Hs.127390	ESTs	5.1
463752	AL120800		gb:KCFZp76Zp152_r1_762 (synonym: hme2) Homo sa	5.1
451683	A1808954	Hs.207673	ESTs	9.1
401464	AF039241	Hs.9028	histone deacetylase 5	5.0
436812	AW256067		gb:UA-H-BMD-gp-g-09-04(Ls1) NCL_GCAP_Sub5	3.7
410758	BE336988		gb:601062419F1 NIH_MGC_10 Homo sapiens cDNA	8.7
412637	AA115097	Hs.261513	ESTs	8.4
419166	AA234638	Hs.233684	ESTs	8.3
423738	AA389165	Hs.67500	ESTs	8.1
413813	M69566	Hs.76961	hepatocarcinoma-derived growth factor 1	8.0
416211	R14625		gb:ygA5003_r1 Soares infant brain 1N10 Homo sapiens	8.1
443131	A033833	Hs.132698	ESTs	7.9
415866	T10115	Hs.92423	KIAA1566 protein	7.9
401330	AB12097	Hs.163308	ESTs	7.8
439426	AT131502	Hs.143135	ESTs, Weakly similar to FAFY_HUMAN PROBABLE	7.8
408141	U62005	Hs.45152	ESTs, Moderately similar to neurogenic basic-helix-loop	7.7
419015	T75262	Hs.14463	ESTs	7.6
411573	BE563565	Hs.65290	ESTs	7.5
415386	AA235887	Hs.143868	ESTs	7.5
439562	D76260	Hs.288097	ESTs	7.5
434738	AA836255		gb:ad17e002_s1 NCL_GCAP_GCB1 Homo sapiens cDNA	7.4
403283			predicted exon	7.4
415881	Z43123	Hs.144513	ESTs	7.4
412732	AW933300		gb:RC2-BN0033-180200-015-g06 BN0033 Homo sapie	7.4
441247	AA118681	Hs.128051	ESTs	7.4
442866	N57659	Hs.114541	ESTs, Weakly similar to neuronal thread protein AD7c	7.3
426929	BE154680		gb:PK6-AT0344-071219-003-c00 HT0344 Homo sapie	7.3
420352	BE268635		gb:5901117374F1 NIH_MGC_16 Homo sapiens cDNA	7.2
421418	AA506639		gb:ab68g05_s1 NCL_GCAP_GCB1 Homo sapiens cDNA	7.2
413597	AW302885	Hs.117183	ESTs	7.1
454102	AW752363		gb:RCD-CT0201-27099-0911403 CT0201 Homo sapien	7.1
445407	A1806287	Hs.201217	ESTs	7.1
467604	A1004397	Hs.130558	ESTs, Weakly similar to similar to O-sialoglycoprotein	7.1

WO 02/102235

PCT/US02/19297

40942			predicted exon	6.9
40756	R86193		gbcy30R5.r1 Soares fetal liver spleen 1NfLS Homo sa	6.9
422046	A833462		gbcy30R5.r1 NCL_CGAP_UH1 Homo sapiens cDNA c	6.9
441284	AA927676	Hs.196542	ESTs	6.9
446224	AW450551	Hs.13308	ESTs	6.9
424043	AL077260	Hs.15394	death-associated protein kinase 1	6.9
453987	AW009077	Hs.232947	ESTs	6.9
449593	AA167642	Hs.14632	ESTs	6.9
431877	AA521204	Hs.105507	ESTs	6.8
411337	AW837349		gbcy2/LT0038-270300-108-412 LT0038 Homo sapie	6.8
410596	AA374186		gbcy2/LT0038-270300-108-412 LT0038 Homo sapie	6.8
417792	AA205576		gbcy2/LT0038-270300-108-412 LT0038 Homo sapie	6.7
406364			predicted exon	6.7
452238	F01811	Hs.107931	ESTs, Moderately similar to S22703 voltage-gated pola	6.7
415288	R15794	Hs.141027	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	6.7
407437	AF220284		gbcy30R5.r1 NCL_CGAP_UH1 Homo sapiens cDNA c	6.7
439126	AF085984		gbcy30R5.r1 NCL_CGAP_UH1 Homo sapiens cDNA c	6.6
452453	AB02519		gbcy30R5.r1 NCL_CGAP_UH1 Homo sapiens cDNA c	6.6
431800	AW452768	Hs.162045	ESTs	6.5
426380	AI291267	Hs.146950	ESTs, Weakly similar to unnamed protein product [H.s]	6.5
449529	AB004659	Hs.230333	ESTs	6.4
437755	AW204256	Hs.291887	ESTs	6.4
443007	AI480289	Hs.211026	ESTs	6.4
435686	AA927676	Hs.110039	ESTs	6.4
420051	N15096	Hs.44745	ESTs	6.4
425006	AB22299	Hs.173369	ESTs	6.4
433923	AB23453	Hs.146625	ESTs	6.4
408159	H63977	Hs.118526	ESTs	6.3
434844	AF157116	Hs.301355	hypothetical protein LOC56757	6.3
430197	AA468888	Hs.107857	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFA	6.3
440332	AI218517	Hs.188051	ESTs	6.3
450061	AI797034	Hs.201115	ESTs	6.3
445694	AW850176		gbcy30R5.r1 NCL_CGAP_UH1 Homo sapiens cDNA c	6.3
422105			predicted exon	6.3
409090	W96067	Hs.103105	ESTs	6.2
405752			predicted exon	6.2
408074	R02723	Hs.124764	ESTs	6.1
452200	Y03366	Hs.30146	homodomain-interacting protein kinase 3	6.1
416310	TS1421	Hs.221396	ESTs	6.1
421976	AL138443	Hs.23450	mRNA for FLJ00323 protein	6.1
429755	NM_001364	Hs.215839	discs, large (Drosophila) homolog 2 (chapsyn-110)	6.0
448732	BE514063		gbcy30R5.r1 NCL_CGAP_UH1 Homo sapiens cDNA c	6.0
453300	AW004045	Hs.203365	ESTs	6.0
431178	AA453884	Hs.218008	Homo sapiens cDNA: FLJ12140, clone COL04089	6.0
449571	AW959755	Hs.288896	Homo sapiens cDNA: FLJ12977, clone NT2P20062	6.0
421349	W01715	Hs.102958	ESTs, Weakly similar to Lysip [S.cerevisiae]	6.0
453282	AK000043	Hs.125822	hypothetical protein FLJ22036	6.0
420618	AA273781	Hs.289698	ESTs	5.9
412490	BE142364		gbcy30R5.r1 NCL_CGAP_UH1 Homo sapiens cDNA c	5.9
449858	AW205979	Hs.196065	ESTs	5.9
423984	AL049925	Hs.225984	DKFZP547G0910 protein	5.9
416453	H59096	Hs.114555	ESTs	5.9
459497	AA825742	Hs.87517	ESTs	5.9
433773	AA759293	Hs.112692	ESTs	5.9
459542	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12 (molten a	5.8
426354	AF073632	Hs.119813	gbcy30R5.r1 NCL_CGAP_UH1 Homo sapiens cDNA c	5.8
410495	N65428		predicted exon	5.8
403277			predicted exon	5.8
444302	AI140115	Hs.225130	ESTs	5.8
439534	AF54576	Hs.124523	ESTs	5.7
404020			predicted exon	5.7
454338	AW381251	Hs.1050	pleckstrin homology, Sec7 and coiled-coil domains 1cy	5.7
420922	AW373747	Hs.183337	ESTs	5.7
420289	NE5534	Hs.95398	8-oxoguanine DNA glycosylase	5.7
426488	AA429575	Hs.243032	ESTs	5.7
445597	H65649		gbcy30R5.r1 NCL_CGAP_UH1 Homo sapiens cDNA c	5.7
411543	AW851248		gbcy30R5.r1 NCL_CGAP_UH1 Homo sapiens cDNA c	5.7
426364	AK382083	Hs.159235	ESTs	5.7
444431	AW513324	Hs.42280	ESTs	5.7
406695			predicted exon	5.7
405641	AF039241	Hs.9028	histone deacetylase 5	5.6
488090	AI282149	Hs.50213	ESTs, Highly similar to FOXD3_HUMAN FORKHEAD	5.6
454629	Z45439	Hs.270425	ESTs	5.6
449312	AF291546		gbcy30R5.r1 NCL_CGAP_UH1 Homo sapiens cDNA c	5.6
441223	AA75067	Hs.132499	ESTs	5.6
422562	AI537170	Hs.173725	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFA	5.6
443650	AA688330	Hs.151444	ESTs	5.6
453714			predicted exon	5.6
444166	AL137443	Hs.10441	hypothetical protein FLJ11236	5.6
459114	BE327696	Hs.280622	ESTs	5.6
420620	AA278807	Hs.173343	ESTs	5.5
458228	AA934985	Hs.184846	ESTs, Weakly similar to R08930.1 [H.sapiens]	5.5
448057	R68996	Hs.153373	src homology 3 domain-containing protein HP-55	5.5
427000	AI187420	Hs.145221	ESTs	5.5

	452351	AA025647	glo255d01.1	Scorae, fetal, head, UNH10W	Home sapi
	493359	B99455	glo255d05.1	Scorae, fetal, liver, apicom	NFLS
	493359	AA055834	44.4553	ESTs	(Coloagors homolog) c
	493359	AW757334	WT77215	ESTs	
	493359	H95167	20.2884	ESTs	early endosome antigen 1, 162D
	493359	W95650	26.8418	ESTs	
	416718	R63017	20.0428	ESTs	
	413236	H16442	12.73738	KIA0266 gene product	
	430603	AF035922	11.13566	ESTs	
	443631	AD29124	13.26241	ESTs	
10	452623	AW29962	19.19602	ESTs	
	433982	AA642418	17.3761	ESTs	
	456790	BE309690		glo255d01-20-260300-01-1-g302	BT720
	440743	AW294070	22.23672	ESTs	
	435613	ADJ27811	10.12507	glo255d05.1	predic
	416671	N94087	26.073	ESTs	Modestly similar to HG14, HUMAN NONHIS
	440231	AW015420	16.16323	ESTs	
	429866	AA460134	16.59540	ESTs	
	431772	AA345232	12.12227	ESTs	
	240209	AB014594	13.13759	KIA0594 gene product	
	426614	A1334063	16.16526	ESTs	
	430663	AW902602	18.30280	ESTs	
	468855	T33061	17.27954	ESTs	
	430404	AW040041		glo255d05.1	predic
25	459415	AB904105	18.122016	ESTs	glo255d05.1-100100-012-c05
	409138	W73159	18.58290	ESTs	BT319
	422047	NM_035323	12.12354	HL Histone family, member T (testis-specific)	
	422047	AW503569	17.28216	ESTs	Weakly similar to gco255d05.1 c. coli
	440108			predicted exon	
30	446253	T12198		glo255d05.1	predic
	430366	AA702376	18.22640	glo255d05.1	predic
	440131	T08331	16.16544	Home sapiens clone 24881 mRNA sequence	
	454607	AB014793	16.42262	hypothetical protein PF01488	
	419761	MT1733	16.93177	interferon, beta 1, fibroblast	
35	451250	AA491275	23.23950	Home sapiens cDNA FLJ12542 fs, clone NT2PM000	
	452390			predicted exon	
	444341	AW796342		glo255d05.1	predic
	444341	AB056060	16.207119	ESTs	Weakly similar to intronic factor D12 receptor pr
	441679	BE502267	16.56996	ESTs	
40	450077	AA523752	12.10858	ESTs	
	450129	AJ010233	10.10576	ref finger protein-like 1 antisense	
	451440	AF502698	17.19713	ESTs	
	421126	MT4587	10.10222	insulin-like growth factor binding protein 1	
	447038	A1357968	16.157812	ESTs	
45	447167	R61575		glo255d05.1	predic
	450104	AW010084		glo255d05.1	predic
	442772	AW503680	16.300513	ESTs	Weakly similar to T1587.2 [C.-tagged]
	450859	AV564262	16.28711	Home sapiens cDNA FLJ13016 fs, clone NT2P3000	
	451640	AA115901	16.23141	Human DNA sequence from clone 74723 on chromosome	
	447167	AJ075234	16.176130	ESTs	
	447090	S79281		glo255d05.1	predic
	438224	AA503999		glo255d05.1	predic
	450859	AW793466	16.82396	Z-3-oligohydroxyl synthetase 1	
55	457356	AA489621	16.191670	ESTs	
	430579	R44428	16.20919	ESTs	
	454747	AD320693	16.145328	ESTs	Weakly similar to ALU1, HUMAN ALU SUBFA
	490306	T38653	12.226410	ESTs	
	433382	T64293	29.291453	ESTs	
60	401287			predicted exon	
	424188	AW954552	16.140334	zinc finger protein	
	440688			predicted exon	
	410152	AW593104	16.23881	ESTs	
	444497	AZ04451	16.149196	ESTs	
65	410175	BE261477		glo255d05.1	predic
	429033	NM_037374	16.194766	glo255d05.1	predic
	410336	BE338606		glo255d05.1	predic
	414332	BE339151	16.18498	glo255d05.1	predic
	415283	ANE15703	16.246872	glo255d05.1	predic
70	434782	AA646263	13.132648	ESTs	
	433403	AF040247		glo255d05.1	predic
	456490	AW846020		glo255d05.1	predic
	452334	AW591925		glo255d05.1	predic
	449590	N49590	17.37204	ESTs	
	433977	AA092425		glo255d05.1	predic
	434767	AF134233	22.26142	ESTs	Weakly similar to ALU1, HUMAN ALU SUBFA
	416192	NM_005036	18.398	peroxisome proliferator activated receptor, alpha	
	450218	AA126333	16.10945	ESTs	predicted exon
	427109			predicted exon	
80	444490	A1151080	16.146830	ESTs	
	423632	AW973801	16.134666	ESTs	
	439683	AA813992	15.291842	ESTs	
	424044			predicted exon	
	459862	AB72227	16.199475	ESTs	

[illegible]

WO 02/102235

PCT/US02/19297

419002	T78625	Hs.268594	ESTs	4.7
425582	AL157586	Hs.23737	ESTs	4.7
416986	H16252	Hs.227263	ESTs	4.7
441133	AA918191	Hs.194457	ESTs	4.7
446323	A1288274	Hs.149868	ESTs	4.7
446347	AI125950	Hs.142864	ESTs	4.7
439481	AF098294	Hs.125844	ESTs	4.6
456388	W78557		gb:4628 Human retina cDNA randomly primed sublibrary	4.6
441864	R34177	Hs.181315	ESTs, Moderately similar to ALU4_HUMAN ALU SJ	4.6
445910	FB3483	Hs.260273	ESTs	4.6
405331			predicted exon	4.6
429773	A1332482	Hs.218791	proteoglycan 1 (mogakaryocyte stimulating factor, arctic)	4.6
422563	BE299342	Hs.19345	Homo sapiens cDNA FLJ13119 fs, clone NT2RP30002	4.6
422890	Z43784	Hs.78713	solute carrier family 25 (mitochondrial carrier; phosphate cytochrome c oxidase subunit Via polypeptide 1	4.6
455663	AL048807	Hs.180714	ESTs	4.6
447639	NT2250	Hs.164144	ESTs	4.5
415612	F12893	Hs.13301	ESTs	4.5
433371	T25451		gb:PT1188 HTCDL1 Homo sapiens cDNA 5'3' similar	4.5
410667	AW936099		gb:Q10-DT0020-210100-005-d04 DT0020 Homo sapie	4.5
410850	AW809575		gb:MNA-S10121-090290-002-a12 ST0121 Homo sapie	4.5
404451			predicted exon	4.5
441705	A1087052	Hs.55993	ESTs	4.5
439697	W79579	Hs.58552	ESTs	4.5
407825	NM_005152	Hs.40202	lymphoid-restricted membrane protein	4.5
429773	BE299342	Hs.123119	MAD (methyl agent) decapentaplegic, Drosophila) ho	4.5
456278	BE300369	Hs.42643	ESTs, Weakly similar to KIAA1016 protein (Hsapiens	4.5
424719	H00452		gb:yv0103.r1 Soares fetal liver sp/cen 1NFL5 Homo sa	4.5
438542	AW297571	Hs.17545	ESTs	4.5
444333	A1645644	Hs.282436	ESTs	4.5
438831	BE263373	Hs.301128	ESTs	4.5
410065	AW812744		gb:RC3-ST0186-181099-012-c09 ST0186 Homo sapien	4.5
458395	AA639843	Hs.61548	ESTs	4.5
458250	A807339	Hs.152174	ESTs, Weakly similar to Z140_HUMAN ZINC FINGER	4.5
423403	BE234583		gb:EST28475 Cornebellum II Homo sapiens cDNA 5' en	4.4
454679	AW813110		gb:CM4-ST0189-651099-02-1406 ST0189 Homo sapien	4.4
443368	A021631	Hs.166788	ESTs	4.5
401004			predicted exon	4.5
425837	AF007567	Hs.159609	insulin receptor substrate 4	4.5
420497	AW206285	Hs.253548	ESTs	4.5
449438	AA927317	Hs.176719	ESTs	4.5
429409	AI694817	Hs.155390	ESTs	4.5
447959	AA55294	Hs.270270	ESTs	4.4
407340	AA819168	Hs.232119	ESTs	4.4
424326	NM_014479	Hs.145296	disintegrin protease	4.4
443479	AF027219	Hs.9443	zinc finger protein 202	4.4
443246	T75157	Hs.285516	ESTs, Weakly similar to hypothetical protein (Hsapien	4.4
414475	BE302555	Hs.119598	ribosomal protein L3	4.4
432075	AW972334		gb:EST359330 MAGE reassortment, MAGM Homo sap	4.4
417906	R24769	Hs.23725	ESTs	4.4
406518	V28077	Hs.79389	net (chicken)-like 2	4.4
441460	A1962478	Hs.222604	ESTs, Moderately similar to ALU4_HUMAN III ALU	4.4
405649	T19427	Hs.181244	major histocompatibility complex, class I, A	4.4
426628	AA380828		gb:EST93827 Activated T-cells VII Homo sapiens cDN	4.4
430635	AW968495		gb:EST380561 MAGE reassortment, MAGM Homo sapi	4.4
406479	BE047329	Hs.144483	ESTs	4.3
446536	A1557139	Hs.129179	Homo sapiens cDNA FLJ13501 fs, clone PLACE10090	4.3
411280	N50617		gb:yv59f02.r1 Soares_mulleppl_sclerotic_2N6HMSF H	4.3
440790	AW983060	Hs.126580	ESTs	4.3
458301	AF003834		gb:AF003834 Clontech HT1149x Homo sapiens cDNA	4.3
442277	AW446914		ESTs	4.3
445463	AF570338	Hs.196109	ESTs	4.3
433426	H69125	Hs.133525	ESTs	4.3
410782	AW504680	Hs.288836	Homo sapiens cDNA FLJ12673 fs, clone NT2RM4002	4.3
423040	AA320749	Hs.205464	KIAA1604 protein	4.3
423430	AW079894	Hs.267480	ESTs	4.3
432072	N62937	Hs.269109	ESTs	4.3
452213	AL110237	Hs.28425	Homo sapiens mRNA; cDNA DKFZp566D0224 (from c	4.3
403635			predicted exon	4.3
441919	AK533602	Hs.128121	ESTs	4.3
416717	H79569	Hs.297726	ESTs	4.3
430595	NM_005092	Hs.245197	tumor necrosis factor (ligand) superfamily, member 18	4.2
429269	AA449013	Hs.59203	ESTs	4.2
415840	BT15955	Hs.21758	ESTs	4.2
451300	AA017086	Hs.237646	EST	4.2
446366	A221551	Hs.239662	ESTs	4.2
441934	BE245833	Hs.169954	hypothetical protein SP192	4.2
459105	NM_014517	Hs.28423	upstream binding protein 1 (UBP-1a)	4.2
455387	BE069037		gb:CV3-ET0379-161259-040-e12 ET0379 Homo sapie	4.2
410507	AA355288		ESTs	4.2
453823	AI137967	Hs.271468	gb:DKFZp761D02315_r1 761 (synonym: hamy2) Homo	4.2
403665	AA017245	Hs.32794	ESTs	4.2
426894	AW981585	Hs.276755	ESTs, Weakly similar to F53B1.2 (C-agona)	4.2
455198	AW956964		gb:CD4-CT0299-291150-031-002 CT0299 Homo sapie	4.2
443609	AW60231	Hs.282941	ESTs	4.2

WO 02/102235

PCT/US02/19297

	427469	AA043084	Has.266347	ESTs	4.2
	417178	NS1636		gbyy67b01.s1 Soams_multiple_sclerosis_2NHMSF H	4.2
	439761	A1190390	Has.50704	Home sapiens mRNA full length insert cDNA clone EU	4.2
5	431982	AW418296	Has.105754	ESTs	4.1
	42641	A1890855	Has.262983	ESTs	4.1
	422128	AW881145		gbcVQ-OT00035-010406-162-a07 OT0033 Homo sapie	4.1
	440156	AF103027	Has.171933	prostate cancer antigen 3	4.1
	419668	A1033066	Has.132777	ESTs	4.1
10	418236	AW994005	Has.172672	hypothetical protein FLJ20093	4.1
	432663	A1984317	Has.122689	ESTs	4.1
	446513	BC522462	Has.121698	Home sapiens cDNA FLJ13463 fs, clone PLACE10034	4.1
	411278	AW984776		gbcVQ-OT0067-010306-121-d01 OT0067 Homo sapie	4.1
	440652	A1216751	Has.143877	ESTs	4.1
15	416608	R11499	Has.189716	ESTs	4.1
	420405	AA743396	Has.186023	ESTs	4.1
	405717			predicted exon	4.1
	435267	N23797	Has.110114	ESTs	4.1
	412228	AW503785	Has.73752	complement component (Sd/Estein Barr virus) recipio	4.1
20	403560	A192721	Has.5120	dyein, cytop/asmic, light polypeptide	4.1
	446162	A1932740	Has.10476	ESTs	4.1
	456157	A1903585		gbcVQ-OT0020-090200-106-g05 OT0020 Homo sapie	4.1
	432474	AA594C42		gbcma65609.s1 NCL_GCAP_Lar1 Homo sapiens cDNA	4.1
	455388	AW836234		gbcVQ-OT0020-090200-106-g05 OT0020 Homo sapie	4.0
25	426456	AA390748	Has.130658	ESTs	4.0
	435957	AA811822	Has.171497	ESTs	4.0
	437934	AW683071	Has.77496	small nuclear ribonucleoprotein polypeptide G	4.0
	459355	BE380047		gbc01159362F2 NH_MGC_53 Homo sapiens cDNA	4.0
	430404	AW969559	Has.137240	Home sapiens mRNA for partial 3'UTR, sequence 2	4.0
30	457740	AW502458		gbcUH-FIN0-abb-4-07-0-CLr1 NH_MGC_50 Homo	4.0
	437935	AA757055	Has.164080	ESTs	4.0
	444530	AV550124	Has.282435	ESTs	4.0
	408065	AA046314		gbcZ4/7h10r1 Soares retina N2b4HR Homo sapiens cD	4.0
	411258	AW634039		gbcVQ-TT0016-091199-053-e09 TT0016 Homo sapie	4.0
35	433822	BE54749	Has.148016	ESTs	4.0
	438637	BE500641	Has.128730	ESTs, Weakly similar to KIAA1214 protein [H.sapiens	4.0
	414571	BE410746	Has.22868	protein tyrosine phosphatase, non-receptor type 11	4.0
	446190	AT72929	Has.256564	ESTs	4.0
	443542	A1927065	Has.146040	ESTs	4.0
	430444	AW295421	Has.121035	ESTs	4.0
40	454673	BE146471		gbcVQ-HIT0216-011199-043-c09 HIT0216 Homo sapie	4.0
	403646	AW501749		gbcUH-HF-ER03-ajm-b-12-0-ULr1 NH_MGC_52 Homo	4.0
	466141	AT51357	Has.268741	Home sapiens cDNA: FLJ2256 fs, clone HRC02850	4.0
	450140	AA159515	Has.6006	ESTs	4.0
45	441636	A1459251	Has.144481	ESTs	4.0
	410877	T83470		gbyd40g06r1 Soares fetal liver spen 1NFLS Homo s	4.0
	401740			predicted exon	4.0
	420122	AA255714	Has.284153	Fanconi anemia, complementation group A	4.0
	424594	AW272467	Has.254655	Unlited	3.9
50	426294	AA374195		gbcEST38289 HSC172 cells 1 Homo sapiens cDNA 5' e	3.9
	411922	AW878280		gbcPMA-PT0019-131299-005-E04 PT0019 Homo sapie	3.9
	452320	AA242873	Has.160412	ESTs	3.9
	431544	AW972822	Has.165248	cytochrome c	3.9
	408932	AW956113		gbcEST358183 MAGE resequences, MAGO Homo sap	3.9
	418132	T32670	Has.117421	ESTs	3.9
55	414372	AA143654		gbcz065602r1 Stratiogene pancreas (S37206) Homo sap	3.9
	400195			predicted exon	3.9
	418900	M59964	Has.1048	KIT ligand	3.9
	445444	AA380876	Has.270	pleckstrin homology, Sec7 and coiled-coil domains, bind	3.9
60	439597	N30015	Has.190389	ESTs	3.9
	442299	AW467791	Has.155561	ESTs	3.9
	413493	AA460136	Has.177638	ESTs	3.9
	438403	AA806607	Has.292206	ESTs	3.9
	440386	AA001308	Has.193213	ESTs	3.9
65	442303	BE568510		gbc01142622F1 NH_MGC_53 Homo sapiens cDNA	3.9
	405481			predicted exon	3.9
	453630	AW021633		gbc120602y1 Morton Fetal Cochlea Homo sapiens cDN	3.9
	415550	AA385143	Has.125719	ESTs	3.9
	416874	H68752	Has.42568	ESTs	3.9
70	445855	AW639822		gbcVQ-LT0036-150209-074-h06 LT0036 Homo sapie	3.9
	416895	298357		gbcHS299652 DKFZ/plazmy1 Homo sapiens cDNA clone	3.9
	440962	A1889951	Has.233477	ESTs, Moderately similar to A Chain A, Scrypa Compl	3.9
	419401	AW804653		gbcVQ-UM0094-160300-135-d05 UM0094 Homo sap	3.9
	406562			predicted exon	3.8
75	402690	BC409855	Has.808	heterogeneous nuclear ribonucleoprotein F	3.8
	435622	AA677428	Has.189731	ESTs	3.8
	402451			predicted exon	3.8
	451577	N56101	Has.32703	ESTs	3.8
	457141	AA521410	Has.41371	ESTs	3.8
	407817	H62553	Has.40400	ESTs	3.8
80	412613	AA553507	Has.265711	Home sapiens cDNA FLJ13089 fs, clone NT21970021	3.8
	418356	LA2563	Has.1165	ATPase, H+K+ transporting, noncatalytic, alpha polypep	3.8
	442537	AW161533	Has.300895	ESTs	3.8
	407448	A301065		gbcHomo Sapiens mRNA, partial cDNA sequence for h	3.8
	456383	A1148037		gbcz41e01r1 Soares_testes_NHT Homo sapiens cDNA	3.8

WO 02/102235

PCT/US02/19297

444651	WS8469	Hs.103120	ESTs	3.8
465067	AW864538	Hs.130645	gt:RC3-CT0255-200100-024-b02 CT0255 Homo sapie	3.8
429657	BE320531	Hs.104972	ESTs	3.8
429142	AA835639	Hs.104972	ESTs	3.8
429274	AJ379772	Hs.99206	ESTs	3.8
437774	AW878199	Hs.291648	ESTs	3.8
427737	AA435986	Hs.178966	ESTs, Weakly similar to AF068289 5 HDOME31P H.s predicted exon	3.8
406671				3.8
413627	BE182082	Hs.246973	ESTs	3.8
438958	R37529	Hs.269924	ESTs	3.8
416512	H70565		gt:R9704r1 Soares fetal liver sapien 1NFLS Homo sa	3.8
423045	AW967472	Hs.301511	ESTs, Highly similar to KP72_HUMAN SERINE/THR	3.8
453361	AA035197	Hs.107375	ESTs	3.7
437243	AA747548	Hs.259122	ESTs	3.7
437987	AW452002	Hs.122963	ESTs	3.7
408781	BE148621	Hs.254602	ESTs	3.7
455895	BE154837		gt:PM1-IT0345-121199-001-c08 IT0345 Homo sapie	3.7
431492	AW612343		gt:hlg97e10.x1 NCL_CGAP_IQd11 Homo sapiens cDN	3.7
413247	AW953939		gt:EST376042 MAGE resequencs, MAGH Homo sap	3.7
422896	NL_002410	Hs.121502	minoxyl (alpha-1,6)-glycoprotein bota-1,6-N-acetyl-g	3.7
431828	AA572994		gt:unzS3F12.x1 NCL_CGAP_Lipo Homo sapiens cDNA	3.7
438872	R64197	Hs.235589	ESTs	3.7
438873	AI824717	Hs.123443	ESTs	3.7
419624	H89044		gt:077056.s1 Soares fetal liver sapien 1NFLS Homo sa	3.7
401983			predicted exon	3.7
428967			predicted exon	3.7
408315	A/W170148		gt:VR4-ST0067-200899-002-B07 ST0067 Homo sapie	3.7
418320	D89581	Hs.84084	amyloid beta precursor protein (cytoplasmic tail)-bindi	3.7
447199	AJ394421	Hs.160910	ESTs	3.7
422890	AA312768	Hs.103846	Homo sapiens cDNA FLJ139652, clone Y79AA10012	3.7
451996	AW514021	Hs.245510	ESTs	3.7
412463	AW553444	Hs.78672	tannin, alpha 4	3.7
448928	ALJ46576	Hs.130198	ESTs	3.7
441951	W51902	Hs.128188	ESTs	3.7
447005	A904244	Hs.153206	ESTs	3.7
434231	AF119901	Hs.250658	hypothetical protein PRO2831	3.7
411039	AL135674	Hs.163348	ESTs	3.7
413137	BE068915		gt:PM0-BT0340-231199-001-b07 BT0340 Homo sapie	3.7
417970	AA309234	Hs.57760	Homo sapiens cDNA:FLJ23119 fs, clone LUG07978	3.7
438786	AW552707	Hs.33759	Homo sapiens cDNA full length insert cDNA clone EU	3.7
458956	ALJ40421		gt:CHKFZp434B0714_r1 434 (synonym: htes3) Homo s	3.7
443501	A078564	Hs.15682	ESTs	3.6
404041			predicted exon	3.6
405122			predicted exon	3.6
404582			predicted exon	3.6
455786	BE090077		gt:RC9-BT0710-300300-021-F02 BT0710 Homo sapie	3.6
411889	AA370573		gt:EST82238 Prostate gland 1 Homo sapiens cDNA 5' e	3.6
428758	ALJ38430	Hs.197772	ESTs	3.6
421776	AW301994	Hs.108183	candidate tumor suppressor p33 ING1 homolog	3.6
430169	AA468531	Hs.188047	ESTs	3.6
407695	AI808007	Hs.68450	ESTs	3.6
454564	AW007573		gt:MFI-ST0068-021299-004-g01 ST0068 Homo sapie	3.6
425902	X52509	Hs.161640	tyrosine aminotransferase	3.6
439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN ALU SU	3.6
428966	AA486555	Hs.178222	ESTs	3.6
428690	AW84490	Hs.580765	ESTs	3.6
437302	AA837146	Hs.180275	ESTs	3.6
443973	AI580083	Hs.176154	ESTs	3.6
453993	AW615224	Hs.252839	ESTs	3.6
413523	A4825721	Hs.246973	ESTs	3.6
429196	NL_001474	Hs.169765	carboxypeptidase M	3.6
424916	AW867440	Hs.23096	ESTs	3.6
424769	H06469	Hs.142553	rat finger protein	3.6
403080			predicted exon	3.6
421521	AI838760	Hs.161795	ESTs	3.6
426549			predicted exon	3.6
446114	AJ275715	Hs.145926	ESTs	3.6
441392	AW451831	Hs.222119	ESTs, Weakly similar to K1CQ_HUMAN KERATIN, T	3.5
424025	AT701852	Hs.301296	ESTs	3.5
446527	AJ526806		gt:PT1.3_03_G05r tumor1 Homo sapiens cDNA 5', mR	3.5
437063	AA351109	Hs.54537	Tax1 (human T-cell leukemia virus type I) binding prot	3.5
448880	AW73006	Hs.231948	ESTs, Weakly similar to ALU8_HUMAN H1 ALU CL	3.5
444931	AW57014		gt:LA9142.x1 NCL_CGAP_G05 Homo sapiens cDNA c	3.5
442999	AW852889	Hs.132395	ESTs	3.5
416238	W90448		gt:zh76d08.s1 Soares fetal liver, sp/oen_1NFLS_s1 H	3.5
432309	BE778508	Hs.106823	H.sapiens gene from PAC 42816, similar to syntrophin 7	3.5
409854	AW501833		gt:UH-GR0p-gp4-d-01-a.U.r1 NHL_MGC_S2 Hom	3.5
414941	C44855	Hs.182159	ESTs	3.5
456337	AW751651	Hs.65819	ESTs	3.5
415296	F05066		gt:H3C01A011 normalized infant brain cDNA Homo s	3.5
423338	AB007991	Hs.127338	KIAP4622 protein	3.5
415618	F12954		gt:H3C3G091 normalized infant brain cDNA Homo s	3.5
405583			predicted exon	3.5
439501	AF217509	Hs.283077	control/normal P4.1-associated protein; uncharacterized bo	3.5

WO 02/02235

PCT/US02/19297

	450897	AA011454	Hs.245122	ESTs	
	431339	AA500204	Hs.257266	ESTs	
	441969	AF733386	Hs.129154	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	
5	431343	AW970903	Hs.300941	Homo sapiens cDNA FLJ11651 fs, clone HEMBA100	
	434317	AF674095	Hs.116323	ESTs	
	414741	FS13321	Hs.25780	Homo sapiens cDNA FLJ12522 fs, clone MAMMA10	
	437077	AW297702	Hs.102815	ESTs	
	431778	AF631241	Hs.47312	ESTs	
	400397	AJ270770	Hs.154485	transcription factor 7-like 2 (T-cell specific, HMG-box)	
	455887	BE154173	Hs.123014	glatPM1-HT0340-201299-004-012 HT0340 Homo sapie	
	434362	W72081	Hs.295446	ESTs	
	409211	AF076835	Hs.290969	glczm9H04Ls1 Skagapone colon HT29 (S37221) Homo	
	414390	BE281040	Hs.102815	glu501156234F1 NH_MGC_21 Homo sapiens cDNA	
	457142	AB24353	Hs.290969	EST	
	423005	LT2970	Hs.123014	anti-Mullerian hormone receptor, type II	
	453363	AB95775	Hs.232623	ESTs	
	418913	BE046745	Hs.137057	glutrh39t06.x1 NOL_OGAP_RDF2 Homo sapiens cDN	
	440016	AW116114	Hs.137057	ESTs	
	405096			predicted exon	
20	435072	AW592176	Hs.116932	ESTs	
	436535	LG9078	Hs.137476	gluHomo sapiens mRNA fragment	
	424001	W67883	Hs.137476	KIAA1051 protein	
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	
25	410387	AA370706	Hs.11252	ESTs, Weakly similar to Weakly similar with the Yye6	
	494543	AW068695	Hs.102815	gluQV4-ST0923-10400-172-05 ST0923 Homo sapien	
	419515	S81944	Hs.30791	gamma-aminobutyric acid (GABA) A receptor, alpha 6	
	410280	AA083558	Hs.261286	ESTs	
	425714	AW363278	Hs.102815	gluEST373531 MAGE resequences, MAGH Homo sap	
30	416895	AW961600	Hs.102815	gluEST373672 MAGE resequences, MAGG Homo sap	
	427935	AW503687	Hs.119424	ESTs, Weakly similar to unnamed protein product (H1a	
	411673	BE064663	Hs.102815	gluRC1-ET0313-110300-015-006 ET0313 Homo sapien	
	453339	AW992699	Hs.252797	ESTs	
	424696	BE435647	Hs.151993	Homo sapiens clone 24706 mRNA sequence	
35	436242	AJ002187	Hs.129469	gluHomo sapiens cDNA FLJ11325 fs, clone PLACE10	
	442837	AJ022082	Hs.50492	ESTs	
	452807	AA028933	Hs.162434	ESTs	
	418110	R43523	Hs.217754	Homo sapiens cDNA: FLJ22202 fs, clone HRC01333	
	433936	AJ208172	Hs.129469	ESTs	
	438177	AT744955	Hs.267072	ESTs, Moderately similar to ALU4_HUMAN ALU SU	
40	401896			predicted exon	
	406237	AL110157	Hs.3843	predicted exon	
	457658	498514	AW363592	Hs.75323	Homo sapiens mRNA: cDNA DKFZp586F2224 (from
	421916	R34441	Hs.101007	Homo sapiens cDNA: FLJ23545 fs, clone LNC08361	
45	413321	NA8146	Hs.269069	ESTs	
	447876	AV654978	Hs.13904	cystathionase (cystathionine gamma-lyase)	
	406157			predicted exon	
	443005	AJ022184	Hs.200918	ESTs	
50	450078	AB81743	Hs.151529	glu3b38g10.x1 NOL_OGAP_Lu24 Homo sapiens cDNA	
	431301	AA502384	Hs.151529	ESTs	
	430202	T85715	Hs.27041	gluY60y02L1 Soares fetal liver spleen TNFSL Homo s	
	428559	H24338	Hs.27041	ESTs	
	459731	BE072188	Hs.88653	gluQV4-ET0536-211299-055-009 ET0536 Homo sapie	
55	420735	AW297440	Hs.88653	ESTs	
	430881	NM_000809	Hs.249112	gamma-aminobutyric acid (GABA) A receptor, alpha 4	
	405836			predicted exon	
	449178	AB633748	Hs.197597	ESTs	
	453265	U61232	Hs.32675	tubulin-specific chaperone e	
60	430700	AA768392	Hs.247812	H2A histone family, member K, pseudogene	
	424498	AT733451	Hs.125212	ESTs	
	446963	AB62968	Hs.178333	ESTs	
	422879	AJ241409	Hs.188092	ESTs	
	419631	AW448930	Hs.5415	ESTs	
65	449570	AA001793	Hs.104671	glu2rh6K06.x1 Soares fetal liver spleen TNFSL S1 H	
	402625			predicted exon	
	412319	AW936903	Hs.104671	gluRC1-DT0029-030200-012-002 DT0029 Homo sapie	
	401350			predicted exon	
	433098	AF065955	Hs.202526	gluHomo sapiens full length insert cDNA clone YR895	
	455659	AJ01565	Hs.25940	ESTs	
70	420749	AJ242956	Hs.25940	v-myc avian myelocytomatosis viral related oncogene, n	
	430689	AB965956	Hs.293219	ESTs	
	454753	AW819212	Hs.30818	gluCM1-ST0263-071299-061 -07 ST0263 Homo sapie	
	444479	AA159480	Hs.30818	Homo sapiens cDNA FLJ13081 fs, clone PLACE2000	
75	413516	BE143807	Hs.102815	gluM99-HT0308-221295-204-x12 HT0308 Homo sapie	
	425541	AA369119	Hs.165796	gluEST618172 Fetal lung II Homo sapiens cDNA 5' end,	
	457107	AA418246	Hs.165796	ESTs, Weakly similar to hMIB.1 [Hsap]sapiens	
	421480	NM_016158	Hs.104671	oxythiocyto transmembrane protein	
	444289	BE287080	Hs.76391	myxovirus (influenza) resistance 1, homolog of murine	
80	417725	RS2525	Hs.21503	ESTs	
	453631	AL046418	Hs.34037	gluDKFZp334N247_r1.434 (synonym: hhs3) Homo sa	
	450692	H50903	Hs.34037	hypothetical protein FLJ23063	
	413357	W47511	Hs.1661	glu2335K06.x1 Soares_sarcomer1 [Hs]oblasts_NIH5-FH	
	415327	H22789	Hs.1661	membrane protein, polyanionic 1 (PSD)	
	457569	AW970021	Hs.291120	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFA	

WO 02/102235

PCT/US02/19297

	448601	R61655	Hs.293690	ESTs	3.3
	438526	AW993033	Hs.287681	Homo sapiens cDNA: FLJ21695 fls, clone COL09372	3.3
	446689	BC307753	Hs.194478	Homo sapiens mRNA: cDNA DKFZp354D1572 (from cold shock domain protein A	3.3
5	426768	AW030337	Hs.270411	ESTs	3.3
	400394	AF040257	Hs.283618	Homo sapiens TNF receptor homolog mRNA, partial cd	3.3
	433665	AA589763	Hs.112630	ESTs	3.3
	424055	AA330028		gk:EST139621 Epithelium Homo sapiens cDNA 5' end,	3.3
10	449562	AA001742	Hs.83722	ESTs	3.3
	431692	AA521315	Hs.194424	ESTs	3.3
	405512			predicted exon	3.3
	440300	A1354717	Hs.223908	ESTs	3.3
	457729	AE121663	Hs.263467	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFA	3.2
	417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	3.2
15	456420	AW041361	Hs.91773	protein phosphatase 2 (formerly 2A), catalytic subunit,	3.2
	404397			predicted exon	3.2
	427145	RS2635	Hs.29935	ESTs	3.2
	406454			predicted exon	3.2
20	441033	BE562555	gb:01336857F1 NIH_MGC_44 Homo sapiens cDNA	3.2	
	408444	AW651639	Hs.263004	ESTs	3.2
	434739	AA044687	Hs.144130	ESTs	3.2
	437090	AA745591	Hs.292053	ESTs	3.2
	423092	BE274837	Hs.123637	putative homeodomain transcription factor	3.2
	424686	US8331	Hs.161899	sarcosylcyan, delta (3&D dihydroxyphenyl-associated glycop	3.2
	443362	AE653464	Hs.195055	ESTs	3.2
	437600	AL300150	gk-Homo sapiens mRNA: cDNA DKFZp547L158 (from	3.2	
	425468	H69317	Hs.162669	ESTs	3.2
	438171	AA831133	Hs.294128	ESTs	3.2
30	407947	AW890158	gk-RC0-CT0379-290100-032-b04 CT0379 Homo sapie	3.2	
	436508	AW183871	Hs.250896	ESTs	3.2
	426743	AA383833	Hs.245022	ESTs	3.2
	457525	AW973800	gk-EST389031 MAGE resequenes, MAGEM Homo sap	3.2	
	413800	AL129238	Hs.192235	ESTs	3.2
35	414193	BE260929	gk-001150906AF1 NIH_MGC_19 Homo sapiens cDNA	3.2	
	456595	BE000537	gk-RC3-BN0072-240200-011-b07 BN0072 Homo sapie	3.2	
	410081	T91029	Hs.13099	ESTs	3.2
	450955	T89966	Hs.16789	ESTs	3.2
	458529	AV552120	Hs.213322	ESTs	3.2
40	424751	AA759482	Hs.293320	ESTs	3.2
	442225	AL305597	Hs.129192	ESTs	3.2
	410990	AW812929	gk-RC3-ST0186-250200-018-c05 ST0186 Homo sapie	3.2	
	435844	AA700857	Hs.293630	ESTs	3.2
	405347			predicted exon	3.2
45	441202	AL632143	Hs.136853	ESTs	3.2
	449594	AV550942	Hs.258132	ESTs	3.2
	454552	AW812066	gk-RC4-ST0173-191099-032-a07 ST0173 Homo sapie	3.2	
	419885	AL042330	Hs.87128	ESTs, Weakly similar to similar to YB64 YEAST [C.e]	3.2
	430118	AL377265	Hs.163267	ESTs	3.2
	430591	C14167	Hs.103538	ESTs	3.2
50	415313	H47205	Hs.194109	ESTs, Weakly similar to ALU0_HUMAN [H] ALU CL	3.2
	445122	AL352790	Hs.181601	ESTs	3.2
	453725	W62543	gk-Hb05 Human retina cDNA randomly primed subclona	3.2	
	453954	AW116338	Hs.75251	DEADH (Asp-Glu-Ala-Asp-His) box binding protein 1	3.2
	428195	AA423849	Hs.79630	M5-14 protein	3.2
55	447505	R78778	Hs.29808	Homo sapiens cDNA: FLJ21122 fls, clone CA605917	3.2
	401671			predicted exon	3.2
	442190	AL337127	Hs.155325	ESTs	3.2
	404708			predicted exon	3.2
	412588	AW930555	Hs.44024	ESTs	3.1
60	431975	AA715001	Hs.291055	ESTs	3.1
	408864	AW870124	Hs.261172	ESTs	3.1
	433811	AW975015	Hs.123136	ESTs	3.1
	431691	AE086511	Hs.292510	ESTs	3.1
	418719	AW975590	Hs.101707	ESTs	3.1
65	431740	NT5450	Hs.153412	ESTs, Moderately similar to A6-1156721 57 PR01777 [H	3.1
	435059	AD01448	Hs.213724	ESTs	3.1
	459344	AW499633	Hs.257976	ESTs	3.1
	431729	AW064714	Hs.162033	ESTs	3.1
	436771	AW975587	Hs.252079	ESTs	3.1
70	434460	AW982866	Hs.55365	Homo sapiens clone IMAGE:112574 mRNA sequence	3.1
	459547	AL400579	Hs.225186	EST	3.1
	427962	AA945682	Hs.133545	Homo sapiens cDNA: FLJ21120 fls, clone CA605691	3.1
	403743			predicted exon	3.1
75	413560	BE148411	gk-AR0-H10214-131299-002-004 H10214 Homo sapie	3.1	
	454372	H93543	Hs.283565	FOS-like antigen-1	3.1
	450016	AA421642	Hs.24309	hypothetical protein FLJ11106	3.1
	428639	AI767756	Hs.82302	ESTs	3.1
	407110	AA013042	Hs.93078	ESTs	3.1
	426133	TT7521	Hs.191124	ESTs	3.1
80	418672	RS4765	Hs.270263	ESTs	3.1
	404416			predicted exon	3.1
	446877	AE594472	Hs.270720	ESTs	3.1
	429553	AA441957	Hs.194114	ESTs	3.1
	425169	H16822	gk-yen26d7.1 Soares infant brain 1N6 Homo sapiens	3.1	

WO 02.102235

PCT/US02/19297

	404134			predicted exon	3.1
	441404	AW63680	Hs.126895	ESTs	3.1
	420075			predicted exon	3.1
5	411676	AW961336	Hs.69705	ESTs, Weakly similar to KIAA0443 (H.sapiens)	3.1
	451048	AA013349	Hs.60602	ESTs	3.1
	447021	A135654	Hs.161406	ESTs	3.1
	404083			predicted exon	3.0
	415835	H05175	Hs.107510	ESTs	3.0
10	402142			predicted exon	3.0
	415820	R53720	Hs.189745	ESTs	3.0
	441140	AW016634	Hs.228994	ESTs	3.0
	445376	AA001278	Hs.59905	ESTs	3.0
	457593	A1735615	Hs.117323	ESTs	3.0
15	411542	AW650767		gb L3-CT0220-031199-025-A05 CT0220 Homo sapien	3.0
	403375			ESTs	3.0
	445561	AI022240	Hs.17924	ESTs	3.0
	406241			predicted exon	3.0
	420306	AA258318	Hs.219226	ESTs	3.0
20	413161	BE068130		gb CM2-BT0368-171295-056-s01 BT0368 Homo sapie	3.0
	448221	BE022615		gb B01440775T1 NIH_MGC_72 Homo sapiens cDNA	3.0
	415920	Z4584		gb H02202121 normalized infant brain cDNA Homo	3.0
	459135	A1902802		gb RC-RT0105-311296-026 ET0105 Homo sapiens cDNA	3.0
	425357	AA355942		gb E8764303 Junkal T-cells VI Homo sapiens cDNA 9'	3.0
25	454724	AA091228		gb ucshn2152.asq.F Human fetal heart, Lambda ZAP Ex	3.0
	429395	AF002071	Hs.201624	hypothetical protein FLJ11209	3.0
	427807	AA405119	Hs.270470	ESTs	3.0
	443598	AW499970	Hs.14822	ESTs	3.0
	437948	AA772920		glv ao73c09.s1 Stratagene schizo brain S11 Homo sapien	3.0
30	418105	AW937488	Hs.178000	ESTs	3.0
	425763	AL042262	Hs.172101	Human DNA sequence from clone RP1-20221 on chro	3.0
	403473			predicted exon	3.0
	427501	A1365280	Hs.131743	ESTs	3.0
	453246	NM_000933	Hs.32539	KIAA1264 protein	3.0
35	404587	M95657	Hs.104134	homeo box (H6 family) 1	3.0
	433964	AV241187	Hs.197025	ESTs	3.0
	453472	AL031925		gb CfXp564M037.1 s64 (synonym: hbr2) Homo sa	3.0
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.0
	435899	W69063	Hs.189914	ESTs	3.0
40	425265	A637528	Hs.175519	ESTs	3.0
	428651	AA954878	Hs.59567	ATPase, H(+)-transporting, lysosomal, noncatalytic acc	3.0
	426593	AY958560		gb E5370030 MAGE resequences, MAGE Homo sapie	3.0
	431899	AA521381	Hs.187726	ESTs	3.0
	422406	AF025441	Hs.116206	Opa-interacting protein 5	3.0
45	448178	AW79482	Hs.170789	ESTs	3.0
	404227			predicted exon	3.0
	440575	AA889870	Hs.128006	ESTs	3.0
	431198	AL047634	Hs.231913	ESTs	3.0
	424221	AF115685	Hs.283040	hypothetical protein PRO2543	3.0
50	459459	AA480445		gb uzs66h.11.1 Soares_tetal_fetus_Nb2HFB_9w Homo	3.0

TABLE 5B:

Key: Unique Eco protocol identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

55	Key	CAT Number	Accession
	427596	100049_1	R88913 R88901 H25352 R01370 H43764 AW044451 W21208
	407647	100756_1	AW860158 AW862385 AW860159 AW862386 AW862341 AW821869 AW821893 AW862690 AW062656
	408066	103649_1	AA048914 AA057231 H38371
60	408315	1051132_1	AW179148 AW179150
	429211	110906_1	AA078619 AA078319 AA078816 AA079026 AA122167 AA111333 AA089899 AA048691 AA068999 AA069038 AA069225 AA069222
	408099	1149033_1	BE154650 BE154785 AW468343 BE154816 BE154697
	409846	1156150_1	AW501748 AW502972 AW502513
	409854	1156229_1	AW501833 AW502145 AW502681
65	409892	1157619_1	AW565113 AW503580
	410065	1174526_1	AW812744 AW818074 AW812725
	410454	1204154_1	AW749041 BE066025 H85202
	410495	1205826_1	N55428 W24040 AW751336 H81987
70	410596	121053_1	AA374168 AW963684 AA086107 AW91986
	410667	121677_1	AW930099 AW935243 AW936097 BE162104 BE162109 AW794263
	410786	121989_1	BE35956 AW900177
	410890	1226008_1	AW909575 BE090626 BE090617 AW936651 AW936552 AW935030 AW936550 AW936481
	410990	1228648_1	AW812928 AW812773 AW813088
	411256	1236790_1	AW834038 AW934040 AW934047 AW845410 BE0303126 AW855479
75	411279	1237516_1	AW854776 AW9356737 AW9353061 AW835247 AW935246 AW935263 AW935240 AW835258
	411280	123758_1	NE0617 H47321 H54159 AW860545 AW863317
	411337	1239217_1	AW827349 AW827355 AW827117
	411542	1240995_1	AW850767 AW851180 AW851358 AW851223 AW851360 AW851222 AW851108
	411543	1249127_1	AW851249 AW851425 AW850305 AW851021 AW850305
80	411673	1252737_1	BE054881 BE153698 AW856575 BE153820 BE046737 BE153674 BE046730 BE060502 BE153536 AW856622 BE155079 BE064651
			BE153695 BE064650 BE064691
	411899	126497_1	AA370573 BE160501 BE160500 BE160498 BE160502 BE160497 N7424 AA095462
	411922	126625_1	AW876200 AW876209 AW876240 AW876146 AW876323 AW876320 AW876171 AW876241 AW876227 AW876243
	412319	1268002_1	AW936933 AW936907 AW936890 AW936914

WO 02/102235

PCT/US02/19297

	413480	129828_1	BE142364 BE142341 AA112025
	417232	132385_1	AW963300 H23107 R22345
	413137	1350383_1	BE066915 BE066942
5	413161	1351262_1	BE068130 BE068135 BE068134 BE068183 BE068184 BE068094
	413247	135544_1	AW963959 AW963971 AA127651 AA376726
	413357	1354155_1	W4761 H3091851
	413516	1374595_1	BE145807 BE145796 BE145851 BE145823 BE145812 BE145809 BE145852 BE145856
	413560	1376621_1	BE148411 BE148415 H59086
	414193	1424706_-2	BE760099
10	414337	1436706_1	BE386906 BE275195 BE274984
	414372	143939_1	AA143654 AW753140 AA213770 AW870855 AA569075 AA492132
	414390	1441570_-1	BE281040
	415296	1533628_1	F05086 F05091 R17158
	415618	1540651_1	J12954 H10624 R11948 R56523 T75190
15	415920	1561733_1	Z45594 H06361 R53285
	416211	1578988_1	R14625 R17552 H29120 R14650
	416238	1590451_1	W90448 H30749
	416612	1603885_1	H70565 N77403 H67949
	416624	1604694_1	HE9044 T47567 H75991 T50292
20	416577	1608621_1	T53470 T94253 H74054
	416856	162674_1	AW961600 AA190217 AA321260
	417178	1655565_1	N51638 TS1674 TS1829
	417762	168750_1	AA205976 AA205930
	418913	180522_1	BE240745 A08748 H817476 AW572513 AA447586 H2B330 AA232486 AA355704 BE271167
25	418401	184454_1	AW804953 AW805017 AA235969
	419696	1886662_1	Z99362 Z99363
	420352	192979_1	BE258635 AW568310 AA258918 AW843305 R14744 A1603388 BE071932 R63620
	421418	202288_1	AA126539 AA291038 AA339274 AW978886
	422046	210744_1	AK339622 H06120 H35401 F07773 F55636
30	422128	211994_1	AW881145 AA490718 H85637 AA304575 T06067 AA331961
	423403	227942_1	AA325483 AW962169 AW962660
	424093	235233_1	AA335026 AA335496 AW966145
	424719	242389_1	H08462 AA344757 AW964502 H00399
	425189	247825_1	H16622 R17322 AA351959
35	425357	260578_-1	AA355842
	426541	252945_1	AA359119 AW663014 D79564
	426714	256333_1	AW963276 AA362296 AA362287
	428294	259994_1	AA374185 AW665180 H35544
	428528	268722_1	AA380828 AW963790 AA380005 AA380080
40	426593	269748_1	AW958560 AA382199 AW444933
	429232	314322_1	T55775 AW96345 AA465986
	430535	319643_1	AW965486 AW965670 AA489922 BE350425
	431075	327638_1	BE267477 AA491488 AW8361723
	431492	333630_1	AW612343 AA922559 AA505025 AA920738 AW972537 AW935564
45	431828	338201_1	AA572994 AA616249 AA710295
	432075	341086_1	AW972634 AA525260 AA525266 AA835021 BE000149 BE000148
	432474	348197_1	AA584422 AW673273 AA548376
	433371	364400_1	T26461 AA585296 AA565306
	433403	36534_-1	AF040247
50	433767	374014_1	AA605245 AA724581 AK241989 AS777274 T47300
	434738	382562_1	AA836260 AA846286 AW974410
	435195	41562_1	AK001084 AA787092 AA829049
	436242	41641_1	AK002187 R66351
	439812	427323_1	AW928087 AA791645 AA810101 AW194180 AW806073 AW897773
55	437500	43772_1	AL390150 AW959162 AA558823
	437948	446966_1	AA772020 D58870 D61151 AW91331
	438224	462650_1	AA933960 AA781181
	438535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
60	439098	46869_1	AF085955 H61581 H60081
	439125	46887_1	AF085984 H59595 H65906
	441033	59007_-1	BE562565
	443283	59452_-1	BE586610
	446597	644513_1	HE05649 AW753545 A0244270
65	446932	651925_1	A0261545 N59134 AW875371 AW875247
	448221	76534_-1	BE622615
	448527	766707_-1	A0525606 BE549857
	448732	77779_-1	BE614063
	449311	804513_1	A0557014 AW684035 A0557036 AW38390
	449570	91016_1	AA001753 AA401871
70	450078	813882_1	A0618743 AW897287 AW897205 AW897284
	452351	91233_1	AA026647 R45716 AW753796
	452453	918300_1	AA02519 AW802518 A0902516
	453472	96337_1	AL037325 AL037331 AL037367
	453530	97021_1	AW021633 AL036730 A0866854
75	453631	979074_1	AL046418 N52738 R23840
	453725	97960_1	W28543 AL119531
	453752	97989_1	AL120806 BE378500
	453823	982596_1	AL137967 BE064480 BE064186
	454102	1011603_1	AW752363 BE147120 N22640
	454487	1216101_1	AW796342 AW796356 BE161430
	454543	1223776_1	AW809858 AW8065476 AW806495 AW805535 AW806623
	454564	122440_-1	AW807573 AW807656 AW807672
80	454573	1226264_1	BE146474 AW833743 AW833609 AW821469 AW821488 AW821541 AW821513 AW821514 AW821549 AW821364 AW821625 AW821577
			AW821541 AW824577

WO 02/102235

PCT/US02/19297

5	454052	1228071_1	AWB12088 AWB12105 AWB12082
	454079	1228029_1	AWB13110 AWB13113
	454274	12128_1	AWB12281P AWB12107P
10	454353	123576_1	AWB10212 AWB19170 BE158474 AWB19172 AWB19213 AWB19200 AWB19256 AWB19254 AWB19178 AWB19214 AWB19215 AWB19233 AWB19171
	454485	123894_1	AWB39522 AWB7819 AWB7688 AWB36919 AWB36987 AWB36906 AWB36912 AWB36993
	454540	124566_1	AWB46202 AWB45174 AWB46532 AWB46181 AWB46458 AWB46206 AWB46432 AWB46553 AWB46197 AWB46198 AWB46180 AWB46459 AWB46530 AWB46550 AWB46512 AWB46470 AWB46458 AWB46192 AWB46552 AWB46557 AWB46531
15	454594	1248637_1	AWB50176 AWB46533 AWB46462 AWB46151 AWB46649 AWB46538 AWB46527 AWB46567 AWB46531
	454595	1250924_1	AWB50517 AWB50513 AWB50542 AWB50451
	454597	1250924_1	AWB53057 AWB53039 AWB53042 AWB53050 AWB53114 AWB53105 AWB53102 AWB53111 AWB53121 AWB53109 AWB53126
20	454598	1250918_1	AWB54538 AWB54549 AWB545412
	454598	1250918_1	AWB55885 AWB55885 AWB55885
	454598	1250918_1	BE069037 AWB536025 BE069178 AWB36034
25	454598	1250918_1	AWB536234 AWB53074 AWB536181 AWB536171 AWB536217 AWB536077 AWB536227 AWB536191
	454598	1250918_1	AWB51925 AWB51919
	454598	1250918_1	BE00537 BE10584 BE180540 BE180542 BE180546 BE072189 BE072229 BE072298 BE072317 BE072238
30	454598	1250918_1	BE090077 BE090079
	454598	1250918_1	BE090090 BE090088 BE090081 BE090093 BE090075
	454598	1250918_1	BE154173 BE154098 BE154096
35	454598	1250918_1	BE154837 BE154679 BE154850 BE154877 BE154835 BE154849 BE154902 BE154905 BE154967 BE154901 BE154904 BE154899
	454598	1250918_1	T12198 T19584 T11583 T15526 T15585 T45876 T15562
	454598	1250918_1	A148037 AA287178 AA236756
40	454598	1250918_1	W25557
	454598	1250918_1	AWB73900 AA57589 AA59886
	454598	1250918_1	AWB500458 AW169000 AF161362 AF150327 AW578353 AW360921 AW360920 AW360902 AW360900 AW360900
45	454598	1250918_1	AF003834 W36292
	454598	1250918_1	A902802 A902783 A902800
	454598	1250918_2	A904385 A904382

TABLE 5C:

Key: Unique number corresponding to an Eos prebset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:499-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

40	400842	7656749	Minus	91553-91757,52720-52843,53962-94079,94624-94907
	401004	722982	Plus	62580-62772
	401267	9801612	Minus	42287-42431
45	401308	9212516	Plus	16390-163949
	401350	963128	Plus	14471-14623
	401740	2982169	Plus	148357-148484,148591-148690
50	401871	8079355	Minus	58153-58305
	401898	8669134	Plus	115129-115294
	401963	3126783	Plus	51382-51521
55	402105	8131588	Minus	22858-24055
	402109	8131678	Minus	171722-171850,173197-173303
	402142	7704595	Minus	23933-30698
60	402451	9795677	Minus	46137-46343
	402897	6598716	Plus	52808-53108,53500-53818
	403277	8072597	Minus	27494-27642
65	403283	8078905	Minus	71124-71866
	403375	9255844	Minus	92584-92795
	403473	9540695	Minus	54241-54437
70	403497	6067111	Plus	7221-7441
	403531	8078842	Minus	75003-78134
	403635	6862664	Minus	157028-157145,161725-161900
75	403714	7210030	Minus	145556-145753
	403743	7652003	Minus	136463-136646
	404020	8655996	Minus	174449-174663
80	404041	8888997	Minus	1334-1503,2483-2585,5230-5337,19556-19604
	404044	9558573	Minus	225767-225830
	404083	9544029	Minus	16555-17082
85	404108	8247074	Minus	63603-64942
	404134	6981900	Minus	40833-40911
	404227	7338233	Minus	93110-93259
90	404416	7332420	Minus	153339-153481,155099-155294
	404451	7638438	Minus	105191-105622
	404582	8739220	Plus	53230-53424
95	404708	8800828	Plus	77522-77658
	404888	9454593	Plus	29554-40430
	405066	8072599	Plus	140344-140697,148510-148591
100	405290	3000649	Minus	75582-75785
	405347	2979802	Minus	977-1115
	405512	946424	Plus	17802-17965,18573-18697
105	405548	1552484	Plus	10078-10446
	405583	4512267	Plus	56211-56353
	405671	2565031	Plus	25805-25923
110	405717	9588573	Plus	11275-11973
	405752	9123305	Plus	91352-91528
	405836	5686282	Minus	5031-5217

WO 02/102235

PCT/US02/19297

	405122	9144087	Minus	30940-31386
	406197	7289592	Minus	47620-47961
	406237	7417725	Plus	30032-30501
5	406241	7417725	Minus	34951-36752
	406265	7417729	Plus	2959-3200
	406364	9256114	Minus	50715-50833
	405454	5558390	Minus	91746-91958
	405451	9854741	Minus	91439-91519
	406562	7711584	Plus	37316-37426
10	406605	8272666	Minus	23275-23493,23729-23903

TABLE 5A lists about 68 genes highly down-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 5A, except the "average" ovarian cancer level was set to the maximum value amongst various ovarian cancers and the "average" normal ovary level was set to the minimum value from various non-malignant ovary specimens, and the ratio was greater than or equal to 2.5 (i.e. 2.5-fold down-regulated in the highest tumor vs. the lowest normal ovary). This has the overall effect of increasing stringency, and reducing the number of false-positives.

TABLE 5A: ABOUT 68 HIGHLY DOWN-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

	Play: Primerkey				
	Ex. Accn: Exemplar Accession				
20	UC ID: UniGene ID				
	Title: UniGene Title				
	ratio: ratio of normal ovary vs. tumor				
25	Play	Ex. Accn	UC ID	Title	ratio
	424851	AA676441	Hs.119059	ESTs	7.9
	437690	AA604362	Hs.180544	ESTs	4.7
	433682	AA642418	Hs.17381	ESTs	4.1
30	407437	AF220264		gbcHomo sapiens MOST-1 mRNA, complete cds.	4.0
	437707	A090363	Hs.251625	ESTs	4.0
	453282	AK000043	Hs.32522	hypothetical protein FLJ20036	4.0
	440987	AA911705	Hs.130229	ESTs	3.8
	443131	A033383	Hs.132699	ESTs	3.6
	431075	BE267477		gbtS116954ZF2 NIH_MGC_7 Homo sapiens cDNA do	3.6
35	412637	AA110567	Hs.261513	ESTs	3.6
	408141	U69205	Hs.45152	ESTs, Moderately similar to neurogenic basic helix-loop	3.5
	420122	AA265714	Hs.264153	Fanconi anemia, complementation group A	3.5
	430653	AW902062	Hs.30260	ESTs	3.4
40	401388			predicted exon	3.4
	410795	BE535686		gbt50106241Bf1 NIH_MGC_10 Homo sapiens cDNA c	3.4
	421418	AA806639		gbcHs06905s1 NCL_CGAP_GCB1 Homo sapiens cDNA	3.4
	480061	A0707034	Hs.201115	ESTs	3.3
	409725	T407001	Hs.50469	EST	3.3
	414739	AA532025		gbcot17a02s1 NCL_CGAP_GCB1 Homo sapiens cDNA	3.3
45	431644	AW972822	Hs.169246	cytochrome c	3.3
	460036	AW753734	Hs.272115	ESTs	3.2
	420457	AW206285	Hs.253546	ESTs	3.2
	435426	A1311802	Hs.143135	ESTs, Weakly similar to FAFY_HUMAN PROBABLE C	3.2
	407896	R65913		gbcys3005s1 Soares fetal liver spleen TNFLS Homo sap	3.2
50	446683	AA167642	Hs.14632	ESTs	3.2
	431582	AW415256	Hs.103754	ESTs	3.1
	452320	AA402673	Hs.160412	ESTs	3.1
	419401	AW804663		gbcQV4-UM0094-160300-135-406 UM0094 Homo sapi	3.1
	402106			predicted exon	3.1
55	444697	A1204451	Hs.146196	ESTs	3.1
	433263			predicted exon	3.0
	455366	AW632234		gbcQV6-DT0020-000200-106-gis DT0020 Homo sapie	3.0
	428599	H24338	Hs.27041	ESTs	2.9
	419002	T78625	Hs.266594	ESTs	2.9
60	404866			predicted exon	2.9
	409090	W59057	Hs.103105	ESTs	2.9
	405605			predicted exon	2.9
	441202	A0632143	Hs.135653	ESTs	2.8
	422046	A0535862		gbcIs50a10x1 NCL_CGAP_U01 Homo sapiens cDNA cl	2.8
65	412865	NS7693	Hs.116451	ESTs, Highly similar to neuronal thread protein ADP-C	2.8
	444431	AW615324	Hs.42280	ESTs	2.7
	426294	AA374185		gbcEST80289.HSC17 cells 1 Homo sapiens cDNA 5' en	2.7
	412480	BE142364		gbcCMM-H10143-270998-062-412 HT0143 Homo sapie	2.8
	419856	AW206979	Hs.193065	ESTs	2.8
70	401464	AF039241	Hs.5025	histone deacetylase 5	2.7
	439126	AF085584		gbcHomo sapiens full length insert cDNA clone Y139F0	2.7
	403277			predicted exon	2.7
	450078	A0681743		gbc33610x1 NCL_CGAP_Lu24 Homo sapiens cDNA	2.7
	450890	A0282149	Hs.50213	ESTs, Highly similar to FXD3_HUMAN FORNHEAD D	2.7
75	420620	AA473807	Hs.173343	ESTs	2.7
	459054	AW738466	Hs.82396	Z'-delta-glucosyltransferase 1	2.6
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-X-Cys), mem	2.6
	454336	AW381251	Hs.1050	pleckstrin homology, Sec7 and cathecolid domains 1cyl	2.6
	454229	Z45430	Hs.270425	ESTs	2.6
	446877	A1555472	Hs.270720	ESTs	2.6
	412588	AW993055	Hs.44024	ESTs	2.6
	449852	AF727277	Hs.199475	ESTs	2.6
	440894	AW686942	Hs.226132	ESTs	2.6
	424029	AS014594	Hs.137579	KIAA0694 gene product	2.6

WO 02/102235

PCT/US02/19297

454102	AW752363	gb:RC0-C10201-270999-011-03 C10201 Homo sapien	2.6	
430922	AW373747	He.183337	ESTs	2.6
42289	N55394	He.36396	5-oxoguanine DNA glycosylase	2.6
410455	N55428	gb:250209.s1 Scans_sensconl_fibroblasts_NHISF He	2.5	
412319	AW93903	gb:RC1-070029-030200-012-022 DT 9029 Homo sapien	2.5	
409099	BE154650	gb:PM3-HT0344-071299-003-c08 HT 0344 Homo sapien	2.5	
445822	A281545	gb:p30007.x1 NC1_CGAP_R011 Homo sapiens cDNA	2.5	
429755	NM_001384	He.215839	dlxs, large (Drosophila) homolog 2 (dlaapsy-110)	2.5
445765	AW294870	He.223672	ESTs	2.5

TABLE 6E:

Play: Unique Eco probe/identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Play	CAT Number	Accession
407896	1003480_1	gb:9113 H65901 H25352 RD1370 H43764 AW044451 W21298
409699	1149033_1	BE154650 BE154765 AW468343 BE154816 BE154667
104935	1205826_1	N95428 W24040 AW751366 H81987
410759	1219395_1	BE353986 AW301777
412319	1280502_1	AW93903 AW530507 AW939098 AW939014
412490	129922_1	BE142364 BE142341 AA112025
19401	184454_1	AW040663 AW805917 AA236960
421418	202288_1	AA806930 AA21008 AA83274 AW378006
422046	210744_1	AA53592 T16529 H15801 F07773 R5636
426294	353894_1	AA374186 AW69169 H58344
431075	327630_1	BE207477 AA451468 AW363723
434738	352652_1	AA836265 AA648266 AW574440
435126	46897_1	AF059394 H55955 H55956
445832	511025_1	AE15485 H55134 AW85371 AW876247
450078	623882_1	AA681743 AW897287 AW867206 AW8907284
454102	1011033_1	AW752363 BE147120 N22640
455368	1287504_1	AW536234 AW536074 AW536181 AW936175 AW936217 AW536077 AW936227 AW936191

TABLE 6C:

Play: Unique number corresponding to an Eco probe/identifier

Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I, et al." refers to the publication entitled "The DNA

sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:469-495

Strand: indicates DNA strand from which exon was predicted

NL_position: indicates nucleotide positions of predicted exons

401308	S212616	Plus	169019-169545
402105	0131083	Minus	22655-40265
403277	8072657	Minus	27494-27842
403283	8076505	Minus	71124-71996
404668	9454553	Plus	38954-40430
406065	6272666	Minus	23275-23453,23723-23903

Table 7A lists about 770 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eco-HuO1 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" ovarian cancer level was set to the 2nd highest amongst various ovarian cancers. The "average" normal adult tissue level was set to the 7th highest amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 7A: ABOUT 770 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Play: Primkey

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene Title

ratio: ratio tumor vs. normal tissues

Play	Ex. Accn	UG ID	Title	ratio
109480	F09255	He.4933	ESTs	23.2
119743	W10242	He.55996	ESTs	22.0
135239	AA283003	He.50768	chromosome-associated polypeptide C	22.0
129571	X51630	He.1145	Wilms tumor 1	20.0
102151	U17280	He.3132	steroidogenic acute regulatory protein	19.6
133841	D49354	He.2142	5-hydroxytryptamine (serotonin) receptor 3A	17.5
132624	AA184819	He.53631	ESTs	15.9
102610	U65011	He.30743	preferentially expressed antigen in melanoma	15.4
101249	L33881	He.1904	protein kinase C, iota	14.5
122802	AA460530	He.256579	ESTs	14.5
135242	M74063	He.57003	cyclin E1	13.6
101804	M89599	He.168840	TTK protein kinase	12.2
123005	AA479726	He.105577	ESTs	12.0
114965	AA250737	He.72472	ESTs	11.5
115636	AA347193	He.62180	ESTs	11.4
132191	AA440431	He.158688	HNA0741 gene product	10.5
121853	AA425687	He.89502	ESTs	10.9
115581	AA435577	He.184942	G protein-coupled receptor 64	10.8
119780	W7267	He.191381	ESTs; Weakly similar to hypothetical protein	10.5
104301	CA65332	He.67163	ESTs	10.3
132932	N59764	He.5398	guanine nucleotidylate synthetase	10.1

WO 02/102235

PCT/US02/19297

105298	AA233469	Hs.26369	ESTs	9.7
108657	AA133260	Hs.62180	ESTs	9.1
113168	TS3592	Hs.161686	EST	9.0
115892	AA435946	Hs.50831	ESTs	8.9
125656	AA199856	Hs.118811	ESTs	8.9
102200	U21551	Hs.157205	branched chain aminotransferase 1; cytosolic	8.8
109355	AA045692	Hs.62637	ESTs	8.6
132572	AA448297	Hs.237825	signal recognition particle 7kD	8.6
119909	AA436666	Hs.59761	ESTs	8.5
108195	AA179645	Hs.73525	RAB6 interacting; kinesin-like (rakbesin6)	8.3
121179	AA422038	Hs.98387	ESTs	8.3
102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	8.0
105317	AA233926	Hs.23635	ESTs	7.8
122520	W87455	Hs.222529	ESTs; Weakly similar to D0992.2 [C.elegans]	7.8
122860	AA317000	Hs.161167	ESTs	7.8
122959	AA478539	Hs.104336	ESTs	7.7
130376	R40873	Hs.155174	KIAA0432 gene product	7.7
123339	AA504263	Hs.101516	ESTs	7.7
134972	U19720	Hs.195252	Human L-myc protein gene; complete cds	7.6
111234	W5207	Hs.21943	ESTs; Weakly similar to ORF YGL22c [S.cerevi]	7.5
123689	AA095555	Hs.259562	ESTs	7.5
123494	AA599786	Hs.112110	ESTs	7.4
131985	AA434329	Hs.36863	ESTs	7.4
105738	AA470145	Hs.25130	ESTs	7.4
108768	AA127741	Hs.61345	ESTs	7.3
106474	AA450212	Hs.42494	Homo sapiens mRNA; cDNA DHFZp5640053 (from d	7.2
123308	AA496211	Hs.103539	ESTs	7.2
106124	AA423967	Hs.7597	ESTs	7.2
111345	N09629	Hs.14559	ESTs	7.1
105200	AA195399	Hs.24641	ESTs	7.1
116416	AA60219	Hs.39382	ESTs	7.1
118446	N0597	Hs.50895	ESTs	7.1
133434	AA278852	Hs.250766	ESTs	7.1
120472	AA251875	Hs.104472	ESTs; Weakly similar to Gag-Pol polypeptide [6.9
115291	AA279843	Hs.122579	ESTs	6.9
111186	N67551	Hs.12844	EGF-like domain; multiple 6	6.9
105776	AA128548	Hs.90847	general transcription factor IIC; polypeptide	6.9
132839	U76189	Hs.61152	oncosome (transcription)-like 2	6.9
134520	N21407	Hs.257325	ESTs	6.9
114724	AA131701	Hs.255287	ESTs; Highly similar to SPERM SURFACE PROTEIN	6.8
116296	AA459533	Hs.62601	Homo sapiens mRNA; cDNA DHFZp569K1318 (from c	6.8
102136	U15552	Hs.85769	acidic 8 kDa protein mRNA	6.7
132725	L41857	Hs.164157	splicing factor; arginine/serine-rich 7 (SKK)	6.5
109648	F04600	Hs.7154	ESTs	6.4
116401	AA500063	Hs.50608	ESTs	6.4
127953	A1367707	Hs.150567	ESTs	6.4
104252	AF002246	Hs.210663	cell adhesion molecule with homology to L1CAM	6.4
120438	AA249441	Hs.99488	ESTs; Weakly similar to YKR0074w [S.cerevi]	6.2
131978	D80008	Hs.36232	KIAA0186 gene product	6.2
134621	U2547	Hs.172655	cleavage stimulation factor; 3' pre-RNA; subo	6.2
122571	AA280738	Hs.128373	ESTs	6.2
102627	U65951	Hs.158174	zinc finger protein 184 (Kruppel-like)	6.1
100651	HG2874-HT3018		Ribosomal Protein L39 Homolog	6.1
118204	N59859	Hs.48443	ESTs	6.0
131386	AA395412	Hs.173135	dual-specificity tyrosine-(T)-phosphorylation	6.0
128997	SI0223		IKK-1+Kruppel-like zinc finger protein (huma	5.9
131228	AA279157	Hs.24485	chondroin sulfate proteoglycan 6 (barnacin)	5.9
106369	AA443828	Hs.25324	ESTs	5.9
108255	AA063157	Hs.173608	ESTs	5.8
125370	AA258743	Hs.151791	KIAA0292 gene product	5.8
130010	N52966	Hs.142838	ESTs	5.8
131945	M87339	Hs.35120	replication factor C (p12val) 1.4 (37kD)	5.7
116238	AA479392	Hs.47144	DMFZP56N0819 protein	5.7
102221	U24575		LM domain only 4	5.6
130759	R00441	Hs.18025	ESTs; Weakly similar to cDNA EST Yk338b7.5 co	5.6
131278	U81523	Hs.25195	endothelial bleeding associated factor (beta-	5.6
101383	M14113	Hs.79345	coagulation factor VIII; procoagulant compon	5.5
131836	AA610086	Hs.32390	DMFZP56F084 protein	5.5
129628	U29727	Hs.11174	cyclic-dependent kinase inhibitor 2A (mekanem	5.5
109523	AA453441	Hs.31511	ESTs	5.5
111772	R26287	Hs.237146	ESTs	5.5
101255	L34930	Hs.148984	mitochondrial translational initiation factor	5.5
108895	AA459585	Hs.26245	ESTs	5.5
104943	AA065217	Hs.198974	ESTs	5.5
129229	AA211941	Hs.109643	polyadenylate binding protein-interacting pro	5.4
102105	U33265	Hs.90073	chromosome segregation 1 (yeast homolog)-like	5.4
109553	AA454967	Hs.5887	ESTs; Highly similar to RNA binding motif pro	5.4
112305	R54622	Hs.25294	ESTs	5.3
123972	C14782	Hs.70337	immunoglobulin superfamily; member 4	5.3
102576	U72514	Hs.12045	putative protein	5.3
105159	AA444941	Hs.4029	glione-amplified sequence-41	5.2
107655	AA025104	Hs.61252	ESTs	5.2
121121	AA399371	Hs.189095	ESTs; Weakly similar to zinc finger protein S	5.2
127152	N76398	Hs.21187	ESTs	5.2

WO 02/102235

PCT/US02/19297

	131646	AA171895	Hs.30057	Human sapiens clone 24749 and 24750 mRNA seque	5.2
	121770	AA421714	Hs.11469	KIAA0696 protein	5.2
	122512	AA408111	Hs.38658	budding inhibited by benzimidazoles 1 (yeas	5.1
5	106870	AA339623	Hs.23505	ESTs	5.1
	100341	DC3506	Hs.8813	synactin binding protein 3	5.1
	118848	H65187	Hs.39001	ESTs	5.1
	120821	AA347419	Hs.366370	Human sapiens mRNA full length insert cDNA clo	5.1
	130690	AA064286	Hs.139033	putatively expressed gene 3	5.1
10	122661	AA454936	Hs.245541	ESTs	5.1
	123169	AA488892	Hs.104412	ESTs; Weakly similar to Gag Pol polyprotein [5.1
	108810	AA130596	HuJ1331	ESTs; Weakly similar to POTENT HEAT-STABLE PR	5.0
	110739	N26101	Hs.7639	Human ring zinc-finger protein (ZNF127-3g) ge	5.0
	120619	AA284372	Hs.111471	ESTs	5.0
15	122792	AA460225	Hs.99519	ESTs	5.0
	128912	AA047344	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen [Hs	5.0
	120223	UB0914	Hs.5057	carboxypeptidase D	4.9
	123890	MT3599	Hs.111461	centroplicans (ferrozidase)	4.9
	101084	L05425		Human sapiens autoantigen mRNA; complete cds	4.9
20	134859	D87716	Hs.90316	KIAA0007 protein	4.9
	115955	AA446121	Hs.44198	Human sapiens BAC clone RS054D04 from 7q31	4.9
	109516	AA423791	Hs.21014	ESTs	4.9
	114932	AA242751	Hs.16218	KIAA0900 protein	4.9
	106672	AA461300	Hs.30643	ESTs	4.8
25	106126	AA244005	Hs.22972	ESTs; Moderately similar to H5AR [Munroscitis]	4.8
	110095	H53483	Hs.124777	ESTs	4.8
	102025	U03911	Hs.78334	mtfS (E. coli) homolog 2 (colon cancer; nonpo	4.8
	133262	U62960	Hs.260656	SRB7 (suppressor of RNA polymerase B; yeast)	4.8
	119708	W67810	Hs.57904	magp-nash1 (Chromophila) homolog; proliferate	4.7
30	120695	AA291458		ESTs	4.7
	126551	AA440990	Hs.103135	ESTs	4.7
	103152	X66533	Hs.77890	guanylate cyclase 1; soluble; beta 3	4.7
	108699	AA121514	Hs.70832	ESTs	4.7
	115094	AA255821	Hs.88095	ESTs	4.7
	121429	AA408293	Hs.193498	ESTs	4.7
35	123203	AA493671	Hs.89709	glutamate-cysteine ligase (gamma-glutamylcyst	4.7
	126802	AA947601	Hs.97096	ESTs	4.7
	130527	C17384	Hs.184227	F-box protein 21	4.7
40	134470	X54942	Hs.63758	CDC25 protein kinase 2	4.7
	100449	D87470	Hs.75400	KIAA0202 protein	4.7
	110970	N51374	Hs.96870	Human sapiens mRNA full length insert cDNA clo	4.7
	115901	AA436403	Hs.68909	ESTs; Moderately similar to Fizzled-6 [H.sapi	4.7
	109799	F10770	Hs.180376	Human sapiens clone 659 unknown mRNA; complete	4.6
	116195	AA465148	Hs.72402	ESTs	4.6
45	132122	U65092	Hs.40403	Chp9300-interacting transactivator; with Glu	4.6
	108990	AA152296	Hs.72045	ESTs	4.6
	109056	AA4160529	Hs.48524	ESTs	4.6
	115837	AA443289	Hs.30991	KIAA0957 protein	4.6
	133520	X74331	Hs.74319	primase; polypeptide 2A (SRM)	4.6
50	131200	AA609427	Hs.210706	ESTs; Moderately similar to E1E ALU SUBFAMIL	4.6
	121369	AA409657	Hs.128791	Human DNA sequence from clone 967N21 on chrom	4.5
	132880	AA444369	Hs.177537	ESTs	4.5
	127386	AA67411	Hs.109726	ESTs	4.5
	129067	W93592	Hs.47343	ESTs	4.5
	122986	AA470653	Hs.102947	ESTs	4.5
55	135286	AA401289	Hs.97849	ESTs	4.5
	130155	L33404	Hs.151254	Kaibin7 (pharyngeal; striatum connectum)	4.5
	106103	AA421104	Hs.12094	ESTs	4.5
	102654	U68494	Hs.24385	Human hbc457 mRNA sequence	4.4
60	107876	AA026315	Hs.61184	Novel human gene mapping to chromosome X	4.4
	109484	AA232225	Hs.463912	ESTs	4.4
	125960	DC3307	Hs.145698	ESTs	4.4
	126992	A1160190	Hs.76127	hcdt (homologous to the ES-AP (UBES3A) carboxy	4.4
	100269	DC8560	Hs.1189	E2F transcription factor 3	4.3
65	134161	U97188	Hs.79440	IGF-1 mRNA-binding protein 3	4.3
	100302	HS1498-HT406		Adrenomedullin-Specific Protein Pp2	4.3
	105542	AA261659	Hs.8241	ESTs; Weakly similar to heat shock protein h	4.3
	109787	F10610	Hs.34853	inhibitor of DNA binding 4; dominant negative	4.3
	110759	N21671	Hs.19025	ESTs	4.3
70	129970	AA478975	Hs.200434	ESTs	4.3
	134866	AA422319	Hs.87792	putative type II membrane protein	4.3
	117693	N40939	Hs.44162	ESTs; Weakly similar to cDNA EST yk342h212.5 c	4.3
	111008	N53388	Hs.7222	ESTs	4.3
	120977	AA398155	Hs.97600	ESTs	4.2
75	105908	AA333808	Hs.71490	KIAA0438 gene product	4.2
	121381	AA405747	Hs.97865	ESTs; Weakly similar to WASP-family protein [4.2
	100693	HG4557-HT4362		Small Nuclear Ribonucleoprotein U1, tcomp	4.2
	107176	AA621762	Hs.7576	ESTs	4.2
	116976	N93629	Hs.93391	ESTs	4.2
80	133703	N63295	Hs.18103	ESTs	4.2
	100540	AA454607	Hs.38114	ESTs; Weakly similar to coded for by C. elega	4.2
	119367	T78324	Hs.90905	ESTs	4.2
	133633	D71262	Hs.75337	nucleolar phosphoprotein p130	4.2
	105520	AA426808	Hs.33065	WD repeat domain 3	4.2
	114264	Z40074	Hs.27595	ESTs	4.1

WO 02/102235

PCT/US02/19297

	116200	AA465358	Hs.118793	ESTs; Highly similar to p621 [H.sapiens]	3.6
	121920	AA428300	Hs.161841	ESTs	3.6
	128609	AA234365	Hs.102456	survival of motor neuron protein interacting	3.6
	101078	LA510	Hs.792	ADP-ribosylation factor domain protein 1; 64k	3.6
5	108693	AA121289	Hs.49597	ESTs; Highly similar to retinoic acid-induced	3.6
	109139	AA176121	Hs.49557	zinc finger protein 261	3.6
	111870	R37775	Hs.16665	ESTs; Weakly similar to hypothetical protein	3.6
	113848	W60080	Hs.27099	DKFZP564J063 protein	3.6
	127947	AI432475	Hs.146327	ESTs	3.6
10	128056	AJ376480	Hs.125449	ESTs; Weakly similar to Na ⁺ K ⁺ channel beta 2	3.6
	129914	U23777	Hs.133121	rearranged L-eye fusion sequence	3.6
	132148	AA263968	Hs.4094	ESTs	3.6
	134644	S83303	Hs.87224	SRF (sex-determining region Y)-box 5	3.6
	115047	AA752627	Hs.22554	homeo box B5	3.6
15	102398	U42659	Hs.1033	Human H33 protein form 1 (N33) gene, exon 1 a	3.6
	127479	AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid) methyl-lysyl	3.6
	105546	AA262030	Hs.5152	ESTs; Weakly similar to katanin p80 subunit 1	3.6
	101483	M24486	Hs.76768	procollagen-proline; 2-oxoglutarate-4-oxo	3.6
	105709	AA291268	Hs.26761	DKFZP569J024 protein	3.6
20	122636	AA454103	Hs.110031	ESTs	3.6
	124792	RA4357	Hs.132784	ESTs; Weakly similar to cDNA EST EMBL701421	3.6
	103621	Z47727	Hs.150675	polymerase (RNA) II (DNA directed) polypolyid	3.5
	106427	AA251330	Hs.28246	ESTs	3.5
	121553	AA412488	Hs.46820	ESTs	3.5
25	151167	AA258421	Hs.43728	hypothetical protein	3.5
	134570	U66615	Hs.172280	SWI/SNF related; matrix associated; coilin dep	3.5
	110787	N24716	Hs.12244	ESTs; Weakly similar to C4B9.1 [C.elegans]	3.5
	131621	U77665	Hs.139120	ribonuclease P (30kD)	3.5
	132813	NT2118	Hs.57436	solute carrier family 11 (proton-coupled tra	3.5
30	116370	AA521256	Hs.236204	ESTs; Moderately similar to NUCLEAR PORE COMP	3.5
	131965	W00146	Hs.35682	ESTs	3.5
	118221	AA262942	Hs.79141	ESTs	3.5
	110933	AA456020	Hs.50948	ESTs; Weakly similar to KIAA0862 protein [H.s	3.5
	123507	AA600176	Hs.112345	ESTs	3.5
35	129801	F11087	Hs.239666	ESTs	3.5
	118084	AA255566	Hs.42484	Home sapiens mRNA; cDNA DKFZp564C053 (from ci	3.5
	123442	AA456863	Hs.111469	ESTs	3.5
	155611	AA253217	Hs.41271	ESTs	3.5
40	100146	D13645	Hs.2471	KIAA0200 gene product	3.5
	115140	AA258030	Hs.55356	ESTs; Weakly similar to supported by GENSCAN	3.5
	115360	AA291950	Hs.5057	carboxypeptidase D	3.5
	130261	D5767	Hs.153678	reproduction 8	3.4
	102824	HG4059-HT4326		Oncogene Anti-Evi-1, Fusion Activated	3.4
	102287	U31814	Hs.3352	histone deacetylase 2	3.4
45	102788	U86602	Hs.74407	nucleolar protein p40	3.4
	115836	N7820	Hs.50264	ESTs	3.4
	102423	U44754	Hs.175512	small nuclear RNA activating complex; polypep	3.4
	106300	AA436840	Hs.19114	high-mobility group (nonhistone chromosomal)	3.4
	106156	AA425354	Hs.4210	ESTs	3.4
50	106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	3.4
	107869	AA426234	Hs.57280	ESTs	3.4
	108187	AA056538	Hs.27942	ESTs; Weakly similar to similar to 1-acyl-gly	3.4
	116123	AA459282	Hs.43756	ESTs	3.4
	116501	W07721	Hs.151363	ESTs	3.4
55	129121	AA127459	Hs.108738	ESTs; Weakly similar to zein [J.melanogaster	3.4
	131638	D87120	Hs.26982	predicted osteoblast protein	3.4
	132662	N34893	Hs.6163	ESTs; Highly similar to CGI-48 protein [H.sap	3.4
	133767	D63875	Hs.173289	KIAA0155 gene product	3.4
	111823	D63875	Hs.24844	ESTs	3.4
60	134372	D63877	Hs.82324	KIAA0157 protein	3.4
	130938	AA013250	Hs.21398	ESTs; Moderately similar to PUTATIVE GLUCOSAM	3.4
	115160	AA253427	Hs.58427	ESTs	3.4
	123978	C20563	Hs.170273	ESTs	3.4
65	106807	AA129898	Hs.45576	ESTs; Weakly similar to PROTEIN PHOSPHATASE P	3.4
	135811	R22296	Hs.52026	ESTs; Weakly similar to beta-TCP protein ESR	3.4
	134654	W23625	Hs.8739	ESTs; Weakly similar to ORF YFR200c [S.cerev	3.4
	106730	AA292701	Hs.5364	DKFZP564J052 protein	3.4
	111295	N73275	Hs.121275	ESTs; Weakly similar to ubiquitin-conjugating	3.3
70	102009	U02680	Hs.53043	protein tyrosine kinase 9	3.3
	114161	Z38904	Hs.222805	ESTs; Weakly similar to KIAA0970 protein [H.s	3.3
	130604	X03635	Hs.1657	estrogen receptor 1	3.3
	100103	AF007875	Hs.5006	dolichyl-phosphate mannosyltransferase polype	3.3
	121746	AA421171	Hs.235645	ESTs	3.3
75	106698	AA463745	Hs.29403	ESTs; Weakly similar to PROBABLE ATP-DEPENDENT	3.3
	134353	S77154	Hs.82120	nuclear receptor subfamily 4; group A; member	3.3
	134154	AA211320	Hs.79404	neuron specific protein	3.3
	133142	F03321	Hs.65674	ESTs	3.3
	124461	N50541	Hs.80285	Home sapiens mRNA; cDNA DKFZP566C1723 (from c	3.3
80	104903	AA065534	Hs.124134	ESTs	3.3
	106772	AA478106	Hs.12692	ESTs; Weakly similar to protein phosphatase-1	3.3
	109704	F09667	Hs.12676	ESTs	3.3
	111131	NA4267	Hs.101777	ESTs	3.3
	115019	AA251905	Hs.48473	ESTs	3.3
	116019	AA450312	Hs.237480	Home sapiens mRNA; cDNA DKFZP434E102 (from ci	3.3

WO 02/102235

PCT/US02/19297

	118528	N87889	Hs.49397	ESTs	3.3
	124027	F03625	Hs.107537	ESTs	3.3
	131699	R91967	Hs.59421	ESTs; Moderately similar to H1 ALU SUBFAMIL	3.3
	111044	N55443	Hs.23625	ESTs	3.3
5	103768	AA089897	Hs.180320	ESTs; Weakly similar to GOLGI 4-TRANSMEMBRANE	3.3
	131682	N49091	Hs.13385	ESTs; Highly similar to CGH-134 protein [Hsa	3.3
	122873	AA089471	Hs.112712	ESTs	3.3
	132936	AB002305	Hs.61111	KIAA0307 gene product	3.3
	130323	X53783	Hs.117950	multifunctional polypeptide similar to SAICAR	3.3
10	126572	AA260794	Hs.258787	ESTs	3.3
	132364	AA479933	Hs.46987	Human DNA sequence from clone 167A19 on chrom	3.3
	105658	AA262914	Hs.10176	ESTs	3.2
	105086	AA147719	Hs.159441	ESTs	3.2
15	118695	H17181	Hs.50081	Human sapiens mRNA full length insert cDNA clo	3.2
	121022	R44536	Hs.140899	ESTs	3.2
	125154	W38419	Hs.24036	ESTs	3.2
	109040	AA041551	Hs.48544	ESTs	3.2
	133453	M68941	Hs.73826	protein tyrosine phosphatase; non-receptor ty	3.2
	124006	D60302	Hs.108977	ESTs	3.2
20	118033	AA455953	Hs.44581	ESTs; Weakly similar to HEAT SHOCK 70 HD PROT	3.2
	106753	AA476944	Hs.7331	ESTs	3.2
	126221	U68075	Hs.50924	GATA-binding protein 6	3.2
	103330	X85373	Hs.77496	small nuclear ribonucleoprotein polypeptide G	3.2
	128526	AA481403	Hs.107213	ESTs; Highly similar to HY-REM4 antigen [Hs	3.2
25	101167	L15302	Hs.153877	zinc finger protein 141 (clone p52-44)	3.2
	104055	AA393755	Hs.117211	ESTs; Highly similar to CG-62 protein [Hsap	3.2
	112817	T10196	Hs.4263	ESTs; Weakly similar to pRedcort	3.2
	126358	AA213459	Hs.100532	transcription factor 17	3.2
	121957	AA426017	Hs.52094	ESTs; Highly similar to DNA-REPAIR PROTEIN CO	3.2
30	122124	AA434257	Hs.186679	ESTs; Moderately similar to H1 ALU SUBFAMIL	3.2
	132231	H59131	Hs.42635	ESTs	3.2
	134272	X76040	Hs.223014	protease; serine; 15	3.2
	115580	AA431719	Hs.61509	ESTs	3.2
	115278	AA279579	Hs.67466	ESTs; Weakly similar to BACH32G11 d [D.melan	3.2
35	134126	R38102	Hs.50421	KIAA0203 gene product	3.2
	128180	AA131252	Hs.109007	ESTs	3.2
	121710	AA419011	Hs.96744	DNFZP586D0823 protein	3.2
	102242	U27186	Hs.32943	retinoic acid receptor responder (tazarotene	3.2
40	104656	AA074860	Hs.120975	ESTs; Weakly similar to hypothetical protein	3.2
	113047	T25867	Hs.7549	ESTs	3.2
	116017	AA261830	Hs.179592	tumor protein p53-binding protein	3.2
	133780	M42419	Hs.76152	dectin	3.1
	129453	AA421213	Hs.111632	Land's protein	3.1
	130363	X36018	Hs.172210	MUF1 protein	3.1
45	106036	AA412505	Hs.10653	ESTs	3.1
	102234	U26312	Hs.8123	chromobox homolog 3 (Drosophila HP1 gamma)	3.1
	108133	AA424346	Hs.107573	siatyltransferase	3.1
	118903	H47357	Hs.6670	ESTs; Moderately similar to weak similarity 1	3.1
	106721	AA465194	Hs.6670	ESTs	3.1
50	107115	AA610108	Hs.27853	ESTs; Highly similar to CQI-124 protein [Hsa	3.1
	133228	N80029	Hs.6381	Human sapiens clone 1400 unknown protein mRNA;	3.1
	104733	AA019498	Hs.23071	ESTs	3.1
	103879	AA228149	Hs.50252	ESTs; Weakly similar to putative [C.elegans]	3.1
	103038	X54941	Hs.77550	ODC28 protein kinase 1	3.1
55	133154	AA128433	Hs.173342	sorting nexin 4	3.1
	114680	AA285112	Hs.100227	ESTs; Moderately similar to similar to murine	3.1
	102437	U49569	Hs.221988	aquaporin 5	3.1
	100352	D64159	Hs.221988	Human sapiens mRNA for 3-7 gene product, parti	3.1
60	133631	Z45570	Hs.173342	Human sapiens Sp 17 gene	3.1
	104236	AB002304	Hs.27916	delta integrin-like and metalloproteinase (tepro	3.1
	108613	AA100957	Hs.69165	ESTs	3.1
	115915	AA436884	Hs.48926	ESTs	3.1
	120640	AA280945	Hs.183933	ESTs	3.1
	124086	H03099	Hs.101819	ESTs	3.1
65	130375	U91931	Hs.155172	adipocyte-related protein complex 3, beta 1 sub	3.1
	131632	AA443671	Hs.29826	ESTs	3.1
	131523	H88801	Hs.201676	M phase phosphoprotein 10 (US small nuclear	3.1
	115827	AA427390	Hs.44426	ESTs; Weakly similar to PHOSPHOLIPID HYDROPER	3.1
	108628	AA131584	Hs.71435	DNFZP584D0463 protein	3.1
70	112198	R49483	Hs.221159	ESTs; Weakly similar to ZINC FINGER PROTEIN H	3.1
	123980	AA621785	Hs.170006	methylmalonate-semialdehyde dehydrogenase	3.1
	131538	Z29331	Hs.28505	ubiquitin-conjugating enzyme E2H (homologous	3.1
	108616	AA208070	Hs.24968	ESTs	3.1
	101228	L27706	Hs.82516	Hisaplepin containing TCP1; subunit 6A (zeta	3.1
75	100280	D42065	Hs.155314	KIAA0005 gene product	3.1
	132744	X54326	Hs.55921	glutaryl-prolyl-lysine synthetase	3.1
	103105	X81970	Hs.78913	proteasome (prosome; macropain) subunit; alpi	3.1
	106984	AA521201	Hs.71726	ESTs	3.1
	105127	AA158132	Hs.11817	ESTs; Weakly similar to contains similarity 1	3.1
80	102302	U33052	Hs.69171	protein kinase C-like 2	3.1
	117708	N45114	Hs.44678	ESTs	3.1
	111514	N74574	Hs.13322	ESTs; novel gene from PAC 117720; chromos	3.0
	123902	AA409089	Hs.168147	ESTs	3.0
	130356	X84373	Hs.155017	nuclear receptor interacting protein 1	3.0

WO 02/102235

PCT/US02/19297

128420	AI088155	Hs.14146	ESTs; Weakly similar to unknown [H.sapiens]	3.0
106746	AA126974	Hs.43388	ESTs	3.0
127236	AG341816	Hs.96558	encoding inhibited by benzimidazoles 1 (yeast)	3.0
114206	Z03001	Hs.7859	ESTs	3.0
107071	AA609053	Hs.35198	ESTs	3.0
104957	AA074919	Hs.10026	ESTs; Weakly similar to ORF YJL0636 [S.cerevisiae]	3.0
124073	1105394	Hs.127376	KIAA0555 gene product	3.0
130869	AA1121100	Hs.2057	uridine monophosphate synthetase (protista pho)	3.0
101232	L28197	Hs.242894	ADP-ribosylation factor-like 1	3.0
104276	CG2193	Hs.85222	ESTs; Weakly similar to RZ090_2 [H.sapiens]	3.0
120160	N90960	Hs.247277	ESTs; Weakly similar to transformation-related	3.0
126584	Mt.1433	Hs.101650	retinol-binding protein 1, cellular	3.0
100405	D96425	Hs.82733	nidogen 2	3.0
101335	L49054		Home sapiens [3.5(p25.1p34)] fusion gene NP	3.0
108761	AA127514	Hs.61603	ESTs	3.0
111346	N99829	Hs.13259	ESTs	3.0
144988	AJ251089	Hs.84576	ESTs; Weakly similar to photoreducin; retinal [H.]	3.0
116038	AA440336	Hs.48589	ESTs; Weakly similar to finger protein 1ZF6;	3.0
116545	D20313	Hs.74899	ESTs	3.0
117873	N49997	Hs.46624	ESTs	3.0
121463	AA411745	Hs.239691	ESTs; Weakly similar to KIAA0554 protein [H.s]	3.0
128625	AA242816	Hs.102652	ESTs; Weakly similar to KIAA0437 [H.sapiens]	3.0
131185	M25753	Hs.23960	cyclin B1	3.0
134380	D38073	Hs.179555	minichromosome maintenance deficient [S. cerevisiae]	3.0
106740	AA263206	Hs.10852	ESTs	3.0
130319	AA291710	Hs.21276	collectin type IV, alpha 3 (Globopectin antigen)	3.0
134423	W6151	Hs.83006	ESTs; Highly similar to CG1-139 protein [H.s]	3.0
104896	AA054228	Hs.23165	ESTs	3.0
134407	X72964	Hs.32794	calretinin (20kD calcium-binding protein)	3.0
105370	AA445994	Hs.21131	ESTs	3.0
112253	R53545	Hs.20562	Home sapiens clone 24411 mRNA, sequence	3.0
090918	AA156980	Hs.114992	ESTs	3.0
114239	Z39742	Hs.222478	ESTs	3.0
114469	AA250778	Hs.57747	ESTs	3.0
115028	AA60752	Hs.71589	Home sapiens mRNA; cDNA DKFZp664P0623 (from c)	3.0
115286	AA279803	Hs.52204	ESTs	2.9
106909	AA393827	Hs.20104	ESTs	2.9
113811	W49426	Hs.4878	ESTs	2.9
107243	D58994	Hs.44782	ESTs	2.9
134469	U08234	Hs.112378	LIM and senescent cell antigen-like domains 1	2.9
134064	D67685	Hs.78893	KIAA0244 protein	2.9
123270	AJ024352	Hs.70337	immunoglobulin superfamily; member 4	2.9
117377	T57597	Hs.11774	protein (polydip-tryptidyl chitinase isomerase)	2.9
132763	NT4897	Hs.5563	DEAD-box (Arg-Glu-Ala-Asp-His) box polypeptide	2.9
109010	AA156480	Hs.444229	dual specificity phosphatase 12	2.9
130095	F01831	Hs.14538	ESTs	2.9
106616	AA458249	Hs.8715	ESTs; Weakly similar to Similarly with snail	2.9
102427	XPT303		H.sapiens mRNA for Pig-12 protein	2.9
133980	D00760	Hs.181309	proteasome (prosome; macropain) subunit; alpha	2.9
111363	N90430	Hs.5616	ESTs	2.9
105344	AA235303	Hs.3645	ESTs	2.9
134498	M5150	Hs.84131	threonyl-RNA synthetase	2.9
117910	N80826	Hs.12940	zinc-fingers and homeobox 1	2.9
118903	N90774	Hs.132207	ESTs; Moderately similar to III ALU SUBFAMIL	2.9
121713	AA419198	Hs.105577	ESTs	2.9
129080	II19307	Hs.108607	ESTs	2.9
129404	AA172056	Hs.111123	ESTs	2.9
129457	X55330	Hs.207776	aspartylglucosaminidase	2.9
130352	D87450	Hs.154978	KIAA0281 protein	2.9
133415	X89599	Hs.73149	paired box gene 8	2.9
126049	AA287115	Hs.59997	ESTs	2.9
131257	AA258042	Hs.24908	ESTs	2.9
134480	AA024654	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subco	2.9
116734	F13789	Hs.53796	DKFZP660223 protein	2.9
105020	AA126719	Hs.25262	ESTs	2.9
114985	AA251010	Hs.87007	ESTs	2.9
105651	AA282481	Hs.18439	ESTs	2.9
101714	M68874		Human phosphatidylcholine 2-acetyltransferase (pP	2.9
123398	AA621265	Hs.105514	ESTs	2.9
106907	AA411462	Hs.13042	ESTs; Weakly similar to vcll 1 [H.sapiens]	2.9
109450	AA232163	Hs.173042	ESTs; Weakly similar to III ALU SUBFAMILY J	2.9
104685	AA010530	Hs.9599	Human PAC clone GSD25M02 from 7q21-q22	2.9
106677	AA115629	Hs.116531	ESTs	2.9
116028	AA452112	Hs.42644	bioreducin-like	2.9
105404	AA243303	Hs.21167	ESTs	2.9
132365	AA598694	Hs.46541	Home sapiens PAC clone DJ0804A10 from 7q32-q3	2.9
119638	W52480	Hs.56148	ESTs; Moderately similar to NY-REN-58 antigen	2.9
124637	N80116	Hs.75798	Human DNA sequence from clone 1183021 on chro	2.9
130358	AA287735	Hs.154118	Human DNA sequence from clone 1185524 on chro	2.9
105640	AA281623	Hs.7525	ESTs; Weakly similar to KIAA0742 protein [H.s]	2.9
131818	Z39297	Hs.3261	neuronal pentonin II	2.9
119298	T23820	Hs.154578	cyclin T2	2.9
128742	OX0763	Hs.251531	proteasome (prosome; macropain) subunit; alpha	2.9
115069	AA253876	Hs.86919	ESTs; Weakly similar to III ALU SUBFAMILY J	2.9

WO 02/102235

PCT/US02/19297

	116142	AA460649	Hs.39457	ESTs	2,7
	105612	H05509	Hs.24638	ESTs	2,7
	103153	X07019	Hs.76724	coatamer protein complex; subunit beta 2 (bat	2,7
5	102046	U07151	Hs.182215	ADP-ribosylation factor-like 3	2,7
	104567	R64634	Hs.101469	ESTs	2,7
	112666	T23539	Hs.7165	zinc finger protein 259	2,7
	115135	N67713	Hs.63960	ESTs; Weakly similar to Ig [J.Neovectus]	2,7
	123065	AA465724	Hs.152119	ESTs	2,7
	124315	H94932	Hs.6506	v-rat simian leukemia viral oncogene homolog	2,7
10	124447	N49030	Hs.149345	Human sapiens mRNA; cDNA DKF Zp566L141 (from c	2,7
	132634	H77546	Hs.57658	ESTs; Highly similar to MY-REN-49 antigen [H	2,7
	107529	Y12065	Hs.5052	nuclear protein [KDED repeat]	2,7
	130648	AA075427	Hs.17296	ESTs; Weakly similar to lyedridin	2,7
	106685	AA461551	Hs.16251	ESTs; Highly similar to 73 kDa subunit of cle	2,6
15	133848	AA055297	Hs.76728	ESTs	2,6
	134980	AA022375	Hs.50906	15 kDa telomere protein	2,6
	128571	AA402271	Hs.105778	Homo sapiens mRNA for putative Ca2+-transport	2,6
	106846	AA485223	Hs.34392	ESTs	2,6
	115852	W61546	Hs.24966	ESTs	2,6
20	132336	AA462517	Hs.2730	jan D polo-oncogene	2,6
	132623	U21858	Hs.60676	TATA box binding protein (TBP)-associated fac	2,6
	114365	Z41688	Hs.19853	ESTs	2,6
	114182	Z38909	Hs.22285	ESTs	2,6
	133370	AA158807	Hs.72157	DKFZ5641922 protein	2,6
25	108818	AA480920	Hs.3542	ESTs	2,6
	133501	W16684	Hs.74284	ESTs; Moderately similar to Similar to Scere	2,6
	100530	HG1869-HT1904		Male Enhanced Antigen	2,6
	133653	AA430332	Hs.252387	pharyngeal tumor-transforming 1	2,6
	108917	AA131978	Hs.123648	ESTs	2,6
30	122249	AA436679	Hs.258453	ESTs; Highly similar to CG4-07 protein [H.sap	2,6
	119598	W45531	Hs.94642	ESTs	2,6
	119902	W84865	Hs.40943	Human DNA sequence from clone 167A16 on chom	2,6
	133272	AA465016	Hs.63923	hathrin 10	2,6
	132675	AA425365	Hs.51884	ESTs; Weakly similar to 60S RIBOSOMAL PROTEIN	2,6
35	130459	AA460264	Hs.155683	XIA06377 gene product	2,6
	133083	N70533	Hs.6456	chaperonin containing TCP1; subunit 2 (beta)	2,6
	131130	T16399	Hs.23255	nucleoporin 158D	2,6
	112045	R43317	Hs.26312	glycine amplified on chromosome 1 protein [Hu	2,6
40	116146	AA460701	Hs.193200	ESTs	2,6
	122378	AA448100	Hs.103617	ESTs	2,6
	103134	W65724	Hs.2839	Norrie disease [pseudoglioma]	2,6
	133355	AA491236	Hs.72605	ESTs	2,6
	115652	AA426266	Hs.38178	ESTs	2,6
45	104975	AA086071	Hs.50758	chromosome-associated polypeptide C	2,6
	134691	M59979	Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	2,6
	112869	T03313	Hs.4747	dyskeratosis congenita 1; dyskerin	2,6
	100052	AF002231	Hs.75618	RA211A; member RAS oncogene family	2,6
	102635	U68838	Hs.79378	cyclin A1	2,6
	104490	N71503	Hs.43087	ESTs; Weakly similar to dyskerin [H.sapiens]	2,6
50	106813	AA479922	Hs.181022	ESTs	2,6
	106872	AA487507	Hs.18282	ESTs; Highly similar to unknown [H.sapiens]	2,6
	107022	AA595041	Hs.28666	programmed cell death 10	2,6
	107113	AA610073	Hs.23900	ESTs; Weakly similar to oligopnein-1 like p	2,6
55	113281	T66300	Hs.112356	Homo sapiens mRNA for lipoyltransferase; comp	2,6
	115586	AA395216	Hs.52423	ESTs	2,6
	115779	AA424183	Hs.70945	ESTs	2,6
	122895	AA469946	Hs.105325	ESTs	2,6
	124726	R15740	Hs.104576	carbohydrate (keratan sulfate Gal-6) sulfotrans	2,6
60	123775	R34659	Hs.12420	ESTs	2,6
	131951	AA251926	Hs.38738	boviferin uninhibited by benzimidazoles 1 (yeas	2,6
	132518	D57575	Hs.50584	ESTs	2,6
	134612	AA451712	Hs.171581	ESTs; Highly similar to ubiquitin C-terminal	2,6
	130313	AA620323	Hs.154320	ubiquitin-activating enzyme E1C (homologous t	2,6
65	131971	R70167	Hs.36111	ESTs	2,6
	133175	AA134787	Hs.69666	ESTs	2,6
	102083	U10323	Hs.75117	Interleukin enhancer binding factor 2; 45D	2,6
	125670	AA432621	Hs.82665	CD47 antigen (Rb-related antigen; integrin-as	2,6
	121822	AA426107	Hs.37016	ESTs; Moderately similar to S1D domain-bindin	2,6
70	105719	AA465171	Hs.236844	ESTs	2,6
	130029	AA236412	Hs.236510	ESTs; Moderately similar to PTF27 [Musculus	2,6
	124328	H57781	Hs.14415	ESTs; Highly similar to CGH-100 protein [H.s	2,6
	105387	AA236951	Hs.10836	chromosome 1 open reading frame 9	2,6
	103073	X59417	Hs.74077	proteasome (prosome; macropain) subunit; dph	2,6
75	116204	AA465000	Hs.51745	ESTs; Moderately similar to TRANSCRIPTION FAC	2,6
	135339	D56265	Hs.127942	Homo sapiens mRNA full length insert cDNA co	2,6
	125390	H95094	Hs.75187	translocase of outer mitochondrial membrane 2	2,6
	102504	U52077	Hs.247948	Human mitonri transposase gene; complete con	2,6
	131076	H44386	Hs.22666	ESTs	2,6
	114056	Z38342	Hs.27007	chromosome condensation 1-like	2,6
80	120402	AA234339	Hs.50282	GTP-binding protein ragB	2,6
	102125	U74650	Hs.107973	sialyltransferase	2,6
	134653	AA452818	Hs.87336	ESTs	2,6
	101659	S80343	Hs.100332	argyl-5RNA synthetase	2,6
	116766	H13280	Hs.56097	ESTs	2,6

WO 02/102235

PCT/US02/19297

104954	AA074514	Hs.26213	ESTs; Weakly similar to protein [H.sapiens]	2.5
103771	AA127524	Hs.21934	ESTs	2.5
116439	AA610668	Hs.43213	PBRF gene product	2.5
133869	U96782	Hs.178761	26S proteasome-associated pact1 homolog	2.5
132792	AA401903	Hs.242985	hemoglobin; gamma G	2.5
126620	AA010686	Hs.239720	ESTs; Weakly similar to KIAA0091 protein [Hs]	2.5
122285	AA191353	Hs.222965	ESTs; Weakly similar to KIAA0390 protein [Hs]	2.5
116516	AA401136	Hs.48617	ESTs	2.5
102983	X17620	Hs.118638	non-metastatic cells 1; protein [NM23A] expe	2.5
106288	AA435636	Hs.24338	ESTs	2.5
107444	W03391	Hs.51511	proliferation-associated 2CA; 28kD	2.5
104895	R16007	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous	2.5
128917	AA204876	Hs.206097	oncogene TC21	2.5
102299	U32907	Hs.165545	37 kDa leucine-rich repeat (LRR) protein	2.5
115363	AA0202071	Hs.155769	activator of S phase kinase	2.5
133399	AA445417	Hs.155395	Homo sapiens mRNA for putative glucosyltransfer	2.5
133752	D50927	Hs.18395	isolated-liver kinase 1	2.5
132724	AA417962	Hs.55498	geranylgeranyl diphosphate synthase 1	2.5
106743	AA476352	Hs.21938	ESTs; Weakly similar to KIAA0704 protein [Hs]	2.5
128949	AA192993	Hs.3650	a dihydrogen and metalloproteinase domain; 12	2.5
126816	AI040346	Hs.4943	hepatocellular carcinoma associated protein;	2.5
106826	AA398243	Hs.21906	ESTs; Moderately similar to similar to NEDD-4	2.5
110841	N31610	Hs.18045	ESTs; Weakly similar to parial CDS (C.elegan	2.5
111987	RA2038	Hs.6763	KIAA0942 protein	2.5
132649	AA185378	Hs.54502	ESTs; Weakly similar to 605 RIBOSOMAL PROTEIN	2.5
103038	D64657	Hs.165482	minichromosome maintenance deficient (mxc); S	2.5
130800	AA223386	Hs.19574	ESTs; Weakly similar to katanin p60 subunit [2.5
114481	AA033562	Hs.151672	ESTs	2.5
113404	T02323	Hs.70337	hemoglobin superfamily; member 4	2.5
100260	D38491	Hs.174135	KIAA0117 protein	2.5
103663	Z22634	Hs.150402	activin A receptor; type 1	2.5
104673	R68952	Hs.29780	ESTs	2.5
105026	AA126338	Hs.22744	ESTs; Weakly similar to ZINC FINGER PROTEIN 1	2.5
106024	AA269158	Hs.27163	ESTs; Weakly similar to KIAA0052 [H.sapiens]	2.5
106157	AA426367	Hs.32094	ESTs	2.5
107243	D69489	Hs.34727	ESTs	2.5
109920	H05733	Hs.30568	ESTs	2.5
105981	H03652	Hs.26090	ESTs; Weakly similar to T20B12.1 (C.elegans)	2.5
114518	AA046407	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like 1	2.5
114768	AA149007	Hs.182339	Ets homologous factor	2.5
118906	N81000	Hs.94433	ESTs	2.5
119026	N89826	Hs.55229	ESTs; Weakly similar to DMR-NS PROTEIN [H.sap	2.5
131712	X05612	Hs.30261	KIAA0857 protein	2.5
132233	X04706	Hs.93574	homeo box D3	2.5
132740	AA227751	Hs.55896	ESTs	2.5
115299	AA2078650	Hs.73291	ESTs; Weakly similar to similar to the beta 1	2.5
128820	F10338	Hs.103529	Protein of GAT42	2.5
124049	F10523	Hs.74619	primase; polypeptide 2A (58kD)	2.5
128781	X85372	Hs.105466	small nuclear ribonucleoprotein polypeptide F	2.5
121361	AA045494	Hs.183028	ESTs	2.5
134133	X03320	Hs.180383	dual specificity phosphatase 8	2.5
109502	U61678	Hs.78760	small acidic protein	2.5
116876	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity to Ye	2.5
132874	AA426778	Hs.55069	ESTs	2.5
108646	F04543	Hs.6528	DKF-ZP64C0423 protein	2.5
111197	N60093	Hs.22929	ESTs	2.5
102968	X16396	Hs.154672	methylene tetrahydrofolate dehydrogenase (NAD	2.5
124911	R89992	Hs.123645	ESTs	2.5
106028	AA489657	Hs.12311	Homo sapiens clone 25570 mRNA sequence	2.5
116988	H02627	Hs.6153	y88b12.51 Scarsa cella K28-R/R Homo sapiens	2.5
131076	X02057	Hs.22965	secretory granule; neuroendocrine protein 1 (2.5
133678	X78627	Hs.76366	translin	2.5
100420	D66983	Hs.118893	p53-responsive gene 2	2.5
133743	W07710	Hs.181724	Homo sapiens mRNA; cDNA DKF-ZP694F083 (hom of	2.5
124665	AA448164	Hs.95153	ESTs; Highly similar to CGH-73 protein [H.sapi	2.5
115117	AA256492	Hs.49307	poly(A) polymerase	2.5
124682	N68477	Hs.108408	ESTs; Highly similar to CGH-78 protein [H.sapi	2.5
104771	AA029911	Hs.24594	ESTs; Highly similar to CGH-53 protein [H.sapi	2.5
103059	AA043844	Hs.62863	ESTs	2.5
109028	AA281261	Hs.35696	ESTs; Weakly similar to putative zinc finger	2.5
105961	AA195256	Hs.61779	ESTs	2.5
119789	W73140	Hs.50916	kallitoxin 5	2.5
130512	AA046324	Hs.181271	ESTs; Highly similar to CGH-120 protein [H.sapi	2.5
134022	U25195	Hs.6153	Fragile X mental retardation; autosomal humal	2.5
104769	AA025887	Hs.114774	ESTs; Weakly similar to 10L ALU SUBFAMILY J	2.5
125787	AA744748	Hs.29403	ESTs; Weakly similar to PROBABLE ATP-DEPENDEN	2.5
131775	AA469566	Hs.31921	KIAA0645 protein	2.5

TABLE 7B:

Play: Unique Eos probaset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

[illegible]

Table BA lists about 54 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Hu01 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissue was greater than or equal to 4.0. The "average" ovarian cancer level was set to be the 3rd highest amongst various ovarian cancers. The "average" normal adult tissue level was set to be the 4th highest amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was calculated.

TABLE 9A: ABOUT 54 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUE

Pkey: Primekey
 Ex. Accn: Exemplar Accession
 UG ID: UniGene ID
 Title: UniGene Title
 ref: refseq tumor vs. normal

35	Play	Enr. Acct.	UG ID	Title	ratio
	130041	HA.3034	Ha.2142	5-hydroxytryptamine (serotonin) receptor 3A	12.1
	101249	L33881	Ha.1904	protein kinase C, η	11.8
	132268	AA233006	Ha.50786	chromosome-associated polypeptide C	11.5
	102610	U65011	Ha.30743	proliferately expressed antigen in melanoma	11.0
40	115336	AA341793	Ha.32106	ESTs	10.9
	129675	US1630	Ha.1146	Wilms tumor 1	9.3
	105298	AA233469	Ha.26389	ESTs	9.0
	121279	AA422036	Ha.98367	ESTs	7.3
	104301	D43332	Ha.6763	ESTs	7.0
	132191	AA449431	Ha.159888	KIA00741 gene product	6.8
	102136	U15552	Ha.85769	acidic 82 kDa protein mRRI	6.7
	101804	M86689	Ha.16840	TTK protein kinase	6.5
	132182	AA442827	Ha.237525	signal recognition particle 72kD	6.5
	106738	AA470146	Ha.25130	ESTs	6.0
	108857	AA133250	Ha.62180	ESTs	5.8
	115291	AA479943	Ha.122579	guanine-monomorphose synthetase	5.8
	132632	U69764	Ha.93988	ESTs	5.0
	115401	AA509963	Ha.59808	splicing factor, arginine/histidine-rich 7 (SPLD)	5.7
	126057	L41087	Ha.184187	HKR-T1=Kruppel-like zinc finger protein (hms)	5.6
55	129097	S60222	Ha.257325	ESTs	5.5
	134320	N12407	Ha.30347	general transcription factor IIC; polypeptide	5.5
	108778	AA126546	Ha.24485	chondroindin sulfate proteoglycan 8 (bancan)	5.2
	111228	AA279157	Ha.47144	CDZP56N0619 protein	5.2
	116238	AA479302	Ha.47144	ESTs	5.1
	103055	AA043562	Ha.62637	ESTs	5.1
60	129259	U76189	Ha.61152	oncosomes (multiple) like 2	5.1
	115902	AA436866	Ha.85761	ESTs	5.1
	120438	AA243441	Ha.39488	ESTs; Weakly similar to ORF Y19074w (Scorv)	4.9
	123404	AA597066	Ha.112110	ESTs	4.9
	109648	F04600	Ha.7154	ESTs	4.9
65	132624	AA1164819	Ha.53381	ESTs	4.9
	111234	N69287	Ha.21943	ESTs; Weakly similar to ORF YGL221c (Scorv)	4.9
	135202	M74093	Ha.9700	cyclin E1	4.9
	130245	AA479726	Ha.105577	ESTs	4.9
	110296	AA459033	Ha.62601	Homo sapiens mRNA; cDNA CDZp56BK13 1b (iron C	4.9
70	112344	U173016	Ha.102074	Ribosomal Protein L35 Homolog	4.8
	106115	N69820	Ha.10159	ESTs	4.8
	102627	U65651	Ha.158174	zinc finger protein 164 (Kruppel-like)	4.5
	106459	AA449741	Ha.4029	gamma-aminified sequence 1	4.5
	123335	U33266	Ha.90073	chromosome segregation 1 (yesl homolog) like	4.5
75	120306	AA119141	Ha.109643	polyadenylate binding protein-interacting pro	4.4
	120376	R40873	Ha.157174	KIA00442 gene product	4.4
	122019	AA284322	Ha.111471	ESTs	4.4
	122802	AA490530	Ha.266579	ESTs	4.4
	116416	AA409219	Ha.39692	ESTs	4.4
80	115804	AA256921	Ha.80095	ESTs	4.4
	126802	AA547061	Ha.97006	ESTs	4.4
	126892	AA1160190	Ha.76127	hert (homologous to the ER-AP (UBR3A) carboxy	4.1
	106816	AA556781	Ha.21214	ESTs	4.1
	131985	AA263529	Ha.30563	ESTs	4.1

WO 02/102235

PCT/US02/19297

			AAP61263	NA1430	AWB30477	W35765	BE354358	NA366256	NA1771	N34873	AA088105	A1242138	AW148523	AI378761	N50882
			AS27448	AWB66230	AW129910	AW670347	NS1596	AW2221	AW172283	HW6242	AW153559	NS1720	AW153559	NS1720	AW153559
			AWB0122	AS356442	AW60122	N20686	N24067	AW154918	N24676	AW471270	AW590456	RR6820	AA264334	N24060	AW149626
			AW500584	AW033568	AW503215	AA007408	AW13506	AW422627	HW5551	AA232357	DE2680	AW682745	HW6206	AA016288	AA485886
5	132532	4312_1	AW10719	BE28110	AW123835	NML00375	U10660	AW651756	BE279938	CB3008	AW19878	AA5441	NS1596	AW139300	AW328252
			AA434241	AW581866	AW469248	BE548103	T93004	NA8944	AA22615	AA564948	AW003484	AW1780423	AW1575445	AW007590	AW174159
			AA359256	AW47433	AW135089	AA584371	AA326053	AW176387	NS5614	AA384000	AA432135	AW1000	AW174857	AW174857	AW174857
			AW673412	BE063175	AW174408	AA20011	R100723	AT753769	AA192261	AW003565	AW272574	AT753729	DD2571	BE337645	NA1130
			U60011	NML00615	AW182053	BE38350	BE407839	BE409930	BE408826	AW070292	AA132589	AA136204	AW365852	AW365735	
10	100610	9336_1	BE22732	AW303255	AW411196	AW171284	AW757329	AW375366	AW170884	AW178333	AW178424	AW1365725	AW025440	AW1712852	
			AW70598	AW117782	AW581496	BE455516	BE204747	AW120342	AA333316	AW170932	BE204742	AW171363	AW153529	AW113545	
			AI10101	AW147493	AW619174	BE207404	AW147492	NL13210	AW351950	AW152825	AA521444	AW145044	AW162904	AW090634	AA128305
			AW51253	NA112799	BE207425	AA145594	AW020682	NM02468	AW1041742	AA163844	AW125933	AW135089	AA200022	AA555458	AA393083
			AI590104	AW501225	AA566758	AA566951	AA567431	AW106726	AW064200	AW1160726	AA561726	AA115726	AA115726	AA115726	AA134743
			AW153559	AW58187	AW005042	AA352502	AW680389	AW675030	BE373356	DD24565	AW110282	BE254796	AW188604	AA134743	
			BE13208	AA189377	AW182114	BE373947									
			AI202198	AA1160639	U065611	AA321623	U52098	AI119453	AA455712	N00800	NA46550	AW7223	NT5923	AW010571	AA155657
			AT57408	AI13121	AT57558	AW827561	AI135471	AA180473	NT8785	AI119983	AT118528	AW422307	AT335776	NA3140	NS9181
			AWB4182	AA132071	AW1467	AW823398	HW8000	D19525	AA504633						
20	132725	29101_1	NML00621	NA100215	U41807	U22343	BE379905	BE5671070	BE274305	BE336518	AW1023523	AA229271	AA08518	BE504485	AA580279
			AA46481	AA140671	AW180428	BE453450	DE5685	AA852399	AI3630020	WT7796	AA178713	R10056	AI933201	AT738336	BE174301
			AW16222	AA564912	AA244152	AW611553	BE500235	AA211023	AA323016	AA089174	AA119631	AA48229	AT68045	AI690437	N30025
			AT59552	AA553572	BE464500	AW777315	AA133721	AW070190	AI533848	AW674581	EA4177	AW510690	AW07869	AA436176	AA350759
			BE502074	AA217850	AA493038	AW080072	AW178071	AW1236153	AA333053	AA380468	AW126971	AW082325	AA352718	AA352156	AA61057
			WT3351	AA241153	HW8024	AA468072	AW0678	AA080711	AI333591	AI593853	AA262811	U10865	AA0404	AA214465	AT72522
25			AW57283	AA21467	AA334640	AW187810	AA207255	AA81588	HW6265	AA363470	AW179119	AA611483	AA2113	AA362156	AW183585
			AW002238	AA507624	W95150	AA446490	AW048025	AA582400	AA362221	AI238373	RS0503	AA230812	AT11937	AW475688	AA473446
			HW1993	PI13487	D19554	AA452807	BE065842	AA354306	AW149633	AA2379472	AW092406	AW007640	AW103519	HW0325	AA307760
			AW172803	AA142801	AA135025	AA005431	AA230561	AA230147	AW180002	AA265039	AW180096	AW149007	AA471202	AW125692	
			W05045	AA241406	AA044744	AA1950517	BE457493	AW474113	AA1465310	BE328705	AI511573	AW243963	BE25822	AW173020	AW079558
			AI140387	AA3851969	NM1299438	AT12170	AW167816	AA22435	AI307116	BE459519	AI371116	AA281748	AA107103	AA769749	BE551197
			U57045	AA338778	BE236291	AA142852	AW106571	AW598868	AA511241	AA254822	AI14414	AA004346	AW047025	AA2149	AW594133
			AT331343	AA335452	AW178084	AA478564	AA551166	AA141231	AA359507	AW094280	AW180533	HW1219	AW178366	AW47500	AA107018
			AW101338	AA511302	AW102807	BE051518	RS08711	BE375653	F10586	AA249625	BE241586	AW102809	AW153070	AA148447	
			AW043150	AA71407	AA013303	AA170634	AW048087	BE566015	BE52280	DE56918	AW1967342	R98280			
			AA302656	BE155915	RA3705	HW159100	HW0794	AA832454	AW091438	AA354538	AA363354	AA948272	AA228143	AA097263	AI325280
40			AI122948	AW486970	AW025907	WT0055	AA211175	AA104362	AA452706	AW063034	AA480708	AW11207	AW023390	AW13027	
			AW10667	AA215585	AA373796	AA253901	AW055234	AA1945079	AA275261	AA265049	AA383290	AA200218	AA002818	AA152695	
			BE56604	HW8579	AA020468	AA340341	AA338291	AA361003	AA494361	AI234151	AW19536	NA3354	AA138758	AW105405	
			AW585809	AW001421	AW106205	AW085317	AI140633	AA347104	AA002547	AW88507	AW472686	AA54028	AW102456	AA2438	BE324838
			AA1019132	AA501463	HW4120	AW14702	AW67483	DE50022	AA663595	BE337472	AW139344	AA140037	W00400	AA230939	HW5808
			AW172803	BE019150	AA57451	AA17446	BE215733	AW1057467							
			AA354343	AA52255	AT117108	BE336917	NML00547	U91705	U70705	BE566709	BE369818	BE299351	BE560809	BE093048	AA483040
			AT102375	BE485894	AA427803	AI18804	DE58801	AA303353	U46218	BE530704	AA187596	AA225545	AA231321	DE31197	AA1080047
			AA24833	AW007368	AI250857	AA741475	AI146832	AA169615	AW089621	AT127428	AA1036	AA120612	AA191730	AA245584	AA08611
			HW674708	AW385373	AA505682	AA0355172	AW147195	AA302235	AW673348	AA325044	AW151235	AA142734	W101036	AA272366	AW082471
			FA14432	AA044615	AW08819	AW100846	AA407580	AT743308	AA338972	AA180743	AA453807	AI013975	AT27557	AW173020	AW079558
			AW104577	AA195464	W013702	AW197351	AA332874	AA335240	AA143496	BE38222	AW066033	AA102272	W07006	AA011347	HW5428
50	132939	11857_1	AD039284	AF000419	AW022636	BE082610	AW367997	AA491410	AA337477	AA336421	W05356	AW173685	AA180708	T66134	
			AA347838	AW022547	AW054726	AW101001	AA431566	AI253595	AW04259	AW469314	U70150	AW172001	AA232945	AA12387	AW87304
			AA101030	AW001450	AA563453	AA584443	D81618	AA568458	HW1930	AA334445	W052767	NA7777	AA483784	AA428915	AW52052
			AT330743	W01792	U435031	AW106791	AW989636	AA220345	AT239913	AI220102	AA435875	AW067531	AI377049	AI039173	AW172633
			AW023632	BE440048	BE440013	AW57463	AI038774	AW020492	AA465800	AA501952	AA342058	AA505255	DE1870	W37125	AW190489
55			AW569693	AA526628	AT262717	T66158									
			AW081165	AI154512	AW080822	AA350413	BE208274	AW001402	AA307065	AW054678	W308708	AW036526	AW369115	AW13690906	
			AW173235	BE209307	AW035194	AW399125	AW364187	HW42625	T75602	AA131938	BE071339	AW136503	AA585505	AA21571	AW061322
			AA361077	AW136898	AW301099	AW118577	AW178885	AA688497	HW2996	AA599349	AW1970825	AW165131	AA243224	AA002110	AA136947
60			BE234243	AA131901	AW063630	AW085168	AW159250	RG0506	AA131923	AA520283	AA045678	AW040972	AA194498	AA029048	AA484588
			AA553463	AA26002	NS6920	AW089702	CO145	RS65414	AA7100						
			AA168491	AA176251	AA1809748	AA185268	AA421244	AW573029	BE590341	AA651915	AT216376	AA215585	AW471780	AW172159	AW181980
			AW151159	AW159270	AW167590	AW180776	AW1757338	AA148511	AI138378	AA504187	AI420817	AW129130	AW036929	WT1567	AW1651403
			AW060533	AW1573108	HW44208	AW093732	AA361519	BE501089	AA439153	AW191485	AW293934	AA335358	AA222050	AA0303978	AW153247
			AT1551	U16758	AW160838	AW0407423	BE040485	AW1473769	AW147507	AA159619	AW188635	AA1345	U43532	HW1682	NS1177
			AW207405	AA125184	F02087	AA041498	W43028								
			BE091005	BE451675	AW337738	AW368083	AI13769	AA5377820	AW369190	AW153239	AW072695	BE379572	AA120173	AW1732	AW091450
			AW091450	BE191358	NS0375	BE091354	BE091365	BE091366	BE091367	BE091368	AA353603	RA455101	N21407	AW170981	AI361577
			AA262557	AA325443	AW081822	AW083088	AA168883	BE1210	AW563074	AA46374	AA135502	AA007587	NS1596	CO2695	
			BE554118	AI137578	AA055456	AW087074	AA149654	AW087074	AA149654	AW087074	AA149654	AW087074	AA149654	AW087074	AA149654
			AW385096	BE150744	AW380468	AW380546	BE150713	DD0020	HW0899	AA464378	DE150731	AW136845	BE091345		
			AI351817	HW37312	AW038829	W14053	BE202150	BE536901	AW14078	HW95578	BE018482	BE54405	NS8337	AW167104	AW439993
			AW307086	AW457070	AA562960	AT215685	AT215684	BE342011	AI186210	AW771831	TA5421	AA454294	AA453419	W95471	AA628312
			AA304686	AW157075	AW536873	T54121									
			AA037145	U054747	NML001324	NA11516	AA147711	NA143605	BE334465	AA337531	AA032327	AA003307	BE259438	BE259565	AA370898
			AA337272	AA166682	BE304387	BE293036	RS0607	AA218696	W7270	AA590540	AA591431	AA255445	AA255445	BE090721	AW901419
			AW090424	AA363564											

WO 02/10223

CT/US02/19297

[illegible]

WO 02/122235

PCT/US02/19297

122802	267993_1	A1763813 A1769315 A1743691 A1915545 A46179473 C21435 N50944 N50902 AW978102 H23837 BE087536 AA316516 A687303 A6571661 A655465 A684252 A681066 A664008 A6826160 A659843 AA42421 AA460330 BE042776 AW273200 AW273223 AW167285 AW083571 A654306 A6517486 A61A104706 AW273214 BE139512 AW169467 AW130022 AW167419 A1268465 AW150010 H50001 A1915745 AW08910	
5	123494	21202_1	AW175919 AW175011 AF135100 NM_014050 AF078860 BE018005 AK000285 AF151038 BE245156 AW175007 AA345114 BE019758 BE019209 W25509 AA314339 AA306674 AA337956 AW564843 AW300412 N46796 AA316235 AA314286 R15696 BE350333 I57134 N46143 AW068462 AA923517 AA068223 A118513 A6837523 A1938320 A3030273 A6522276 N46739 AA3049717 AA3052772 N302940 AA80765 A671677 A102109 AA094552 A465252 A461781 A174447 AW52254 A077790 AW051083 AW14067 N60801 AA57185 A151244 A433106 A1719760 AA45308 AA63056 AA300975 A636920 AW075033 A4264393 AW089867 AA475335 A332539 BE301513 AA452920 AA645475 A1166871 A0879412 A658171 A375985 BE220535 A688811 AW514909 AW062346 AA539796 BE330848 A650048 A023075 A112804 A19150433 A08929
10	116295	11967_2	AW145502 Z45342 A1002825 AL046382 A4442545 AW914171 BE220243 AW068852 AA043037 AYC29245 A665892 A038768 H26330 BE463534 A1628252 AA36138 A0277291 AA489033 AA741238 A1029064 A300253 A125761 Z38417 C01353

Table 9A lists about 382 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected from 35403 probesets on the Affymetrix-Eos-Hu01 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult ovaries was greater than or equal to 10. The "average" ovarian cancer level was set to the 2nd highest amongst various ovarian cancers. The "average" normal adult ovaries level was set to the arithmetic mean amongst various non-malignant ovaries. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues (see Table 7A) was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 9A: 382 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

25	Play: Primkey Ex. Accn: Exon/Exon Accession UG ID: UniGene ID Title: UniGene title ratio: ratio tumor vs. normal tissues			
30	Play	Ex. Accn	UG ID	Title
35	134554	L33530	Hs.173596	CD24 antigen (small cell lung carcinoma clust
40	102827	X12878	Hs.85114	keratin 18
45	115909	AA436666	Hs.56781	ESTs
50	123169	AA488862	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [
55	115674	AA408542	Hs.71520	ESTs
60	102163	U20758	Hs.313	secreted lipocalin protein 1 (lecithin:lecithin, heme
65	101839	M30306	Hs.682	membrane component; chromosomal c; surface ma
70	115221	A4252942	Hs.76741	ESTs
75	100309	A4043644	Hs.22663	ESTs
80	121953	AA428687	Hs.56502	ESTs
85	133504	W56070	Hs.74318	desmoplakin (DPL DPL)
90	103546	Z14244	Hs.75752	cytochrome c oxidase subunit I1iib
95	100147	X12368	Hs.135340	cathepsin B (proteolytic factor 2) (lysosomal Hk
100	102676	X17042	Hs.15618	proteolysin 1, secretory granule
105	130967	AA134138	Hs.182579	Homo sapiens leucine aminopeptidase mRNA; com
110	102008	U02880	Hs.82543	protein tyrosine kinase 9
115	126960	AA311790	Hs.167156	ESTs
120	103111	X63167	Hs.71719	epididymis-specific; whey-acid protein type
125	133828	AA453783	Hs.78550	Homo sapiens mRNA; cDNA DKFZ56481264 (from c
130	111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [Lysapine]
135	102803	U88619	Hs.28125	claudin 10
140	104843	AA465217	Hs.159674	ESTs
145	106055	AA577118	Hs.21103	Homo sapiens mRNA; cDNA DKFZ56480736 (from cl
150	120655	AA287347	Hs.238205	ESTs
155	102568	L16398	Hs.154572	methylene tetrahydrofolate dehydrogenase (NAD
160	104052	AA393164	Hs.57644	mammaglobin 2
165	105105	AA175945	Hs.73825	RAB5 interacting; kinesin-like (kinesinlike)
170	101332	L47776	Hs.79525	Homo sapiens (coll line HL-6) alpha topoisomere
175	106167	AA425906	Hs.7955	ESTs
180	101042	J05428	Hs.10319	UDP glucosyltransferase 2 family; polypeptide
185	125552	X08290	Hs.15550	Homo sapiens mRNA; cDNA DKFZ56481264 (from c
190	101201	L25234	Hs.2255	matrix metalloproteinase 7 (matrilysin; strom
195	126410	R51912	Hs.12409	sonatalectin
200	134326	L16306	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)
205	125739	AA426557	Hs.52137	y-myc avian myeloblastosis viral oncogene h
210	132254	L20628	Hs.430	placatin 1 (lipoican)
215	112610	R73932	Hs.23643	ESTs
220	101441	M21005	Hs.100000	S100 calcium-binding protein A8 (calgranulin
225	116345	AA59361	Hs.19067	HER3 receptor tyrosine kinase (c-erbB3; EREB3
230	100880	AA133334	Hs.129811	ESTs
235	133859	U06782	Hs.176761	S65 proteasome-associated pad1 homolog
240	107295	T34527	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine polypeptid
245	106210	AA426239	Hs.10338	ESTs
250	134711	J04011	Hs.86674	cytochrome b-245; beta polypeptide [chronic g
255	125789	A362972	Hs.62128	ST4 oncogenic lipophilic glycoprotein
260	107222	D51235	Hs.82609	tumor rejection antigen (gp96)
265	102260	U2386	Hs.155957	karyophilin alpha 2 (RAG cohort 1; importin a
270	134691	M69379	Hs.80474	prostaglandin-endoperoxide synthase 1 (cycloo
275	105588	A4279215	Hs.10867	ESTs
280	130718	N70166	Hs.18376	ESTs
285	111185	N67551	Hs.12644	EGF-like domain; multiple 6
290	131985	W60146	Hs.35962	ESTs
295	132903	AA235044	Hs.5685	Homo sapiens clone 25166 mRNA sequence
300	114359	Z41589	Hs.133483	ESTs; Moderately similar to H1 chloride chan

WO 02/102235

PCT/US02/19297

	129229	AA211941	Hs.109643	poly(ADP-ribose) binding protein-interacting pro	17.2
	129351	AA167268	Hs.62349	Human ras inhibitor mRNA; 3' end	17.2
	110709	X22222		yw3405.51 Morton Fetal Cerebral Homo sapiens	17.1
	111182	TSS234	Hs.9676	Human DNA sequence from clone 30M3 on chromo	17.0
5	116892	AA435946	Hs.50831	ESTs	17.0
	123114	AA485407	Hs.105235	ESTs; Moderately similar to KIAA0454 protein	17.0
	123442	AA598853	Hs.111496	ESTs	17.0
	123339	AA594253	Hs.101515	ESTs	16.9
	123681	AA609550	Hs.255552	ESTs	16.9
10	131941	D62657	Hs.35086	ubiquitin-specific protease 1	16.8
	120649	AA287115	Hs.95957	ESTs	16.8
	102139	U18332	Hs.21726	dual specificity phosphatase 5	16.8
	118522	AA331393	Hs.43758	ESTs	16.7
	135243	AA215333	Hs.97101	putative G protein-coupled receptor	16.6
15	131257	AA250042	Hs.24906	ESTs	16.5
	106506	AA233692	Hs.65952	ESTs; Weakly similar to III ALU SUBFAMILY SX	16.3
	132701	AA279389	Hs.55220	BCL2-regulated autophagene 2	16.3
	134449	L34155	Hs.83450	laminin: alpha 3 (nicotin (150K)); kalinin (16	16.3
	126180	R18070	Hs.3712	ubiquitin-cytochrome c reductase; Rieske iron	16.3
20	106124	AA423987	Hs.7507	ESTs	16.2
	115263	AA262071	Hs.152769	activator of S phase kinase	16.2
	117688	R34055	Hs.44648	ESTs	16.1
	131245	AA620599	Hs.24786	DKFZP564E1962 protein	16.1
25	101674	M61916	Hs.82124	laminin: beta 1	16.0
	125819	AA330535	Hs.161469	ESTs	16.0
	134039	S78559	Hs.76572	laminin: alpha 4	15.9
	130648	AA075427	Hs.17296	ESTs; Weakly similar to [prediction	15.9
	102823	U09914	Hs.5057	carboxypeptidase D	15.8
30	129470	AA447854	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564E222 (from et	15.7
	115544	AA400124	Hs.234007	ESTs	15.7
	132543	AA417152	Hs.5101	protein regulator of cyclinase 1	15.7
	130155	L33404	Hs.151254	kallikrein 7 (chymotrypsin; stratum corneum)	15.7
	101008	J04152	Hs.753	Fc fragment of IgG; low affinity Iiia; recept	15.7
35	120472	AA251875	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprotein [15.6
	115844	H64398	Hs.38331	ESTs	15.6
	106753	AA476944	Hs.7331	ESTs	15.6
	114767	AA148885	Hs.154443	minichromosome maintenance deficient (S. cere	15.5
	114768	AA149007	Hs.182339	Ets homologous factor	15.5
	123710	AA24352	Hs.70337	immunoglobulin superfamily; member 4	15.5
40	101507	M27492	Hs.82112	Interleukin 1 receptor; type 1	15.4
	102519	U29359	Hs.80295	Parklike cell protein 4	15.4
	102610	U50111	Hs.30743	preferentially expressed antigen in melanoma	15.4
	111244	N65555	Hs.24724	10F4-amplified sequences with leucine-rich tan	15.4
	120404	AA234521	Hs.85657	KCA-1015 protein	15.3
45	130455	X17055	Hs.155956	N-acetyltransferase 1 (arylamine N-acetyltran	15.2
	129519	AA298786	Hs.112242	ESTs	15.1
	106553	AA454957	Hs.5587	ESTs; Highly similar to RNA binding motif pro	15.0
	109502	AA233837	Hs.44755	ESTs; Weakly similar to membrane glycoprotein	14.9
50	115967	AA445887	Hs.42911	ESTs	14.9
	104635	AA004415	Hs.106105	ESTs	14.9
	134133	X83920	Hs.180383	dual specificity phosphatase 6	14.8
	134444	X04470	Hs.251754	secretory lysocyte protease inhibitor (antit	14.8
	132998	Y00652	Hs.170121	protein tyrosine phosphatase; receptor type;	14.8
55	131997	D82399	Hs.136644	Homo sapiens clone 23714 mRNA sequence	14.6
	134056	R27358	Hs.7886	ESTs; Weakly similar to Pelfo associated prot	14.6
	101249	L33581	Hs.1594	protein kinase G, iota	14.5
	105286	AA233469	Hs.26369	ESTs	14.5
	109719	AA620307	Hs.27379	ESTs	14.5
	115839	AA429038	Hs.40541	ESTs	14.5
60	122802	AA406830	Hs.258579	ESTs	14.5
	123956	AA243021	Hs.132225	UDP-Galactose 4-epimerase 1;4- galactoseyltransf	14.3
	130269	AA284694	Hs.169332	nucleoside-like protein 1	14.3
	134374	D26533	Hs.8235	ESTs	14.3
	106370	AA443841	Hs.18675	spouty (Drosophila) homolog 2	14.2
65	130019	AA297170	Hs.12175	collagen; type IV; alpha 3 (Goodpasture anti	14.1
	132323	U21658	Hs.80679	TATA box binding protein (TBP)-associated fac	14.1
	107968	AA034020	Hs.61539	ESTs	14.1
	125390	H65094	Hs.75187	translocase of outer mitochondrial membrane 2	14.1
70	107148	AA621131	Hs.5889	ESTs; Weakly similar to W01A11.2 gene product	14.1
	110786	N54730	Hs.15450	ESTs	14.0
	109481	AA233342	Hs.90960	ESTs; Weakly similar to WD40 protein Clao 1 [13.9
	105646	AA282147	Hs.5888	ESTs	13.9
	105090	AA412251	Hs.12802	development and differentiation enhancing fac	13.8
75	132616	AA253330	Hs.5344	adaptor-related protein complex 1; gamma 1 su	13.7
	133230	S62240	Hs.58838	ras homolog gene family; member E	13.7
	124803	R45480	Hs.164695	cyclin K	13.6
	121381	AA405747	Hs.37865	ESTs; Weakly similar to WASP-family protein [13.6
	106200	AA195399	Hs.24641	ESTs	13.5
	106527	AA281245	Hs.23317	ESTs	13.5
80	114896	AA251010	Hs.87807	ESTs	13.5
	118036	N52844	Hs.199008	ESTs	13.5
	134572	N79749	Hs.87627	ESTs; Weakly similar to cDNA EST EMBL700542	13.5
	110915	N46252	Hs.23724	ESTs	13.3
	117994	N51919	Hs.47398	ESTs	13.3

WO 02/102235

PCT/US02/19297

	132550	AA029597	Ha.170195	bore morphogenic protein 7 (patogenic prot	13.3
	124315	H94932	Ha.8906	v-rat simian leukemia viral oncogene homolog	13.2
	102547	U57911	Ha.46538	chromosome 11 open reading frame 6	13.2
	126134	W19228	Ha.100748	ESTs	13.2
5	111805	R33468	Ha.24651	ESTs	13.1
	106983	AA521195	Ha.10887	similar to lysosome-associated membrane glyco	13.0
	106486	AA52141	Ha.17171	ESTs	13.0
	110787	X26716	Ha.12244	ESTs; Weakly similar to C44B9.1 [Calepans	13.0
10	122850	AA654414	Ha.112159	ESTs	13.0
	131535	AA504642	Ha.28436	ESTs; Weakly similar to coded for by C. eleg	13.0
	116188	AA464728	Ha.18498	ESTs	13.0
	107243	Z59489	Ha.34727	ESTs	12.9
	126300	C20976	Ha.110165	ESTs; Highly similar to ribosomal protein L26	12.9
	134487	R38185	Ha.83954	Homo sapiens unknown mRNA	12.8
15	102348	U37519	Ha.87539	aldehyde dehydrogenase 8	12.8
	131839	H83622	Ha.33010	KIAA0555 protein	12.8
	119520	W47520	Ha.56009	Z-5'-phosphorylase synthetase 3	12.8
	120802	AA343533	Ha.128777	ESTs; Weakly similar to predicted using Genot	12.7
	102250	U28014	Ha.74122	casease 4; apoptosis-related cysteine proteas	12.7
20	105539	AA258973	Ha.26242	ESTs	12.7
	114965	AA250737	Ha.27422	ESTs	12.7
	118001	NS2151	Ha.47447	ESTs	12.7
	100448	D87459	Ha.57652	EGF-like domain; multiple 2	12.6
	130200	D59375	Ha.75525	cathecolamin	12.6
25	131075	Y02347	Ha.22195	secretory granule; neuroendocrine protein 1 (12.6
	102496	AA265323	Ha.25264	DKFZP434B126 protein	12.5
	102925	AA193592	Ha.42300	ESTs; Weakly similar to !!! ALU SUBFAMILY SQ	12.5
	118215	NS2195	Ha.77910	3-hydroxy-3-methylglutaryl-Coenzyme A synth	12.5
	134388	M15841	Ha.82575	small nuclear ribonucleoprotein polypeptide B	12.5
30	103657	AA459790	Ha.167498	PAIN binding protein 6	12.4
	130350	S67325	Ha.83788	propionyl Coenzyme A carboxylase; beta poly	12.4
	109883	F09308	Ha.27807	ESTs	12.3
	127463	AA411745	Ha.239681	ESTs; Weakly similar to KIAA0554 protein [Hs	12.3
	102876	X29653	Ha.174142	colony stimulating factor 1 receptor; format	12.2
35	101804	M86990	Ha.169640	TTK protein kinase	12.2
	128017	H13108	Ha.107968	ESTs	12.1
	106812	AA394125	Ha.20814	ESTs; Highly similar to CGI-27 protein [Hsap	12.1
	105459	AA49741	Ha.4029	glutamate-amplified sequence-41	12.0
	107059	AA365846	Ha.23044	RAO51 (S. cerevisiae) homolog [E col RecA ho	12.0
40	107080	AA609210	Ha.19221	ESTs	12.0
	110799	N28101	Ha.7838	Human ring zinc-finger protein (ZNF 127-Xp) ge	12.0
	112253	R51818	Ha.104222	Homo sapiens mtDNA; cDNA DKFZp665L034 (from d	12.0
	116780	H11084	Ha.155242	protein kinase C, delta	12.0
	120314	AA194168	Ha.221040	KIAA1038 protein	12.0
45	123005	AA479726	Ha.105577	ESTs	12.0
	132572	AA448287	Ha.237825	signal recognition particle 72kD	12.0
	110661	H58817	Ha.5139	ESTs; Weakly similar to UBQUITIN-CONJUGATING	12.0
	101923	S70266		HNL-mesenchymal lipocalin (human, ovarian canc	11.9
	134892	H06625	Ha.92414	ESTs	11.8
50	105816	AA257971	Ha.21214	ESTs	11.8
	102448	AA226968	Ha.22826	ESTs	11.7
	109130	AA172240	Ha.20161	ESTs; Weakly similar to IgE receptor beta sub	11.7
	119565	AA448121	Ha.44198	Homo sapiens BAC clone RGS4D04 from 7q31	11.7
	116135	AA460314	Ha.94179	ESTs	11.7
55	116284	AA487262	Ha.237809	ESTs; Weakly similar to hypothetical protein	11.7
	132384	AA479653	Ha.47467	Human DNA sequence from clone 167A10 on chrom	11.7
	134763	Y09216	Ha.173135	dust specificity tyrosine (Y)-phosphorylation	11.7
	125136	W21479	Ha.129051	ESTs	11.7
	133928	NS4096	Ha.77768	ubiquitin-conjugating enzyme E2E 1 (homologou	11.6
60	117285	N28530	Ha.93701	ESTs	11.5
	127007	AA296980		EST11857 Uterus tumor 1 Homo sapiens cDNA 5'	11.5
	130567	L27493	Ha.1608	replication protein A3 (14kD)	11.5
	138073	AA462000	Ha.94030	Homo sapiens mRNA; cDNA DKFZp686E1624 (from c	11.5
	119140	AA258030	Ha.50556	ESTs; Weakly similar to supported by GENSCAN	11.4
65	116336	AA347193	Ha.52180	ESTs	11.4
	133240	D01161	Ha.65613	ESTs	11.3
	106521	AA453431	Ha.14732	multic enzyme 1; NAD(P)-dependent; cytosolic	11.3
	107674	AA411027	Ha.41143	KIAA0881 protein	11.3
	114149	Z38514	Ha.27195	ESTs	11.3
70	132478	H29205	Ha.45890	KIAA4246 protein	11.2
	104252	AF002246	Ha.210863	cell adhesion molecule with homology to L1CAM	11.2
	102436	U46499	Ha.790	microsomal glutathione S-transferase 1	11.2
	108726	AA465339	Ha.7141	ESTs	11.2
	100116	D02654	Ha.77443	actin gamma 2; smooth muscle; enteric	11.2
75	110970	NS1374	Ha.96570	Homo sapiens mRNA full length insert cDNA do	11.2
	130417	U58522	Ha.155485	huntingtin-interacting protein 2	11.2
	132006	AA142857	Ha.234896	ESTs; Highly similar to gominin [Hs]aptons	11.2
	107853	AA024427	Ha.59461	DKFZP434C245 protein	11.2
	133467	Y02461	Ha.78712	aminotransferase; delta; cytosolic 1	11.1
80	100438	D67448	Ha.91417	topoisomerase (DNA) II binding protein	11.1
	102654	U68494	Ha.24385	Human hbc547 mRNA sequence	11.1
	103172	X58742	Ha.116774	integrin, alpha 1	11.1
	106856	AA46183	Ha.155329	ESTs; Weakly similar to similar to oxysal-	11.1
	108255	AA063157	Ha.127608	ESTs	11.1

WO 02/102235

PCT/US02/19297

	124306	H93575	Hs.227146	Homo sapiens mRNA; cDNA DKFp554J142 (from d	11.1
	125057	X52495	Hs.214742	CDW52 antigen (CDMPATH-1 antigen)	11.1
	128846	AA455958	Hs.104049	basement membrane-linked gene	11.1
5	129025	AA209992	Hs.103441	ESTs; Weakly similar to testicular lektin B1-	11.0
	107038	AA009528	Hs.42743	ESTs; Weakly similar to predicted using Genef	11.0
	134480	AA024654	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha sub	11.0
	115262	AA279112	Hs.84994	ESTs	11.0
	102580	U60608	Hs.152981	CDP-diacylglycerol synthase (phospholipase cy	10.9
10	106914	AA458934	Hs.179912	ESTs	10.9
	107115	AA010138	Hs.27893	ESTs; Highly similar to CGI-124 protein (H.s.a	10.9
	115764	AA421562	Hs.104111	anterior gradient 2 (Xenopus laevis) homolog	10.9
	121770	AA421714	Hs.11469	KIAA0958; protein	10.9
	132191	AA449431	Hs.158988	KIAA0741 gene product	10.9
	133214	U10859	Hs.250911	interleukin 13 receptor; alpha 1	10.9
15	133914	N33611	Hs.77542	ESTs	10.9
	101913	S82507	Hs.80100	UDP-N-acetyl-L-alpha-D-glucosamine:polypeptid	10.8
	102559	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	10.8
	104147	AA451992	Hs.226799	ESTs; Highly similar to HSPC939 protein (H.s.a	10.8
20	106474	AA450212	Hs.42484	Homo sapiens mRNA; cDNA DKFp554C063 (from d	10.8
	115881	AA433577	Hs.149442	G protein-coupled receptor 64	10.8
	129950	M31516	Hs.1399	decay accelerating factor for complement (CD5	10.8
	132783	N74897	Hs.5663	DEAD1 (Acp-Glu-Ala-Asp) box polypeptide	10.8
	133784	AA214306	Hs.76173	ESTs	10.8
	134248	AA262577	Hs.80624	ESTs	10.8
25	102555	AA278302	Hs.15349	ESTs; Weakly similar to partial CD5 (Calegan	10.8
	127999	AA837495	Hs.60851	ESTs; Weakly similar to Wiskott-Aldrich syndr	10.8
	108040	AA041551	Hs.48644	ESTs	10.8
	130367	Z38501	Hs.8786	ESTs; Weakly similar to Hs. ALU SUBFAMILY SQ	10.7
	106339	AA084977	Hs.54568	ESTs; Weakly similar to protein B (H.sapiens)	10.7
30	111345	N68620	Hs.14559	ESTs	10.7
	115583	AA308913	Hs.45231	LDLC1 protein	10.7
	128995	T17440	Hs.107418	ESTs	10.7
	101396	M15796	Hs.76996	proliferating cell nuclear antigen	10.6
35	121214	U64271	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dioxygen	10.6
	101275	L37936	Hs.3273	Ta translation elongation factor; mitochondrial	10.6
	104680	AA007150	Hs.14846	Homo sapiens mRNA; cDNA DKFp554D016 (from d	10.6
	106939	AA100394	Hs.69449	Human DNA sequence from BAC 15E1 on chromosom	10.6
	112041	RA5500	Hs.22829	ESTs	10.6
	114208	Z39301	Hs.7659	ESTs	10.6
40	116837	N67974	Hs.75431	fibrinogen; gamma polypeptide	10.6
	106919	AA490885	Hs.21766	ESTs	10.6
	116984	AA474587	Hs.91109	ESTs	10.6
	106338	AA268610	Hs.32597	ring finger protein (C3H2C3 type) 5	10.6
45	102200	U21551	Hs.157205	branched chain aminotransferase 1; cytosolic	10.6
	116710	F10577	Hs.70312	ESTs	10.5
	119780	W72987	Hs.191381	ESTs; Weakly similar to hypothetical protein	10.5
	112896	T23538	Hs.7165	zinc finger protein 259	10.5
	100029	X54489	Hs.789	GRO1 oncogene (melanoma growth stimulating ac	10.5
50	101255	L34500	Hs.145894	mitochondrial translation initiation factor	10.4
	107032	AA599472	Hs.247509	succinate-CoA ligase; GDP-forming; beta subun	10.4
	126617	A087461	Hs.104590	ESTs	10.4
	114475	Z39093	Hs.27263	ESTs	10.4
	132073	N67408	Hs.35516	ESTs	10.4
55	101469	M22877	Hs.189248	Human somatic cytochrome c (HCS) gene; comple	10.3
	102487	U46589	Hs.221968	aquaporin 5	10.3
	104201	Q45332	Hs.6763	ESTs	10.3
	127236	A0341818	Hs.96958	building uninhibited by benzimidazoles 1 (yeas	10.3
	101465	M22612	Hs.241395	protease, serine; 1 (trypsin 1)	10.3
60	113805	W45957	Hs.250617	ESTs	10.2
	133538	Y00264	Hs.174469	amylid beta (A4) precursor protein (protease	10.2
	159789	F10770	Hs.180378	Homo sapiens clone 659 unknown mRNA; complete	10.2
	113523	T90037	Hs.106866	ESTs	10.2
	116195	AA465148	Hs.72402	ESTs	10.2
65	134542	X57025	Hs.85112	insulin-like growth factor 1 (somatomedin C)	10.2
	129298	Z39265	Hs.235359	YD191 protein	10.2
	119357	T78324	Hs.90005	ESTs	10.2
	134470	X54942	Hs.837558	CDK28 protein kinase 2	10.2
	134288	AA430008	Hs.8117	ESTs	10.2
70	105127	AA158132	Hs.118117	ESTs; Weakly similar to contains similarity t	10.1
	119227	H07046	Hs.35225	ESTs; Weakly similar to MBNL protein (H.sapie	10.1
	115188	AA261819	Hs.86367	ESTs	10.1
	132632	N59764	Hs.5398	guanine-mono-phosphate synthetase	10.1
	124049	F10523	Hs.74519	pininase; polypeptide 2A (SBLD)	10.1
	100079	AB002365	Hs.233114	KIAA0657 protein	10.0
75	113987	W67494	Hs.9541	ESTs; Moderately similar to COMPLEMENT C1Q SU	10.0
	117280	N22107	Hs.172241	ESTs	10.0

TABLE 99:

Play: Unique Fos probe/seq identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Play	CAT Number	Accession
100661	2182_1	BE023001 L05095 AA383604 AW996416 NS3295 AA480213 AW571519 AA603655

WO 02/102235

PCT/US02/19297

[illegible]

Table 10A lists about 733 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix Eos-HUG3 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" ovarian cancer level was set to be about the 80th percentile amongst various ovarian cancers. The "average" normal adult tissue level was set to the 90th percentile value amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator, before the ratio was evaluated.

TABLE 10A: ABOUT 733 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

	Pkey	Ex. Acn	UG ID	Title	ratio
	Ex. Acn: Exemplar Accession				
	UG ID: UniGene ID				
	Title: UniGene title				
	ratio: ratio tumor vs normal tissues				
65	Pkey	Ex. Acn	UG ID	Title	ratio
	439238	T27013	Hs.3132	steroidogenic acute regulatory protein	56.1
	416179	X51630	Hs.1145	Wntes tumor 1	33.5
	400292	AA260/37	Hs.7247.2	BMP1-IR, bone morphogenetic protein receptor	30.0
	452838	U95011	Hs.30743	Preferentially expressed antigen in melanoma	29.5
70	415111	AT32617	Hs.162382	ESTs	26.1
	422965	HS450/2	Hs.122579	ESTs	23.1
	410529	H47223	Hs.30543	ESTs	27.4
	403259	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromelysin 2)	25.2
	449524	AB24049	Hs.27532	gcb1a1093.01, NID_5GAP_1H1 Homo sapiens cDNA	23.7
75	477455	D31152	Hs.79729	collagen, type X, alpha 1 (Schm) medially secretory granules, neuroendocrine protein 1	21.9
	428192	H33932	Hs.2265	ESTs	21.3
	446243	AA069771	Hs.77465	ESTs	21.3
	430691		Hs.103536	ESTs	21.2
	444763	AK001468	Hs.62180	ESTs	20.6
	407038	AA404572	Hs.268693	EST	20.1
80	423739	AA308155	Hs.97600	ESTs	19.7
	436962	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular matrix p	19.0
	451110	AB055040	Hs.321584	ESTs	18.2
	414717	AB05605	Hs.168640	ITK, protein kinase	16.6

WO 02/102235

PCT/US02/19297

	452065	AI377431	Hs.129372	ESTs	9.1
	424086	AI351010	Hs.103267	lysyl oxidase	9.1
	442975	BE523033	Hs.23826	Homo sapiens clone TCCCTA00142 mRNA sequence	9.1
5	415208	AW291168	Hs.41295	ESTs	9.0
	407166	RA5175	Hs.117193	glycylglycyl 1.1 Scares infant brain 1N16 Homo s	9.0
	445537	AJ245671	Hs.12844	EGF-like domain; multiple 6	8.9
	405269	AA579363	Hs.22912	Homo sapiens cDNA FLJ13352 fls, clone OVARC10	8.9
	433527	AW236613	Hs.133020	ESTs	8.9
10	409928	AL137163	Hs.57549	hypothetical protein d47384	8.8
	423020	AA383092	Hs.1608	replication protein A3 (14C)	8.7
	425665	AK001050	Hs.159066	ESTs	8.6
	443204	AW205578	Hs.29643	Homo sapiens cDNA FLJ13103 fls, clone NT2P930	8.6
	449453	AI572096	Hs.9012	ESTs	8.6
15	453878	AW964440	Hs.19025	ESTs	8.6
	450505	NM_004572	Hs.25051	phosphatase 2	8.6
	407001	U12471	Hs.247954	Human bromodomain-1 gene, partial cds	8.6
	414315	Z24878		gh.HS65D0052 STRATA.GENE Human skeletal muscle	8.5
20	425492	AL021918	Hs.158174	zinc finger protein 184 (Knappel-like)	8.5
	436181	AA660339	Hs.28836	KIAA1571 protein	8.5
	436396	AI503487	Hs.299112	Homo sapiens cDNA FLJ11441 fls, clone HEMBA10	8.5
	413384	AW146266	Hs.25130	ESTs	8.4
	453370	AI470523	Hs.182356	ESTs, Moderately similar to translation init	8.4
	409041	AR033025	Hs.50081	KIAA1199 protein	8.4
25	447078	AW685727	Hs.301570	ESTs	8.4
	445674	WS1178	Hs.154140	ESTs	8.3
	433393	AF033584	Hs.98074	atrophin-1 interacting protein 4	8.3
	434386	AF064254	Hs.40785	VERY-LONG-CHAIN ACYL-CoA SYNTHETASE	8.3
30	421155	HE7879	Hs.102267	lysyl oxidase	8.2
	435394	BC5719623	Hs.27693	COX-124 protein	8.2
	400098	AA022719	Hs.615356	STEAP1	8.1
	409092	AI735263	Hs.172606	ESTs	8.1
	440250	AA676179	Hs.134650	ESTs	8.1
	408143	AW025980	Hs.139666	ESTs	8.1
35	407771	AL138372	Hs.62713	ESTs	8.1
	419038	AI533323	Hs.77496	ESTs	8.1
	431725	X55724	Hs.2839	Norrie disease (pseudoglioma)	7.9
	431750	AA514966	Hs.283705	ESTs	7.9
	435635	AF220350	Hs.181385	uncharacterized hematopoietic stem/progenitor	7.9
40	441826	AW008603	Hs.128915	phospholipase related	7.9
	417728	AW138437	Hs.24790	KIAA1573 protein	7.8
	418845	AA552986	Hs.68232	chromobox homolog 5 (Drosophila HP1 alpha)	7.8
	421039	NM_003478	Hs.101299	cullin 5	7.8
	440999	AA151520	Hs.279525	hypothetical protein PRO2605	7.8
	429809	AF002246	Hs.210653	cell adhesion molecule with homology to L1CAM	7.8
45	415139	AW975942	Hs.43524	ESTs	7.7
	405192	AA263143	Hs.24695	RAD51-interacting protein	7.7
	423982	AW896292	Hs.137206	Homo sapiens mRNA: cDNA DHFZp564H1663 (from c	7.7
	438211	AK001191	Hs.80881	polynucleotide (DNA directed), gamma	7.7
50	463101	AV549959	Hs.24395	Human hbo547 mRNA sequence	7.5
	428921	AA037145	Hs.172866	cleavage stimulation factor, 3' pre-RNA, subu	7.5
	433330	AW207094	Hs.132816	ESTs	7.5
	438759	AL359055	Hs.57700	Homo sapiens mRNA full length insert cDNA, clo	7.5
	427660	AT741320	Hs.114121	Homo sapiens cDNA: FLJ23226 fls, clone CAE006	7.5
55	422095	AI868872	Hs.289665	centriole (microtubule)	7.5
	438478	AA328108	Hs.53631	ESTs	7.4
	412170	U16552	Hs.73729	very low density lipoprotein receptor	7.4
	428954	AF100761	Hs.194678	WNT1 inducible signaling pathway protein 3	7.4
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	7.4
60	439262	AA832333	Hs.124399	ESTs	7.4
	458420	AY28513	Hs.59203	ESTs	7.3
	423952	AA98178	Hs.121553	hypothetical protein FLJ20641	7.3
	457030	AG017740	Hs.173381	dihydropyrimidinase-like 2	7.3
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	7.2
65	409916	BE213625	Hs.57435	solute carrier family 11 (proton-coupled diva	7.2
	415307	NI13529	Hs.531659	Matrix metalloproteinase 1 (interstitial collag	7.2
	420300	AL045633	Hs.44259	ESTs	7.2
	424001	W57833	Hs.137475	KIAA1051 protein	7.2
	400330	X03635	Hs.1657	Estrogen receptor 1	7.1
70	40238			0	7.1
	413573	AI733859	Hs.149089	ESTs	7.1
	428071	AF212845	Hs.182339	transcription factor ESE-3B	7.1
	447164	AF026941	Hs.17518	Homo sapiens cigs mRNA, partial sequence	7.1
	453062	AW207638	Hs.81903	ESTs	7.1
75	425965	AY131888	Hs.172792	ESTs, Weakly similar to hypothetical protein	7.1
	442520	AB193953	Hs.209122	ESTs	7.1
	445142	AT754693	Hs.145968	ESTs	7.0
	417791	AW965339	Hs.111471	ESTs	7.0
	418524	AA305075	Hs.65769	acidic 62 kDa protein mRNA	7.0
80	451787	AW953865	Hs.565120	ESTs	7.0
	452909	NM_015368	Hs.33985	pannixin 1	7.0
	453516	NM_003462	Hs.33846	dynein, axonemal, light intermediate polypapi	7.0
	436281	AW411194	Hs.120051	ESTs	7.0
	448937	AW819642	Hs.241135	transmembrane protein vesalzin, hypothetical p	6.9
	414142	AW356397	Hs.155042	ESTs	6.9

WO 02/102235

PCT/US02/19297

	448776	BE302464	Hs.30057	transporter similar to yeast MRS2	6.9
	419423	D28488	Hs.96315	KIAA007 protein	6.9
	420968	ALJ40974	Hs.102051	Homo sapiens mRNA; cDNA DKFZp5648222 (transl)	6.8
5	429971	AI873678	Hs.91789	ESTs	6.8
	413597	AW302885	Hs.117183	ESTs	6.8
	415138	C18366	Hs.78045	tissue factor pathway inhibitor 2 TFP2	6.7
	437476	AL390172	Hs.118811	ESTs	6.7
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	6.7
10	421184	NM_003616	Hs.102456	survival of motor neuron protein interacting	6.7
	410227	A6009284	Hs.61152	evostoses (multiple)-like 2	6.6
	446826	N75217	Hs.257046	ESTs	6.6
	438187	R28363	Hs.24296	ESTs	6.6
	445459	AI478629	Hs.158466	ESTs	6.6
15	422291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae), h	6.6
	410011	A6002641	Hs.57595	PPTAIRE protein kinase 1	6.6
	410292	A4843067	Hs.124194	ESTs	6.5
	415716	NS9294	Hs.301141	Homo sapiens cDNA FLJ11689 fs, clone HEMBA10	6.5
	424770	AA425652		glwz46505.1 Soares_kat4_jctis_Nb2HFR_9w Ho	6.5
20	438122	A620270	Hs.129837	ESTs	6.5
	439820	AL362204	Hs.263853	Homo sapiens mRNA full length insert cDNA do	6.5
	444743	AA045648	Hs.11817	nucleic (nucleoside diphosphate linked moiety X	6.5
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.5
	418203	X54942	Hs.833758	CDC28 protein kinase 2	6.5
	439901	N73885	Hs.124189	ESTs	6.5
25	429758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fs, clone PLACE20	6.4
	404552			0	6.4
	404599			0	6.4
	418503	AA243542	Hs.137422	ESTs	6.4
	420149	AA255920	Hs.88095	ESTs	6.4
30	440411	N30296	Hs.156971	ESTs, Weakly similar to Weak similarity with	6.4
	449108	AI140683	Hs.98328	ESTs	6.4
	425097	AB002364	Hs.27918	ADAM-TS3 : a disintegrin-like and metallopro	6.4
	453519	H87648	Hs.33322	H.sapiens novel gene from PAC 117F20, chromos	6.4
	410273	BE328477	Hs.291523	ESTs	6.3
35	434486	AA678816	Hs.117142	ESTs	6.3
	454036	AA374756	Hs.93500	ESTs, Weakly similar to unnamed protein produ	6.3
	403381			0	6.2
	421308	AA687322	Hs.192843	ESTs	6.2
40	419346	AI830417	Hs.88095	glwz946(12.x1 NCL CGAP_CL11 Homo sapiens cDNA	6.2
	445140	AA356170	Hs.26750	Homo sapiens cDNA; FLJ21908 fs, clone HEPD30	6.2
	453047	AW023798	Hs.289026	ESTs	6.2
	442573	H53306	Hs.7507	Branched chain aminotransferase 1, cytosolic,	6.2
	410102	AW246508	Hs.279277	ESTs	6.1
	410004	AI268027	Hs.299116	ESTs	6.1
45	413335	AI513318	Hs.48442	ESTs	6.1
	428454	A1221919	Hs.173438	hypothetical protein FLJ10582	6.1
	427510	Z47542	Hs.173512	small nuclear RNA activating complex, polyprep	6.1
	451229	AW967707	Hs.48473	ESTs	6.1
	452641	AW952893	Hs.237826	signal recognition particle 72kD	6.1
50	433172	AB037841	Hs.102552	hypothetical protein ASH1	6.1
	425485	L18984	Hs.1904	protein kinase C, beta	6.1
	437177	AL040256	Hs.122583	ESTs	6.0
	423440	R25234	Hs.143434	contactin 1	6.0
	430510	AW162916	Hs.241578	hypothetical protein PRO2577	6.0
55	433252	AB040957	Hs.151343	KIAA1524 protein	6.0
	434889	AA645887	Hs.148425	Homo sapiens cDNA FLJ11980 fs, clone HEMD810	6.0
	438954	AA740151	Hs.138426	ESTs	5.9
	435032	AA150797	Hs.109276	lactenin protein	5.9
	424590	AA996359	Hs.45821	hypothetical protein FLJ20066	5.9
60	444078	BE346919	Hs.10290	US: cAMP-specific 40 kDa protein (hPrp8-bind)	5.9
	418379	AA218940	Hs.157516	fdgpt-like 1	5.9
	438081	H49546	Hs.288964	ESTs	5.8
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	5.8
	450459	A5971193	Hs.299254	ESTs	5.8
65	433512	AF078164	Hs.61158	Homo sapiens Ku70-binding protein (KUB3) mRNA	5.8
	449048	Z45051	Hs.22920	similar to S66-01 (rat) glucose induced ge	5.8
	417251	AW015242	Hs.99488	ESTs; Weakly similar to ORF YK0074w (S.cerevi	5.7
	429181	AW979104	Hs.294009	ESTs	5.7
	454933	BE141714		glc40(3)HT0101-051099-032-04 HT0101 Homo sapi	5.7
70	456553	AA721325	Hs.189058	ESTs, Weakly similar to cAMP-regulated guanine	5.7
	430371	D87466	Hs.240112	KIAA0275 protein	5.7
	425371	D49441	Hs.155981	mesothelin	5.7
	424513	BE385854	Hs.143894	mitochondrial translational initiation factor	5.6
75	423016	AI157604	Hs.169115	ESTs	5.6
	438109	AI076821	Hs.71357	ESTs, Moderately similar to ALU7_HUMAN ALLU SU	5.6
	407137	T97307	Hs.199067	v-erb-b2 avian erythroblastic leukemia viral	5.6
	407945	X69208	Hs.606	ATPase, Cu++ transporting, alpha polypeptide	5.6
	415555	AW000980	Hs.44870	ESTs	5.6
	417630	AW504786	Hs.132808	epithelial cell transforming sequence 2 oncog	5.5
80	419752	AA248573	Hs.152618	ESTs	5.5
	422093	AF151852	Hs.111449	CG-54 protein	5.5
	424583	AF017445	Hs.150526	thucase-1-phosphatase guanylyltransferase	5.5
	423686	AA308923	Hs.240770	nuclear cap binding protein subunit 2, 20kD	5.5
	425234	AW083022	Hs.145425	Homo sapiens cDNA FLJ11980 fs, clone HEMEB10	5.5

WO 02/102235

PCT/US02/19297

	453279	AW893940	Hs.59698	ESTs	5.5
	424188	AW564552	Hs.142834	zinc finger protein	5.5
	453984	AA336529	Hs.36232	KIA0168 gene product	5.5
5	424641	AS001106	Hs.151413	g1a maturation factor, beta	5.5
	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.5
	427975	A153965	Hs.122460	ESTs	5.5
	424620	AA101043	Hs.151554	kallistatin 7 (clonotypic; citraum comunt)	5.5
	424914	AW166551	Hs.59515	Homo sapiens cDNA FLJ14007 fs, clone Y79A10	5.5
10	417955	AW974175	Hs.188751	ESTs	5.4
	418946	A1798941	Hs.132103	ESTs	5.4
	419953	AA743276	Hs.301652	ESTs	5.4
	422352	U07374	Hs.57205	huntinglin interacting protein 1	5.4
	422670	AA371612	Hs.115351	ESTs	5.4
15	432837	AA310693	Hs.279512	HSPC072 protein	5.4
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.4
	495227	LA0554	Hs.85195	ESTs, Highly similar to K035625 (p34) fus	5.4
	425217	AU076995	Hs.155174	CDX5 (cell division cycle 5, S. pombe, homolog)	5.4
	422638	NM_001809	Hs.1594	centromere protein A (TKO)	5.4
20	450434	AA166950	Hs.18645	ESTs, Weakly similar to partial CD6 (Coleman)	5.4
	432279	AA605166	Hs.165165	ESTs, Moderately similar to ALUR_HUMAN ALU SU	5.4
	413384	NM_004041	Hs.75334	exonuclease (multiple) 2	5.3
	420328	Y15062	Hs.95870	stauilin (Drosophila, RNA-binding protein) hom	5.3
	436586	A1308852	Hs.167028	ESTs	5.3
25	435793	AB037374	Hs.4593	ESTs	5.3
	422395	BE545325	Hs.272280	Homo sapiens mRNA for Lsm5 protein	5.3
	426154	NM_001651	Hs.154550	collagen, type IX, alpha 1	5.2
	453253	AA382267	Hs.10553	ESTs	5.2
	429944	R13949	Hs.226440	Homo sapiens clone 24681 mRNA sequence	5.2
30	434981	AA614308	Hs.123693	ESTs	5.2
	413263	AA645333	Hs.130953	ESTs	5.2
	405506	NM_006163	Hs.54599	NCK adaptor protein 1	5.2
	412848	AA121514	Hs.70832	ESTs	5.2
	421246	AW982362	Hs.300961	ESTs, Highly similar to AF151805 1 CG4-47 pw	5.2
35	431546	AB343273	Hs.5711	Homo sapiens cDNA FLJ13016 fs, clone NT2RF30	5.2
	412719	AW016610	Hs.125911	ESTs	5.2
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncogene h	5.1
	424078	AB006525	Hs.130533	paternally expressed gene 3	5.1
40	433658	AA833737	Hs.201709	ESTs	5.1
	434265	AA648511	Hs.130544	Homo sapiens cDNA: FLJ123093 fs, clone LNS070	5.1
	453911	A1503857	Hs.4007	Sarcolemmal-associated protein	5.1
	415530	A1733881	Hs.72472	BMPP-1b; bone morphogenetic protein receptor	5.1
	442717	R63652	Hs.180591	ESTs, Weakly similar to R06F5.5b (C. elegans)	5.1
45	422386	AB02461	Hs.72330	ESTs	5.0
	406731	AA125895	Hs.56145	thymosin, beta, identified in neuroblastoma c	5.0
	419699	AA248998	Hs.31246	ESTs	5.0
	420313	AB022230	Hs.59427	KIAA1013 protein	5.0
	422505	AL129652	Hs.124185	ESTs; (HSA)PAP protein (programmed cell death	5.0
	429733	F13297	Hs.165386	Homo sapiens clone Z3575 mRNA sequence	5.0
50	434160	BE561156	Hs.114275	ESTs	5.0
	433094	AB960129	Hs.277523	EST	5.0
	436612	AW290067	Hs.277523	gb.UH-BWD-ajp-g-09-0-U.11 NCL_CGAP_Sub6 Ho	5.0
	432415	T16971	Hs.285014	ESTs	4.9
	406117			0	4.9
55	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	4.9
	447505	AL045296	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F003 (from cl	4.9
	445621	AB97144	Hs.52950	ESTs, Weakly similar to SACR37P7.g [J. mangr	4.9
	453001	AW131636	Hs.191250	ESTs	4.9
	410581	BE540255	Hs.6954	Homo sapiens cDNA: FLJ122044 fs, clone HEP091	4.9
60	418811	AK001407	Hs.66663	hypothetical protein FLJ10545	4.9
	439754	A161288	Hs.133437	ESTs, Moderately similar to gonadotropin indu	4.8
	437212	AF165021	Hs.210775	ESTs	4.8
	447312	AA143345	Hs.39308	activating transcription factor 1	4.8
	406732	NM_016122	Hs.56140	NY-FEN-58 antigen	4.8
65	434690	AB67675	Hs.145416	ESTs	4.8
	444172	BE147740	Hs.104586	ESTs	4.8
	424539	L02911	Hs.150402	activin A receptor, type I	4.6
	416577	SE3308	Hs.87224	SRY (sex determining region Y) box 5	4.6
	450576	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (from cl	4.6
70	420179	NF4530	Hs.21168	ESTs	4.7
	450375	AW05847	Hs.8850	a disintegrin and metalloproteinase domain 12	4.7
	415247	S65791	Hs.85764	fragile X mental retardation 1	4.7
	420690	BE139590	Hs.122406	ESTs	4.7
	425420	BE539911	Hs.234545	ESTs	4.7
75	420694	AF021696	Hs.183505	similar to SALL1 (rat (Drosophila) like	4.7
	419131	AA406293	Hs.301622	ESTs	4.7
	422278	AF072873	Hs.114218	ESTs	4.7
	451684	AF216751	Hs.26813	CDA14	4.6
	420296	AA305627	Hs.135336	ATP-binding cassette, sub-family C (CFTR/MRP)	4.6
	450425	AW056614	Hs.447621	Homo sapiens mRNA; cDNA DKFZp340C0227 (from c	4.6
80	417168	AL133117	Hs.61576	Homo sapiens mRNA; cDNA DKFZp586L1121 (from c	4.6
	425496	AF158827	Hs.203963	hypothetical protein FLJ10339	4.6
	442617	AA314937	Hs.85858	ESTs	4.6
	443298	AB007771	Hs.125445	hypothetical protein FLJ12495	4.6
	452735	AW352555	Hs.18878	hypothetical protein FLJ21620	4.6

WO 02/102235

PCT/US02/19297

5	457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ12663 fls, clone COL088	4.5
	459851	AA7289		gb 3607.x1 Scans, NSF_F0_9W_OT_PA_P_S1 Hom	4.6
	421977	WA1497	Hs.110165	ribosomal protein L26 homolog	4.6
	429441	AJ224172	Hs.204096	lipophilin II (atropogelin family member), pro	4.6
	449722	BE280074	Hs.23990	cyclin B1	4.6
	431869	AA30658	Hs.267695	UOP-Garbeta/Garbeta beta 1.3-galactosyltransferase	4.5
	425178	H16097	Hs.161927	ESTs	4.5
	429657	NM_003816	Hs.244242	a disintegrin and metalloproteinase domain 9	4.5
	436556	AJ364997	Hs.7572	ESTs	4.5
10	400534			0	4.5
	417845	AL117461	Hs.82719	Homo sapiens mRNA: cDNA DKFZ598F1822 (from c	4.5
	421213	NM_012247	Hs.124027	SELECTOPHILATE SYNTHETASE - Human selenium d	4.5
	440350	AA628207	Hs.264916	Homo sapiens cDNA FLJ12908 fls, clone NT29P20	4.5
15	441006	AW606267	Hs.7627	CG-40 protein	4.5
	414569	AF105299	Hs.115258	Prostate cancer associated protein 1	4.5
	447824	AB171226	Hs.170337	ESTs	4.5
	425506	NM_006366	Hs.155205	basic leucine zipper nuclear factor 1 (JEM-1)	4.5
	411630	AU2349	Hs.71119	Potential prostate cancer tumor suppressor	4.4
	432842	AW574093	Hs.279525	hypothetical protein PRC2695	4.4
20	413472	BE242670	Hs.75379	solute carrier family 1 (glut high affinity	4.4
	414599	AB115023	Hs.76330	synuclein, alpha (non A4 component of amyloid	4.4
	412733	AA984472	Hs.74554	KIAA0080 protein	4.4
	419790	U79260	Hs.93201	glyoxyl-3-phosphate dehydrogenase 2 (mitochond	4.4
25	435377	AF732713	Hs.43845	ESTs	4.4
	445355	W15187	Hs.23872	low density lipoprotein receptor-related prot	4.4
	435900	AW003582	Hs.225414	ESTs, Weakly similar to ALU8_HUMAN ALU SURFAM	4.4
	443881	R64512	Hs.237146	Homo sapiens cDNA FLJ14234 fls, clone NT27P40	4.4
	423026	AA381267	Hs.12244	Homo sapiens cDNA: FLJ23581 fls, clone LNC138	4.4
	408821	AB770372	Hs.46538	chromosome 11 open reading frame 8, fetal ly	4.3
30	416241	NQ2639	Hs.300983	ESTs	4.3
	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA POLYME	4.3
	459532	AW291468	Hs.117305	ESTs	4.3
	461613	NM_010117	Hs.27182	phospholipase A2-activating protein	4.3
35	454193	BE411183		gb H1007.1-191169-001-404/H10071 Homo sapi	4.3
	418478	U58945	Hs.11174	cyclin-dependent kinase inhibitor 2A (melanoma	4.3
	400609			0	4.3
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fls, clone LNC055	4.3
	416413	R56736	Hs.117573	ESTs, Weakly similar to antigen of the monoc	4.3
40	453038	AK010189	Hs.27556	hypothetical protein FLJ10097	4.3
	418993	AT50878	Hs.57409	thrombospondin 1	4.3
	410361	BE391804	Hs.62861	guanylate binding protein 1, interferon-induc	4.2
	400763	AL343212		gb DNFZp34H0623_r1 434 (synonym: hbs3) Homo	4.2
	459501	AJ368480	Hs.816	SPY box determining region Y-box 2, partial	4.2
	408908	BE296227	Hs.48915	serine/threonine kinase 15	4.2
45	413582	AW295947	Hs.71331	Homo sapiens cDNA: FLJ21971 fls, clone HEP057	4.2
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	4.2
	425524	R38235	Hs.12407	ESTs	4.2
	447153	AA485202	Hs.173912	eukaryotic translation initiation factor 4A,	4.2
50	447406	BE518050	Hs.282882	ESTs	4.2
	449347	AV548748	Hs.295991	ESTs	4.2
	414279	AW021691	Hs.3894	DNFZP564C1940 protein	4.2
	425865	AA438738	Hs.183171	Homo sapiens cDNA: FLJ22002 fls, clone HEP066	4.2
	407672	AB039723	Hs.40735	hitzell (Xenopus) homolog 3	4.2
	421502	AF111865	Hs.105339	solute carrier family 34 (sodium phosphate),	4.2
55	436406	AW105723	Hs.125346	ESTs	4.2
	438209	AL120469	Hs.6111	KIAA0037 gene product	4.2
	443663	AA137043	Hs.9693	programmed cell death 6-interacting protein	4.1
	454556	AW807073		gb MFRA-ST0062-031199-018-d06/ST0062 Homo sapi	4.1
60	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fls, clone NT29P20	4.1
	412593	Y07558	Hs.74658	early growth response 3	4.1
	416566	NM_003814	Hs.733178	cyclin A1	4.1
	426342	AF093419	Hs.169378	multiple PCZ domain protein	4.1
	428417	AK001699	Hs.184227	F-box only protein 21	4.1
65	429317	AA331552	Hs.285016	solute carrier family 5 (inositol transporter	4.1
	446880	AJ311837	Hs.108546	Homo sapiens cDNA FLJ12534 fls, clone NT29P40	4.1
	422988	AW573947	Hs.97321	ESTs	4.0
	434657	AA641876	Hs.191840	ESTs	4.0
	412494	AL133900	Hs.732	ADP-ribosylation factor domain protein 1, 54k	4.0
70	443271	BE588658	Hs.195704	ESTs	4.0
	421437	AW521262	Hs.104535	ESTs	4.0
	401644			0	4.0
	405095			0	4.0
	418417	R77182		gb y65602.r1 Scans placenta Nb2HP Homo sapi	4.0
	420907	AA28927	Hs.57846	ESTs	4.0
75	429529	AA54190	Hs.193811	ESTs, Moderately similar to reduced expressio	4.0
	457726	AJ217477	Hs.194591	ESTs	4.0
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein type	4.0
	453403	BE465539	Hs.61179	Homo sapiens cDNA FLJ13391 fls, clone PLACE16	4.0
	442768	AA04534	Hs.48468	ESTs, Weakly similar to ALU8_HUMAN ALU SURFAM	4.0
80	413430	R22479	Hs.24650	Homo sapiens cDNA FLJ13047 fls, clone NT29P30	4.0
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	4.0
	425892	D90041	Hs.155565	NAT1; arylamine N-acetyltransferase	4.0
	407792	AD77716	Hs.39384	peptide secreted ligand homologous to Ix1	4.0
	405353	BE439638	Hs.44299	hypothetical protein	4.0

WO 02/102235

PCT/US02/19297

	421178	A1879089	Hs.102397	GIST-3 for gonadotropin inducible transcript	3.9
	423334	AF163474	Hs.96744	DKFZP56D0823 protein, Prostate androgen-regu	3.9
	417531	NM_003157	Hs.1087	serine/threonine kinase 2	3.9
5	458924	BE242158	Hs.24427	DKFZP565D1646 protein	3.9
	400195			0	3.9
	401480			0	3.9
	413360	AW63690		gblh21g03.x1 NCL_CGAP_L8 Homo sapiens cDNA	3.9
	410908	AA121696	Hs.10592	ESTs	3.9
	420150	A1572490	Hs.99785	ESTs	3.9
10	422805	AA436989	Hs.121017	H2A, histone family, member A	3.9
	424638	AB174744	Hs.131329	ESTs	3.9
	428555	NM_002214	Hs.148908	integrin, beta 8	3.9
	431699	NM_001173	Hs.267531	Homo sapiens cDNA: FLJ12952 fig, clone NT2RP20	3.9
	433703	AA210863	Hs.3532	nemo-like kinase	3.9
15	437144	AL049466	Hs.7859	ESTs	3.9
	432728	A1516076	Hs.230708	ESTs	3.9
	430447	W17054	Hs.241451	SWI/SNF related, matrix associated, actin dep	3.9
	440594	AW445167	Hs.126036	ESTs	3.9
20	400938	AA059013	Hs.22607	ESTs	3.9
	427051	BE178110	Hs.173574	ESTs	3.9
	447658	AF153855	Hs.18885	COP-116 protein	3.9
	457211	AW972565	Hs.32399	ESTs, Weakly similar to Similar to Ena-VASP1	3.9
	443475	AL066470	Hs.134482	ESTs	3.9
	433447	U29156	Hs.3281	neuronal protein II	3.9
25	420933	AW594506	Hs.104630	ESTs	3.8
	437938	A1650087		ESTs; Weakly similar to Gag-Pol polyprotein [3.8
	408829	NM_006042	Hs.46364	heparan sulfate (glucosamine) 3-O-sulfotransf	3.8
	422520	H55585	Hs.198308	tryptophan rich basic protein	3.8
30	441859	AW194564	Hs.126022	ESTs, Weakly similar to FIG1 MOUSE FIG-1 PROT	3.8
	437702	A1076965	Hs.122848	ESTs	3.8
	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	3.8
	400564	AA045857	Hs.51943	fracture callus 1 (rat) homolog	3.8
	429474	AA453441	Hs.31511	ESTs	3.8
	431555	BE175190		gblh21g04.H10577-010500-165-g04 H10577 Homo sapi	3.8
35	454018	AW016892	Hs.214552	ESTs	3.8
	426320	W47595	Hs.165300	transforming growth factor, beta 2	3.8
	439635	AA477288	Hs.94881	Homo sapiens cDNA: FLJ22759 fig, clone HS156	3.8
	417517	AF001178	Hs.82286	PDP4 [processing of precursor, S. cerevisiae]	3.8
40	446402	AB811145	Hs.165724	ESTs	3.8
	450236	AA162298	Hs.24684	KIAA1376 protein	3.8
	410804	U64820	Hs.55521	Machado-Joseph disease (spinocerebellar ataxi	3.8
	400268			0	3.8
	412217	A1910847	Hs.13442	ESTs	3.8
	421928	AF013758	Hs.109649	polyadenylate binding protein-interacting pro	3.8
45	417300	A1765227	Hs.55610	solute carrier family 30 (zinc transporter),	3.8
	414136	AA812434	Hs.178227	ESTs	3.8
	453945	NM_005171	Hs.39508	activating transcription factor 1	3.7
	400240			0	3.7
50	407877	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fig, clone HS1073	3.7
	405581	AF081513	Hs.25195	endometrial bleeding associated factor (lelt-	3.7
	418223	NM_014733	Hs.83790	KIAA305 gene product	3.7
	411704	A1482220	Hs.71473	hypothetical protein FLJ110074	3.7
	432712	AG016247	Hs.288031	sterol-C5-desaturase (flnqap ERG3, delta-5-de	3.7
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.7
55	402820			0	3.7
	406260	BE173621	Hs.292478	ESTs	3.7
	416421	AA134006	Hs.76306	eukaryotic translation initiation factor 4E	3.7
	418282	AA216536	Hs.98133	ESTs	3.7
60	418454	AA315308		gblh21g095 Colon carcinoma (HCC) cell line	3.7
	418658	AW407957	Hs.87150	Human clone A9A3UR11 (CHCn)GTGn repeat-con	3.7
	422220	AA49854	Hs.48837	hypothetical protein FLJ12565	3.7
	432824	AK001173	Hs.279012	hypothetical protein FLJ110921	3.7
	439907	A0853978	Hs.124577	ESTs	3.7
65	447479	AS037534	Hs.18685	Homo sapiens mRNA for KIAA1413 protein, part I	3.7
	451073	A1738306	Hs.200593	ESTs	3.7
	450377	AS033091	Hs.24936	ESTs	3.7
	414343	AL036166	Hs.75914	coated vesicle membrane protein	3.7
	448807	A1571940	Hs.7945	ESTs	3.7
	442821	BE319129	Hs.8762	Pulvinar type II membrane protein	3.7
70	426300	U15939	Hs.165228	delta-like homolog (Discohep)	3.7
	418068	AW971155	Hs.239902	ESTs, Weakly similar to prollyl 4-hydroxylase	3.7
	411263	BE297802	Hs.65360	kinasin-like 6 (mitotic centromere-associated	3.7
	443054	AF148186	Hs.8939	yeast-associated protein 65 kDa	3.7
75	421154	AA284333	Hs.207631	Homo sapiens cDNA: FLJ14289 fig, clone PLACE10	3.7
	411402	BE297855	Hs.65935	NRAS-related gene	3.7
	450447	AF212223	Hs.25010	hypothetical protein PT5-2	3.6
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.6
	434228	Z42047	Hs.283978	ESTs, KIAA0073 gene product	3.6
	434164	AW020701	Hs.148135	ESTs	3.6
80	409533	AW965543	Hs.21291	mitogen-activated protein kinase kinase kinase	3.6
	402222			0	3.6
	404915			0	3.6
	404996			0	3.6
	411560	AW851186		gblh21g0220-150200-071-H05 CT0220 Homo sapi	3.6

WO 02/102235

PCT/US02/19297

	417950	AL079741	Hs.163114	Homo sapiens cDNA FLJ14236 fs, clone NT2RP40	3.6
	429010	AA136653	Hs.1975	Homo sapiens cDNA: FLJ21007 fs, clone CAE038	3.6
	429338	NM_014633	Hs.173288	KIAA0155 gene product	3.6
5	439255	BE194500		gbcRCA-11T0469-23C300-014-e10.11T0469	3.6
	458242	BE295688	Hs.28465	Homo sapiens cDNA: FLJ21899 fs, clone HEP024	3.6
	415115	AA214228	Hs.127751	hypothetical protein	3.6
	455458	W00712	Hs.32990	DKFZP568F084 protein	3.6
	441205	AW137627	Hs.176504	ESTs	3.6
	452693	T79153	Hs.48589	zinc finger protein 228	3.6
10	417389	BE203064	Hs.82045	Midline (neurotrophin growth-promoting factor 2)	3.6
	448105	AW591433	Hs.170575	ESTs, Weakly similar to 11MS2_HUMAN TRANSMEMBR	3.6
	451922	BE586817	Hs.261498	hypothetical protein FLJ21667	3.6
	440048	AA587451	Hs.158469	ESTs, Weakly similar to envelope protein (Hs	3.5
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)-like	3.5
15	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564M2464 (from c	3.5
	405955			0	3.5
	422546	H87863	Hs.151380	ESTs	3.5
	407845	AA426202	Hs.40403	Cbp/p300-interacting transactivator, with Glu	3.5
	408730	AF560717	Hs.47144	DKFZP569N0819 protein	3.5
20	401517			0	3.5
	413775	AW040934	Hs.75538	nucleolar GTPase	3.5
	417177	NM_004458	Hs.81452	glycyl-acyl-Coenzyme A ligase, long-chain 4	3.5
	427943	AW569075		gbEST371145 MAGE resequences, MAGE Homo sapi	3.5
	439107	AL049134	Hs.27895	ESTs	3.5
	447258	AS29413	Hs.363675	Homo sapiens cDNA: FLJ22418 fs, clone HRC085	3.5
	412504	AW078324	Hs.47144	DKFZP569N0819 protein	3.5
	427134	AA389409	Hs.173561	EST	3.5
	430273	AI311127	Hs.125522	ESTs	3.5
30	436571	AW137159	Hs.146151	ESTs	3.5
	433007	NM_014168	Hs.278639	HSPC057 protein	3.5
	453745	AA952989	Hs.63908	Homo sapiens HSPC316 mRNA, partial cds	3.5
	400531	AF151054	Hs.39069	hypothetical protein	3.4
	433345	A081545	Hs.152982	EST cluster (not in UniGene)	3.4
	409400	AA343529	Hs.104570	hNF1A (neurospirovadin)	3.4
35	407596	BE6913		gby33055.1 Soares fetal liver spleen 1NFLS	3.4
	453779	N35187	Hs.43388	ESTs	3.4
	444858	AI199738	Hs.208275	ESTs, Weakly similar to unnamed protein produ	3.4
	447858	N67079	Hs.152235	NADH dehydrogenase (ubiquinone) 1 beta subcom	3.4
40	246165	AA347748	Hs.3621	ESTs, Weakly similar to KIAA1015 protein (Hs	3.4
	407854	AF029291	Hs.40539	chromosome 5 open reading frame 1	3.4
	404103			0	3.4
	403729			0	3.4
	404232			0	3.4
45	423687	AA329633	Hs.130011	ESTs, Highly similar to Z117_HUMAN ZINC FINGE	3.4
	423372	AK000584	Hs.183887	hypothetical protein FLJ22104	3.4
	439741	BE379546	Hs.6904	Homo sapiens mRNA full length insert cDNA clo	3.4
	414147	AA584377	Hs.126890	ESTs	3.4
	443358	R04433	Hs.105514	Human DNA sequence from clone RP4-534K7 on ch	3.4
	450926	AI744361	Hs.205691	ESTs, Weakly similar to zinc finger protein P	3.4
50	458477	NM_000314	Hs.10712	phosphatase and tensin homolog (mutated in mu	3.4
	421379	Y15221	Hs.103982	small inducible cytokine subfamily 9 (Cys-X-C	3.4
	452822	X05609	Hs.289817	Homo sapiens cDNA: FLJ22521 fs, clone HS0055	3.4
	441111	AA905967	Hs.126594	ESTs	3.4
55	447519	U40258	Hs.23448	ESTs	3.4
	448913	AA430680	Hs.16529	transmembrane 4 superfamily member (tetraspan	3.4
	449581	AB98517	Hs.181605	ESTs	3.4
	455132	BE219771	Hs.237145	Homo sapiens cDNA FLJ14234 fs, clone NT2RP40	3.4
	448196	AA262105	Hs.40394	Homo sapiens cDNA FLJ14208 fs, clone NT2RP30	3.4
	422511	AA158177	Hs.118722	lucosyltransferase 5 (alpha (1,6) glucosylat	3.4
60	414133	AA538809	Hs.42745	ESTs	3.4
	417037	AL077905	Hs.11103	transforming growth factor, beta 1	3.4
	450516	AJ002655	Hs.21943	NF3 (Nrg1) interacting factor 3, S.pombe homo	3.4
	407796	AA195509	Hs.272239	lymphocyte activation-associated protein	3.3
65	419200	AW955405	Hs.263556	(Homo sapiens mRNA; cDNA DKFZp564H1116 (from c	3.3
	423161	AL046227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564H1116 (from c	3.3
	445679	AA348668	Hs.55800	Homo sapiens cDNA: FLJ21488 fs, clone NT2RP420	3.3
	435014	BE580889	Hs.10026	ribosomal protein L17 isoform	3.3
	446619	AU076643	Hs.313	saccharid phosphatoprotein 1 (osteopontin, bone	3.3
70	439170	AA352365	Hs.155539	ESTs	3.3
	429850	AJ537276	Hs.225841	DKFZP343D193 protein	3.3
	428943	AW086180	Hs.37636	ESTs, Weakly similar to KIAA1392 protein (Hs	3.3
	445817	NM_003642	Hs.13340	histone acetyltransferase 1 (alpha (1,6) glucosylat	3.3
	438905	H09912	Hs.48269	vacuolin related kinase 1	3.3
	411134	W22952	Hs.1678	cellular retinoic acid-binding protein 1	3.3
75	403552	AA453137	Hs.63176	ESTs	3.3
	409517	X90780	Hs.54668	troponin I, cardiac	3.3
	414304	AJ521275	Hs.165998	DKFZP564M2423 protein	3.3
	430427	AA344378	Hs.143359	ESTs	3.3
	436662	AA522813	Hs.126595	ESTs	3.3
80	440304	BE159984	Hs.125399	ESTs	3.3
	447385	F12863		gbt5HSCFE081 normalized infant brain cDNA Hom	3.3
	451177	A989716	Hs.18034	ESTs	3.3
	428949	AA442153	Hs.104744	ESTs, Weakly similar to AF208855 1 BM-013 (H	3.3
	451743	AW074266	Hs.23071	ESTs	3.3

WO 02/102235

PCT/US02/19297

	421515	Y11339	Hs.105352	GaNAc alpha-2, 6-sialyltransferase 1, long f	3.3
	448351	AW444551	Hs.725832	ESTs	3.3
	435102	AW895053	Hs.769117	F-box only protein 8	3.3
5	418216	AA662240	Hs.263099	AF15q14 protein	3.3
	401508			0	3.3
	437108	AA434051	Hs.80624	Home sapiens cDNA: FLJ23442 f1, clone HS1009	3.3
	416630	U82801	Hs.79361	kallidin 6 (neurokin, zyme)	3.3
	445171	BE281128	Hs.90039	TONGU1	3.3
10	458627	AW066642	Hs.97964	ESTs; Weakly similar to WASP-family protein [3.3
	412076	X69999	Hs.73149	paired box gene 8	3.3
	414080	AA135257	Hs.47763	ESTs; Weakly similar to T12540 hypothetical p	3.3
	401197			0	3.3
	422134	AW179019	Hs.112110	ESTs	3.3
	409044	AI129556	Hs.33033	ESTs	3.3
	416196	HD7332	Hs.93958	ESTs	3.3
	436461	AA378597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	3.2
	436525	AA721428	Hs.26145	Home sapiens cDNA FLJ14127 f5, clone MAMMA10	3.2
	405142	AL136877	Hs.50756	chromosome-associated polypeptide C	3.2
	428819	AL136623	Hs.193914	KIAA0575 gene product	3.2
	428726	NM_016625	Hs.101361	ESTs; Weakly similar to hypothetical protein	3.2
	421261	AA600653	Hs.86153	ESTs	3.2
	446219	AI267344	Hs.146627	ESTs	3.2
	457574	H88717	Hs.27774	ESTs; Highly similar to AF161349 1 HSPC086 [H	3.2
25	409172	Z95399	Hs.116145	ESTs	3.2
	413886	TG7012	Hs.75373	prothelin	3.2
	434167	AA627098	Hs.99103	ESTs; Weakly similar to I36426 T-complex prot	3.2
	446060	AA830611	Hs.88086	ESTs	3.2
	448254	AA629900	Hs.22929	ESTs	3.2
30	452843	BE247449	Hs.31052	hypothetical protein FLJ10525	3.2
	411383	AW977437	Hs.58771	B-factor, propeptide	3.2
	453775	NM_002916	Hs.36120	replication factor C (activator 1) 4 (37kD)	3.2
	406410	AW963897	Hs.44743	KIAA1435 protein	3.2
	442025	AW987434	Hs.11810	ESTs; Weakly similar to CD412 [C.elegans]	3.2
35	417006	AW973606	Hs.60758	aspartyl-ATP synthetase	3.2
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotransf	3.2
	444755	AA431791	Hs.163001	ESTs	3.2
	402829			0	3.2
	451693	AF151679	Hs.26705	CGH-121 protein	3.2
40	419925	AW900392	Hs.93795	DKEZP59602223 protein	3.2
	434651	BE367162	Hs.280588	ESTs; Highly similar to XPB_HUMAN DNA-REPAIR	3.2
	445929	A1009600	Hs.7638	makorin, ring finger protein, 1	3.2
	409365	AA702376	Hs.226440	Home sapiens clone 24821 mRNA sequence	3.2
	410335	AI555499	Hs.161712	ESTs	3.2
45	441020	W79283	Hs.36962	ESTs	3.1
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38kD)	3.1
	413010	AA383273	Hs.76133	transcription factor 6-like 1 (mitochondrial	3.1
	452032	BE246374	Hs.27642	hypothetical protein FLJ11210	3.1
	410456	AW236294	Hs.193404	ESTs; Weakly similar to KIAA1054 protein [Hs	3.1
50	434540	NM_016045	Hs.5164	TH1 drosophila homolog	3.1
	406176	BE363940	Hs.50915	kallikrein 5	3.1
	439460	AL036511	Hs.125316	ESTs	3.1
	417840	AA205681	Hs.39467	ESTs	3.1
	445293	AI420213	Hs.149722	ESTs	3.1
55	408106	AI550492	Hs.42743	hypothetical protein	3.1
	415947	U04045	Hs.78934	mds1 (E. coli) homolog 2 (colon cancer, nonpo	3.1
	410519	AW612284	Hs.130755	ESTs	3.1
	421987	AI133161	Hs.266131	CGH-101 protein	3.1
	440946	AW402306	Hs.6677	hypothetical protein FLJ10483	3.1
60	453931	AL121278	Hs.25144	ESTs	3.1
	454423	AW603665	Hs.179652	nucleosome assembly protein 1-like 1	3.1
	498099	P1306	Hs.27793	Home sapiens mRNA: cDNA DNZp56401763 (from c	3.1
	416735	N40769	Hs.44509	ESTs	3.1
	414245	BE146072	Hs.75650	WAS protein family, member 1	3.1
65	410509	AW696161	Hs.63112	ESTs; Weakly similar to ALUR_HUMAN ALU SUBFAM	3.1
	434525	BE54285	Hs.502523	ESTs	3.1
	405239	AA740875	Hs.44307	ESTs	3.1
	425017	AA463605	Hs.238596	ESTs	3.1
	440772	D61594	Hs.17275	tyrosyl-protein sulfotransferase 1	3.1
70	426514	BE519633	Hs.301122	bone morphogenetic protein 7 (osteogenic prot	3.1
	446133	AA723167	Hs.73769	folate receptor 1 (adult)	3.1
	416792	AB031785	Hs.65442	KIAA1384 protein	3.1
	427526	AU077143	Hs.179565	minichromosome maintenance deficient (S. cere	3.1
	402077			0	3.1
75	443671	AW257620	Hs.130054	ESTs	3.1
	419690	X17360	Hs.278255	homeo box D4	3.1
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	3.1
	409161	AA306105	Hs.50765	SEC22, vesicle trafficking protein (S. cerevi	3.1
	431221	AA448015	Hs.285165	SRB7 (suppressor of RNA polymerase II; yeast)	3.1
80	455584	AB07036	Hs.101819	ESTs	3.1
	445525	BE148666	Hs.14631	ESTs	3.1
	410441	BE28210	Hs.501118016F1 NIH_MGC_17 Home sapiens cDNA	3.1	
	422634	NM_016010	Hs.118821	CG-42 protein	3.0
	420022	AA296263	Hs.126817	ESTs	3.0
	453612	AL120313	Hs.32555	KIAA0379 protein	3.0

WO 02/102235

PCT/US02/19297

5	456844	A/264155	Hs. 152981	CDP-diacylglycerol synthase (phosphatidate cy	3.0
	414641	C14865	Hs. 162159	ESTs	3.0
	407607	AJ331427	Hs. 40094	Human DNA sequence from clone 167A19 on chrom	3.0
	414725	AA769791	Hs. 120355	Home sapiens cDNA FLJ13148 fs, clone NT2P30	3.0
	444420	A148157	Hs. 146796	ESTs	3.0
10	431742	NM_016652	Hs. 268281	CGI-201 protein	3.0
	412519	AF196241	Hs. 73980	Insulin T1, skeletal, slow	3.0
	416348	AJ537167	Hs. 56322	Home sapiens cDNA: FLJ23550 fs, clone LN0096	3.0
	444261	AA288958	Hs. 10724	MUSO23 protein	3.0
	457485	AW001344	Hs. 195969	ESTs	3.0
15	443933	AF091631	Hs. 133501	Home sapiens two pore potassium channel KT3.3	3.0
	442150	AJ368108	Hs. 120604	ESTs	3.0
	414883	AA926960	Hs. 77550	CDC28 protein kinase 1	3.0
	442879	AF032922	Hs. 8813	synactin binding protein 3	3.0
	437949	U78519	Hs. 41654	ESTs	3.0
20	405515	405864	0	0	3.0
	407785	AW027285	Hs. 98279	ESTs	3.0
	426199	AA371865	Hs. 57050	ESTs	3.0
	428324	AF0291787	Hs. 200553	ESTs	3.0
	427738	NM_000316	Hs. 180612	peroxisomal membrane protein 3 (35kD), Zellweg	3.0
25	427837	U87309	Hs. 180941	vacuolar protein sorting 41 (yeast homolog)	3.0
	439430	AF124250	Hs. 65564	breast cancer anti-estrogen resistance 3	3.0
	442039	AW075240	Hs. 128352	ESTs, Weakly similar to p80 [nonovogenic]	3.0
	445978	NM_001938	Hs. 16597	downregulator of transcription 1, TDR-bilin	3.0
	452431	U88879	Hs. 25465	tol-like receptor 3	3.0
30	452841	T17431	Hs. 65412	DEAD(H) (Asp-Glu-Ala-Asp/His) box polypeptide	3.0
	432114	AL036021	Hs. 225597	ESTs	3.0
	445540	AW959626	Hs. 31704	ESTs, Weakly similar to KIA00227 [Hsapiens]	3.0
	442607	AA507576	Hs. 285381	KIA02471 gene product	3.0
	453920	AI133148	Hs. 36502	1 factor (complement)	3.0
35	430000	AW205931	Hs. 99595	ESTs	3.0
	429164	AF688663	Hs. 116586	ESTs	3.0
	453331	AJ240655	Hs. 8865	ESTs	3.0
	448663	BE614599	Hs. 106823	Hsapiens gene from PAC 4295, similar to syn	3.0
	425776	U25128	Hs. 159499	parathyroid hormone receptor 2	3.0
40	401714	401714	0	0	3.0
	429428	AL037544	Hs. 184258	cyclin-dependent kinase 7 (homolog of Xenopus	3.0
	443761	AI525743	Hs. 160603	ESTs	3.0
	451640	AA195001	Hs. 26771	Human DNA sequence from clone 747H23 on chrom	3.0
	442580	AF33682	Hs. 130239	ESTs	3.0

TABLE 10B:

Pkey: Unique Eos probe/identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
50	407598	1003489_1
	408763	113382_1
	410380	1197225_2
	410441	120358_1
		BE288210 AW72315 AW065489 BA290471 AA655921 AA902537 BE327124 R14963 AA085210 AW274273 AJ33594 AJ369742 AJ039658
55	411590	1249443_1
	414315	143512_1
	418417	1760818_1
	418454	175699_1
	419346	184129_1
60	424770	243504_1
	427943	294802_1
	431965	33919_2
	436812	427323_1
	437938	44573_2
65		AW539057 F175190 BE070348
		AW529057 F1731645 AA810101 AW194180 AB90573 AW578773
		AA950887 N10203 R97040 N39369 A308119 AW957617 N5320 A251473 H59397 AW971573 R97278 W01059 AW956771 AA930593
		AA421615 A26201 AB02032 W67891 T83804 U71455 T82301 BE326711 T75102 R34725 AA684322 BE326517 A219788 AA94444
		N52376 F113493 AA027734 AA920521 AW814068 AL134043 AA025363 AA653345 AA0008282 AA458964 AA263144 A1890387 AA950434
70		AT171346 AB68062 AA282915 AW102896 AW672193 AT53273 AW173586 AW150329 A1652832 AT762688 AA88777 AA48882 A1356394
		AW103813 A1539642 AA642789 AA856575 AW505512 A961530 AW629970 BE612681 AW276997 AW131361 AW152843 AA044209
		AW856538 AA180068 AA337499 AW961101 AA251669 A251874 AB18225 AA025082 AB63336 A1856599 AW276905 AB63306 AA872584
		AA480741 AW172629 AW13386 A428323 AA489759 N55628 N22388 HA4725 H50592 T92437 AJ022658 AW67415 AA510305 N80701
		AW613456 AJ373032 A1564269 F06531 H83488 W37181 W78822 H66059 AA062639 R67840 AA300207 AW959581 T63226 F0405
75		BE164500 AA632198 BE164502
		F12693 A372723 F15989
		BE141183 AW117067 AW178162 AW178166 AW178172 AW184583 AW178169 AW178222 AW178213 AW178215 AW178040 AW178051
		AW178161 AW178207 AW178210 AW178214 AW178212 BE140918 BE140917 AW178135 AW178136 AW178205 AW178209 AW178223 AW178220
		AW178206 AW178203 AW178165 AW178168 AW178160 AW178136 AW845878 AW178211 AW178138 AW178105 AW845894 AW178129
80		AW845838 AW845826 AW178216 AW178112 AW178211 AW178224 BE140818 AW178214 AW178130 AW178134 AW178036 AW178108
		AW178133 AW178164 AW178216 AW178171 AW178167 AW178162 AW178103 BE141165 AW178046 BE141566 AW178156
		AW178104 AW178163 AW178093 AW178232 AW178137 AW178140 AW178219 BE141532 AW845901 BE141530 AW178155 BE141536
		BE140957
		AW807073 AW807055 AW807067 AW807276 AW807030 AW807363 AW845892 AW807091 AW807275 AW807284 AW807287 AW845891
	464556	1223878_1
	447385	175912_1
	454193	1650296_1
	454533	1245515_1
		BE141714 AW845993 AW845989

WO 02/102235

PCT/US02/19297

TABLE 10C:

Key: Unique number corresponding to an Eni protocol

Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

5	Key	Ref	Strand	NL_position
10	400534	6961826	Minus	27637-279292
	400566	8118495	Plus	17962-18115,20297-20466
	400503	2611732	Plus	69112-83229
	401197	6710766	Plus	17634-176432
	401480	7321503	Plus	195120-196347,166451-166557,196551-198832
15	401508	7534110	Minus	110776-110883
	401517	7677912	Plus	20278-29770
	401544	8579138	Plus	62656-37900
	401714	6715702	Plus	96494-96681
	402077	8117414	Plus	65014-65105
20	402222	9558106	Plus	3261-3834,3939-4269
	402406	9796239	Minus	110326-110491
	402820	6458583	Minus	92274-92043
	402829	8518414	Plus	101632-101852,102006-102253
	403381	9438267	Minus	26009-26178
25	403515	7656757	Minus	173356-179553
	403729	7543752	Minus	37962-37990
	403854	7709019	Minus	51753-51890,79290-79445
	404108	8247074	Minus	63603-64942
	404232	8218045	Minus	71800-71956
	404552	7243981	Plus	19854-22010
30	404587	7249163	Minus	191320-191591
	404599	8705107	Plus	119443-119733
	404915	7341766	Minus	100515-101087
	404996	6007930	Plus	37939-38145,38652-38938,39727-39872,40557-40674,42361-42450
	405095	6327399	Plus	138877-139005
35	406069	9117732	Plus	68880-69374
	406117	9142932	Plus	54304-54584

Table 11A lists about 222 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 10A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egr, 7tm domains, signal sequences, transmembrane domains). Predicted protein domains are noted.

TABLE 11A: ABOUT 222 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Key: Primerkey

Ex. Acen: Exemplar Accession

UG ID: UniGene ID

Title: UniGene title

PFAM domains: predicted protein structural domains

ratio: ratio tumor vs normal tissue

50	Key	Ex. Acen	UG ID	Title	PFAM domains	ratio
	400282	AA250737	Hs.72472	BMPLR1: bone morphogenetic pro	plasma_Actin_rec	30.0
	400289	X07820	Hs.2256	Matrix Metalloproteinase 10 (Strom	SS,hemopexin,Peptidas	25.2
55	427585	D31152	Hs.179729	collagen; type X; alpha 1 (Schmid m	C1q,Collagen	22.7
	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular m	isp_1	19.0
	436579	NM_005736	Hs.184942	EGF-like domain multiple 6	TM	17.4
	443646	AI065198	Hs.298699	ESTs	TM,SPN,wc,isp_1,EGF	15.1
	436209	AI055047	Hs.254020	ESTs, Moderately similar to unname	TM	14.1
	418601	AA278490	Hs.86368	cathepsin	SS,cathepsin	13.8
60	425532	AF157326	Hs.184786	TSP-interacting protein	TM	13.6
	427344	NM_008699	Hs.21412	5-hydroxytryptamine (serotonin) rec	TM,neur_chan	11.8
	432577	NM_004482	Hs.279611	UDP-N-acetyl-alpha-D-glucosamin	TM,Glycos_transf_2,R6	11.0
	404567	NM_015902	Hs.278428	progestin induced protein (DD5)	TM,EGF,25-UBR1	10.8
65	445537	A2425671	Hs.12844	EGF-like domain multiple 6	SS,M,MEGF	8.9
	405928	AL137163	Hs.57540	hypothetical protein d.47384	TM,NSP_domain	8.6
	407001	U12471	Hs.247954	Human thrombospondin-1 gene, par	TM,wc,isp_1,EGF	8.5
	453370	AI470323	Hs.182556	ESTs, Moderately similar to tralat	ABC,Tam,ABC_membr	8.4
	400288	AA032229	Hs.51535	STEAP1	TM	8.1
	431725	X55724	Hs.2839	Niem disease (pseudoglioma)	SS,Cys_inol	7.9
70	425962	AF902245	Hs.210853	cell adhesion molecule with homolo	TM,EGF	7.8
	412170	D15532	Hs.73729	very low density lipoprotein recepto	TM,MT_recep,La_id_rec	7.4
	428564	AF100781	Hs.194678	WNT1 inducible signaling pathway	SS,GFDP,Cys_inol,isp	7.4
	418007	M13509	Hs.83199	Matrix metalloproteinase 1 (interstia	SS,hemopexin,Peptidas	7.2
75	424001	W57863	Hs.127475	KIAA0151 protein	TM,MT2B_propap,isp	7.2
	456955	AW131888	Hs.177292	ESTs, Weakly similar to hypothelice	TM	7.1
	445142	AI754953	Hs.145958	ESTs	Cadherin_C_term,cathe	7.0
	415138	C18355	Hs.78045	tissue factor pathway inhibitor 2 (TFP	Kunitz_BPTI,G-gamma	6.8
	438167	D26363	Hs.24266	ESTs	7tm_1	6.6
	452907	AB002364	Hs.276216	ADAM-TS3; a disintegrin-like and	TM,MT2B_propap,isp	6.4
80	449048	DA40561	Hs.22390	similar to S58401 (cathe) glucose in	SS	5.8
	425371	D49441	Hs.155981	mesothelin	SS	5.7
	407945	X06026	Hs.505	ATPase, Ca++-transporting, alpha p	TM,E1-E2,ATPase,Hs	5.5
	424530	AA101043	Hs.151264	kalikrein 7 (chymotrypsin-like) seram c	SS,trypsin	5.5
	420352	U97934	Hs.97206	huntingtin interacting protein 1	TM,ENTH1,UEQ	5.4

WO 02/102235

PCT/US02/19297

41384	NM_000401	Hs.75334	exostoses (multiple) 2
42514	NM_001851	Hs.154850	collagen, type IX, alpha 1
411945	AL033527	Hs.92137	v-myc avian myeloblastosis viral
415539	AT133881	Hs.73472	GNPAs-1b, bone morphogenetic pro
438018	AF001160	Hs.5999	hypothetical protein FLJ10298
424539	L02911	Hs.150402	activin A receptor, type I
450375	A000847	Hs.8850	a disintegrin and metalloproteinase d
415184	AF101751	Hs.26813	CD41
400296	A000527	Hs.139336	ATP-binding cassette, sub-family C
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase d
400534	AF000447		predicted exon
425506	NM_003866	Hs.156205	basic leucine zipper nuclear factor 1
419472	B240670	Hs.75379	soluble carrier family 1 (gal1 high aff
449535	W15267	Hs.23672	low density lipoprotein receptor-rela
450208	AK001859	Hs.27595	hypothetical protein FLJ10597
418693	AF190878	Hs.87409	thrombospondin 1
410361	BE391804	Hs.62661	guanylate binding protein 1, interfer
407872	AB039723	Hs.40735	fizzled (Drosophila) homolog 3
421502	AF111856	Hs.105039	solute carrier family 34 (sodium pho
412494	AL133900	Hs.732	ADP-ribosylation factor domain pro
405056	NM_014143	Hs.145296	disintegrin protease
431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic pro
407792	A1077715	Hs.39384	putative secreted ligand homologous
408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-s
450581	AF081513	Hs.25195	endothelial bleeding associated fac
432712	AB015640	Hs.268031	serot-C5-desaturase (human ERG5),
450447	AF122123	Hs.25010	hypothetical protein P15-2
414706	AW340125	Hs.76989	KIAA0097 gene product
417389	BE283964	Hs.82045	Mdixes (zebrafish growth-promoting
400666	X07820	Hs.22259	Matrix Metalloproteinase 10 (Strom
406400	AA343629	Hs.104570	kallikrein 6 (neuropilin/ovastin)
407864	AF069291	Hs.40539	chromosome 8 open reading frame 1
452822	X58569	Hs.288617	Homo sapiens cDNA: FLJ22621 fs,
446913	AA403950	Hs.18523	transmembrane 4 superfamily memb
422611	AA158177	Hs.119722	fucosyl transferase 6 (alpha 1-6) he
423161	AA108227	Hs.124776	Homo sapiens mRNA: cDNA DKFZ
435102	AW895053	Hs.76917	F-box only protein 8
416530	U62801	Hs.75361	kallikrein 6 (neuronin, zyme)
421157			predicted exon
459525	AA721428	Hs.28145	Homo sapiens cDNA FLJ14127 fs,
452943	BE247449	Hs.31082	hypothetical protein FLJ10525
411393	AW197437	Hs.65771	B-factor, propeptide
407891	AW072003	Hs.40393	heparan sulfate (glucosamine) 3-O-s
418836	AB55449	Hs.161712	ESTs
409178	BE383948	Hs.50915	kallikrein 5
421987	AT133101	Hs.286131	CGH-101 protein
447072	DE1594	Hs.17279	tyrosylprotein sulfotransferase 1
426514	BE015633	Hs.301122	bone morphogenetic protein 7 (osteo
449133	AA723157	Hs.73769	folate receptor 1 (adult)
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot
456944	A1264155	Hs.152981	CDP-diacylglycerol synthase (phosph
414725	AA769791	Hs.126355	Homo sapiens cDNA FLJ13145 fs,
407785	AW207205	Hs.98279	ESTs
427738	NM_003018	Hs.180612	peroxisomal membrane protein 3 (35
452431	U88679	Hs.29489	fol-like receptor 3
453020	AT133148	Hs.36662	I factor (complement)
403331	A240963	Hs.8895	ESTs
425776	U25128	Hs.155499	parathyroid hormone receptor 2
424828	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog
407910	AB562274	Hs.41236	fibronectin leucine rich transmembra
426390	AF123595	Hs.41530	disintegrin
407763	AW956972	Hs.172028	a disintegrin and metalloproteinase d
420757	X76592	Hs.99915	androgen receptor (dihydrotestosterone
424406	DS4120	Hs.146409	wingless-type MMTV integrase sit
426549	AA430084	Hs.220029	ESTs, Moderately similar to ARF-1a
419402	X33635	Hs.96572	PI3K protein tyrosine kinase 7
452281	T93500	Hs.26792	ESTs
402040	NM_002407	Hs.97644	mammaglobin 2
418848	AB209691	Hs.193465	ESTs
421901	NM_014918	Hs.114068	KIAA0050 protein
433190	MT6501	Hs.3210	renin
424536	NM_005095	Hs.150390	zinc finger protein 262
433002	AF048730	Hs.279906	cyclin T1
444342	NM_014598	Hs.10867	similar to lysosome-associated mem
430594	AK001179	Hs.247112	hypothetical protein FLJ10902
428490	NM_014791	Hs.184339	KIAA0175 gene product
450171	AL133661	Hs.24583	hypothetical protein: DKFZp434C03
423554	M60516	Hs.16174	glutamine fructose-6-phosphate tran
430116	NAL004736	Hs.227656	zeonitonic and polytopic retrievers
417896	AW067903	Hs.82772	collagen, type XI, alpha 1
424804	H83520	Hs.153678	reproduction 8
430651	AA961694	Hs.105187	kinesin protein 9 gene
414853	U31116	Hs.77551	sarcoplasmic, beta(4D) dystrophin-
448595	AB014544	Hs.21672	KIAA0044 gene product

WO 02/102235

PCT/US02/19297

5	452835	AK001269	Hs.30738	ESTs	TM	2.7
	430919	AAS3429	Hs.66718	RAD54 (S.cerevisiae)-like	SS,Anti_proliferat	2.7
	470281	AE623993	Hs.191533	ESTs	Callosin_sulfux	2.7
	434815	AF155592	Hs.46744	core1 UDP-galactose-4-epimerase	SS	2.6
	432201	AE58613	Hs.135657	TMPRSS3a mRNA for serine protease	trickoli,lypsin	2.6
	430450	R2353	Hs.241469	hypothetical protein	SS	2.6
	448402	BE244226	Hs.21104	RAB1L, member RAS oncogene fam	cas,arf	2.6
	421802	BE261458	Hs.108408	CGI-7 protein	TM	2.6
	452555	Hs.49295	Hs.29202	G protein-coupled receptor 34	TM7tm_1	2.6
10	417742	RE4719	Hs.26312	gloE372A11 WATM Homo sapi	ank,deaf1,FWD,TIG	2.6
	451346	NM_006338	Hs.19292	glione associated on chromosome 1	TM,lg,LR,LRNT,LR	2.6
	433147	AF091434	Hs.43080	platelet derived growth factor C	TM,PDGF,CUB	2.6
	420079	NM_014051	Hs.94896	PTD011 protein	SS,TM	2.6
15	419918	X07070	Hs.93728	pre-B-cell leukemia transcription fac	homeobox,lg,Acyltransfer	2.5
	432350	NM_005895	Hs.774467	proinsulin, isoform 16 (thymus)	ank,deaf1,FWD,TIG	2.5
	406671	AA125947	Hs.285754	mel prolo-oncogene (rasp-cad) gene	phosphase,Sema,Plasmin_re	2.5
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	SS,TIR,lg	2.5
	425330	AW872300	Hs.18110	bone marrow stromal cell antigen 2	TM	2.5
20	433529	AJ575999	Hs.27379	ESTs	EGF,FGF,PDGF,La,Id,ne	2.5
	443552	AF118638	Hs.9599	solute carrier family 25, member 13	TM,milo_carr	2.5
	414385	X00442	Hs.75990	haploctobin	sushi,lypsin	2.5
	417575	AA339449	Hs.82785	phosphatibosylglycinamide formyltr	AFRS,transf,trans,GA	2.5
	449207	AL044222	Hs.23255	nucleoprotein 15530	TM	2.5
25	415107	AA173846	Hs.79015	antigen identified by monoclonal ant	TM,lg	2.4
	421750	AK000756	Hs.107872	hypothetical protein FL20761	TM,PH	2.4
	414912	X27255	Hs.77357	monokine induced by gamma interfe	SS,IL8	2.4
	408137	R42754	Hs.3248	muS (E. coli) homolog 5	TM,MuS,C,MuS_N,P	2.4
	450710	AF065381	Hs.18627	ESTs, Weakly similar to G01447 GP	TM	2.4
30	430221	AV085445	Hs.238126	CS-40 protein	TM,lg	2.4
	425184	BE278288	Hs.155048	Lutheran blood group (Aubergier b a	lg	2.4
	451418	BE387790	Hs.28389	ESTs	TM	2.4
	412277	BE277932	Hs.73799	guanine nucleotide binding protein (TM,G-alpha	2.4
	413719	BE405860	Hs.75498	small inducible cytokine subfamily A	SS,IL8	2.4
	451806	NM_003729	Hs.27076	RNA 3-terminal phosphate cyclase	TM,RCT	2.3
35	418224	NM_002902	Hs.79088	reticulocalbin 2, EF-hand calcium bi	SS,elhand	2.3
	452258	NM_003512	Hs.28777	HGA histone family, member L	histone,Calc_CGRP_I,AA	2.3
	451666	Z43946	Hs.28789	ADPK (podoc secreted protein in ce	SS,STM	2.3
	400880	M84340	Hs.115853	CD59 antigen	TM,CDAP_LY6	2.3
	421340	F07763	Hs.1359	decay accelerating factor for comple	SS,sushi	2.3
40	443986	AE381750	Hs.283437	HTHG29 protein	TM	2.3
	443037	AF050305	Hs.8906	synectin 1	TM,Synectin	2.3
	440516	SA2303	Hs.18121	HN1 cell surface, type 1, N-carbohy	TM,HN1,carbohydr,Cathetin	2.3
	404977	AE394145	Hs.18048	melanoma antigen MAGE-10	TM,MAGE	2.3
	440704	M89241	Hs.182	Insulin-like growth factor binding pr	SS,Iryroglobulin_1,IGF	2.3
45	437952	D63209	Hs.5944	solute carrier family 11 (proton-cou	TM	2.3
	416624	AF74480	Hs.104211	ESTs	Sema,lg	2.2
	410634	AF051152	Hs.63558	tol-like receptor 2	SS,TIR,LR,RCT,LR	2.2
	424687	JO6070	Hs.151738	matrix metalloproteinase 9 (gelatin	SS,fx2,homopauin,Pepl	2.2
	431467	NM_012211	Hs.266257	integrin, alpha 11	TM,FG-GAP,psa	2.2
50	407907	AF152235	Hs.41270	prothogelin-lysin, 2-oxoglutarate 5	SS,Lysyl_Hydro	2.2
	403056	AF220030	Hs.125300	Homo sapiens tyrosine motif protein	SPRY,TM,tm_1	2.2
	400303	AA242758	Hs.79138	Human breast cancer, estrogen regu	SS,STM	2.2
	411789	AF745505	Hs.72157	Homo sapiens mRNA, cDNA DKFZ	lg,LR,RCT	2.2
	414909	AE344699	Hs.77356	transferrin receptor (p80, CD71)	TM,PA,Ribosomal_S2	2.2
55	401131	NM_001051	Hs.258023	Homo sapiens aquaporin 5 (AQP5)	TM,MMP	2.1
	400277	Y02061	Hs.2280	Human mRNA for ribophorin I	TM	2.1
	409317	U20165	Hs.53250	bone morphogenetic protein recepto	TM,phkase	2.1
	409955	AW103394	Hs.727	H.sapiens activin beta-A subunit (ex	TGF-beta,TGFb_propop	2.1
	451253	M8299	Hs.28128	claudin 10	TM	2.1
60	429638	AE16692	Hs.211577	Khechin 1 (kinectin receptor)	TM	2.1
	409267	NM_012453	Hs.52515	transducin (beta)-like 2	TM,WBD40	2.1
	418414	JO4977	Hs.84981	X-ray repair complementing defecti	SS	2.1
	449057	AE037874	Hs.22941	ESTs	TM	2.1
	417695	AA324001	Hs.82380	message a trois 1 (CAK assembly fac	TM	2.1
65	428485	NM_002850	Hs.2280	ribophorin I	TM	2.1
	445796	NM_012421	Hs.13321	rearranged L-myc fusion sequence	TM,zf-C2H2	2.1
	430057	AE453033	Hs.2534	bone morphogenetic protein recepto	TM,Activin_recep,phkine	2.1
	425169	HE1622	Hs.153203	glycm2607.1 Scores infant brain 1	TM,FGF,PH,Ubiquitinog	2.1
70	413053	AE336737	Hs.75184	chitinase 3 like 1 (cartilage glycop	SS,Glyco_Hydro_16	2.1
	421343	BE245444	Hs.283685	hypothetical protein FLJ20396	TM	2.1
	456227	AF019812	Hs.297007	ESTs	TM,Peptidase_M50	2.1
	426261	AE242243	Hs.168670	peroxisomal farnesylated protein	E1-E2,ATPase,Catoin	2.1
	431638	NM_003016	Hs.2820	oxylipin receptor	TM,tm_1	2.1
75	456546	AE800321	Hs.203845	ESTs, Weakly similar to TWIK-rela	TM,E1-E2_ATPase,hy	2.1
	421685	AF189723	Hs.106776	calcium transport ATPase ATP2C1	TM,ABC_tran,ABC_m	2.1
	424099	AF071202	Hs.139336	ATP-binding cassette; sub-family C	TM	2.1
	424930	AE035888	Hs.153203	MyoD family inhibitor	TM	2.1
	410007	AE953687	Hs.57813	zinc ribbon domain containing, 1	TFIS	2.0
80	439135	DE3590	Hs.5057	carboxypeptidase D	SS,Zn_scarOpopt	2.1
	420633	NM_014581	Hs.99526	odorant-binding protein 2B	TM,Upocatin	2.1
	420162	BE379432	Hs.85577	cyclin-dependent kinase 4	phosphase,ant,ArfGap,PH	2.1
	429156	BE244537	Hs.157402	carboxypeptidase receptor A/guanu	TM,ANF_receptor,guan	2.0
	442711	AF151073	Hs.8645	hypothetical protein	TM	2.0
	411872	AW337356	Hs.90918	chromosome 11 open reading frame	TM	2.0

WO 02/102235

PCT/US02/19297

427801	AW979155	Hs.234433	hypothetical protein PRO1068	TM_Aa_trans	2.0
430238	AA000737	Hs.237480	hypothetical protein FLJ20730	TM	2.0
431153	NM_006055	Hs.236846	KDEL (Type-1) endoplasmic reticulum chaperone	TM,ER,Jaamen,recopl	2.0
431846	BE079924	Hs.271550	Urokinase 1B	TM,transmembrane4	2.0
404210	U02478	Hs.103469	Human A-F6 mRNA	TM,RA,DIL,POZ,FI	2.0
435640	AF220053	Hs.54960	undecarboxylated homopolysaccharide	TM,SET,COX,PHD	2.0
417905	AL080062	Hs.10989	DMF2P569023 protein	SS	2.0
412550	AL080116	Hs.74420	origin recognition complex, subunit	SS	2.0
417181	L10123	Hs.1071	surface protein A binding protein	TM	2.0
423945	AA410943	Hs.72472	BMPL-1b; bone morphogenetic protein	TM,kinase,Activin_rec	2.0
411773	NM_006799	Hs.72028	protease, serine, 21 (testin)	SS,tyrosin	2.0
408350	L14601	Hs.78546	Homo sapiens clone 24411 mRNA s	TM,EF,ATPase,Hy	2.0
401093	AB55244	Hs.121620	HYPOTHETICAL 16.4 kDa PROTE	TM,LRCT	2.0
415604	NM_004939	Hs.70600	DEADH (Asp-Glu-Ala-Asp) box	DEAD,helicase,CS,PRY	2.0
448165	NM_005591	Hs.203739	modic recombination (S. cerevisiae)	DNA_repair,Glyco_tran	2.0
415391	AB73927	Hs.79084	mesoderm specific transcript (mouse)	TM,ubiquitylase	2.0
422626	NM_016102	Hs.121748	ring finger protein 16	SPRY,CS-CHC4,zf-B	2.0
465649	AU076617	Hs.16251	cleavage and polyadenylation specif	TM	2.0
427517	D42063	Hs.179025	RAN binding protein 2-like 1	TM,Ran,BP1,zf-RanBP	2.0
411676	AB07114	Hs.71465	squalene epoxidase	TM,Monoxygenase	2.0
432554	AW73813	Hs.279411	NCK-associated protein 1	TM	2.0

TABLE 11B:

Phy: Unique Eos probe set identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Phy	CAT Number	Accession
417742	1998202_1	R84719 Z44680 R12451
425169	247626_1	U16522 R17322 AA351859

TABLE 11C:

Phy: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Durham et al. (1999)" refers to the publication entitled "The DNA sequence of human chromosome 22" Durham, et al. (1999) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NT_position: indicates nucleotide positions of predicted exons

Phy	Ref	Strand	NT_position
400634	0981026	Minus	278337-27922
401197	9719705	Plus	176341-176422

Table 12A lists about 57 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 10A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulated by small molecules (e.g., kinase, peptidase, isomerase, transporter). Predicted protein domains are noted.

TABLE 12A: ABOUT 57 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Phy: Primase

Ex. Accn: Exemplar Accession

UG ID: UniGene ID

Title: UniGene title

PFAM domains: predicted structural domains

ratio: ratio tumor vs. normal

Phy	Ex. Accn	UG ID	Title	PFAM domains	ratio
400292	AA250737	Hs.72472	BMPL-1b; bone morphogenetic protein	kinase,Activin_rec	30.0
400269	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS_Peptidase_M10	25.2
426427	M56699	Hs.169840	TTK protein kinase	kinase	18.7
424935	NM_002497	Hs.153704	NIMA (never in mitosis gene alpha	kinase	16.2
431169	AB032946	Hs.150557	kinesin-like protein 2	kinesin	11.5
453370	AF470523	Hs.182356	ESTs, Moderately similar to translat	ABC_tran	6.4
410007	M13509	Hs.83169	Matrix metalloproteinase 1 (interleu	SS_Peptidase_M10	7.2
425465	L11894	Hs.1904	protein kinase C, iota	SM_Snaphrase_C	6.1
409595	NM_006163	Hs.54589	NCK adaptor protein 1	SH2,SH3	5.2
415539	AT733881	Hs.72472	BMPL-1b; bone morphogenetic protein	kinase,Activin_rec	5.1
424539	L02911	Hs.150402	activin A receptor, type 1	Activin_rec,kinase	4.0
400296	AA305627	Hs.139335	ATP-binding cassette, sub-family C,	TM,ABC_tran	3.6
431899	NM_001173	Hs.267831	Homo sapiens cDNA FLJ12952 l	RNAP,PF,trans	3.9
439560	BE056471	Hs.72620	hypothetical protein FLJ12920	C2,PA,PLC-gamma,PLC-X	4.8
450447	AF212223	Hs.25010	hypothetical protein P15-2	ANF_receptor,kinase	3.6
400666	X07820	Hs.2258	Matrix Metalloproteinase 10 (Strom	SS_Peptidase_M10	3.5
452822	X85689	Hs.28667	Homo sapiens cDNA: FLJ22621 l	EGF,Int3,kinase	3.4
416230	UG2801	Hs.73361	kallistatin 5 (kallistatin, zym)	SS,TM,tyrosin	3.3
411393	AW797437	Hs.69771	B-factor, propeptide	SS,ush,tyrosin,wat,ln3	3.2
444755	AA431791	Hs.183001	ESTs	AAA	3.2
418636	AB554599	Hs.161712	ESTs	kinase,Activin_rec	3.2
409178	BE333948	Hs.267831	kallistatin 5	SS,tyrosin	3.1
406667	M31125	Hs.272620	pregnancy specific beta-1-glycoprot	kinase,Activin_rec	3.1
453920	AI131460	Hs.36602	1 factor (complement)	kinase,Activin_rec	3.0
404653	AA823729	Hs.26322	PI3K protein tyrosine kinase 7	kinase	2.9
419452	U03635	Hs.39572	PI3K protein tyrosine kinase 7	kinase,Activin_rec	2.9
418040	AB020961	Hs.153465	ESTs	kinase,Activin_rec	2.9
428450	NM_014791	Hs.184339	KIAA0175 gene product	TM,kinase,KIA	2.8

WO 02/102235

PCT/US02/19297

5	401323	AL158037		predicted exon	lactonase_B	2.7
	444798	BE242141	Hs.12013	ATP-binding cassette, sub-family E	SH3,phospho_ABC_tran	2.7
	432721	AUS55113	Hs.135557	IMPRESSA, member RAS oncogene fam	indol,tyrosin	2.6
	448402	BE244226	Hs.21084	RAB18, member RAS oncogene fam	ras,arf	2.6
	406971	AA129547	Hs.285754	mel proto-oncogene (hepatocarcin)	phkinase,Sema	2.6
	453418	AL036710	Hs.209527	ESTs	OH,lykinase	2.5
	414386	X00442	Hs.75580	haptoglobin	susk,tyrosin	2.5
	421270	H50337	Hs.108148	ESTs	RbcGAP	2.4
	414695	BE439915	Hs.78913	proteasome (prosome, macropain) su	proteasome	2.4
10	431341	AA307211	Hs.251531	proteasome (prosome, macropain) su	proteasome	2.4
	424005	NM_002914	Hs.139226	replication factor C (activator 1) 2 (4	AAA,Viral_helicase	2.2
	424697	X05073	Hs.151738	matrix metalloproteinase 9 (gelatin	SS,62_Pepsinase_M10	2.2
	416517	AA776987	Hs.79357	proteasome (prosome, macropain) 26	AAA	2.2
	417801	NM_014735	Hs.82292	KIAA0215 gene product	PHD	2.1
15	402659	M97639	Hs.155565	receptor tyrosine kinase-like orphan	pro_isomerase	2.1
	403267	AHA63303	Hs.2334	bone morphogenetic protein recepto	Adiclin_rec,phkinase	2.1
	421941	AA508197	Hs.108850	KIAA0093 protein	TPR,phkinase	2.1
	453078	AF053551	Hs.31594	metacin 2	pro_isomerase	2.1
20	424098	AF071202	Hs.139335	ATP-binding cassette; sub-family C,	TM,ABC_tran	2.1
	411159	AA336342	Hs.59171	protein kinase C- β 2	phkinase,phkinase_C,HPT1	2.1
	407740	AA256547	Hs.52509	ESTs	P450	2.1
	402152	BE378432	Hs.95577	cyclin-dependent kinase 4	phkinase,anti_ArkGap_zas	2.1
	420480	H98994	Hs.193041	ESTs	PI3Ka,PI3_P14_kinase	2.1
25	422156	BE244537	Hs.167382	antimicrobial peptide receptor Argumy	TM,WF_receptor,phkinase	2.0
	423945	A4410943	Hs.72472	SMPPR- β , long-megakaryopoietic pro	TM,phkinase,Adiclin_rec	2.0
	411773	NM_005769	Hs.72026	protease, serine, 21 (feline)	SS,lypsin	2.0
	447298	BE617527	Hs.180450	ribosomal protein S24	PI3Ka,PI4_kinase	2.0
	427817	DA2063	Hs.178825	RAN binding protein 2-like 1	TPR,pro_isomerase	2.0
30	453546	AF042385	Hs.33251	polydiphenyl isomerase E (cycloph	pro_isomerase,rm	2.0

TABLE 12C:

Play: Unique number corresponding to an Eos probost

Ref: Sequence source. The 7 digit numbers in this column are GenBank Identifier (GI) numbers. "Dunham 1, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1989) Nature 339: 255-409-455

Strand: Indicates DNA strand from which exons were predicted

NLposition: Indicates nucleotide positions of predicted exons

Play	Ref	Strand	NLposition
401323	5212516	Plus	213550-214450

Table 13A lists about 1085 genes up-regulated in ovarian cancer compared to normal ovaries. These were selected as for Table 10A, except that the ratio was greater than or equal to 10, and the denominator was the median value for various non-malignant ovary specimens.

TABLE 13A: ABOUT 1085 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL OVARY

Play: Primerkey

Ex Accr: Exemply Accession

US ID: UnGene ID

Title: UnGene title

ratio: ratio(tumor vs. normal ovary)

Play	Ex Accr	US ID	Title	ratio
439706	AW872627	Hs.597815	ESTs	109.2
449519	AU070643	Hs.313	secreted phosphoprotein 1 (osteopontin, bone	107.8
422055	AB688872	Hs.288966	centroplasmic (ferrooxidase)	104.4
447111	AU171574	Hs.17409	cysteine-rich protein 1 (inistatin)	88.3
431139	NM_008103	Hs.2719	epididymis-specific, wavy-acidic protein type	82.8
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (anti	81.9
413858	AW992355	Hs.8364	ESTs	73.9
445291	BE397753	Hs.14523	interferon, gamma-inducible protein 30	72.7
423650	AF017307	Hs.169966	ET4-like factor 3 (ste domain transcription f	68.1
411459	T09957	Hs.70327	cysteine-rich protein 2	66.6
425504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	65.7
416971	RJ4357	Hs.82658	uncoupling protein 2 (mitochondrial, proton c	64.9
453273	AA295454	Hs.24743	hypothetical protein FLJ20171	62.5
446441	AK001782	Hs.15083	hypothetical protein	60.7
428758	AA433886	Hs.98502	Homo sapiens cDNA FLJ14303 fs, clone PLACE20	59.7
441405	Z45957	Hs.7837	Homo sapiens cDNA FLJ10457 fs, clone N12RP10	57.8
441959	AW194554	Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG-1 PROT	55.7
449495	AW772286	Hs.211603	Homo sapiens mRNA, cDNA DKF Zp5648073	55.7
414932	AW330088	Hs.78550	Homo sapiens mRNA, cDNA DKF Zp56481264	55.2
418068	AW971155	Hs.283902	ESTs, Weakly similar to prolly 4-hydroxylase	54.8
425330	L22524	Hs.2255	matrix metalloproteinase 7 (matlysin, ulei	53.4
412335	NM_004415	Hs.74315	desmoplakin (DPL, DPM)	51.4
430034	AB903551	Hs.29885	ESTs	50.7
439318	AW837045	Hs.5527	G protein-coupled receptor 56	50.7
417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (versican)	50.5
407795	AA057538	Hs.38972	lactoperoxidase 1	50.4
429535	AW17720	Hs.172654	vesicle-associated membrane protein 8 (endob	49.7
417308	H90720	Hs.811892	KIAA0101 gene product	48.9
438875	AT124755	Hs.5337	isocitrate dehydrogenase 2 (NADP+), mitochon	48.4
439180	AA393742	Hs.199397	v-erb-b2avian oncoprotein leukemia virus	47.1
426289	M23031	Hs.2253	complement component 2	46.3
405484			0	46.1

WO 02/102235

PCT/US02/19297

425371	D49441	Hs.155981	mesothelin	45.7
425912			0	45.0
443021	AA38548	Hs.8904	Ig superfamily protein	44.6
427897	T18997	Hs.180372	BCL2-like 1	44.3
428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN	44.0
404678			0	43.9
420289	XU7820	Hs.2258	Matrix Metalloproteinase 10 (Stromelysin 2)	43.8
451035	AU078785	Hs.430	plastin 1 (l isoform)	43.8
408484	BE314650	Hs.7476	ATPase, H ⁺ transporting, lysosomal (vacuolar)	42.6
336278	BE396290	Hs.5097	synapophysin 2	42.4
415383	AF113678	Hs.75621	serine (or cysteine) proteinase inhibitor, cl	42.1
420859	AW465367	Hs.100000	S100 calcium-binding protein A6 (calgranulin	42.1
428411	AW291464	Hs.10338	ES1s	41.8
422166	W12424	Hs.112405	S100 calcium-binding protein A9 (calgranulin	41.5
413477	AA150864	Hs.790	microsomal glutathione S-transferase 1	40.7
417130	AW226563	Hs.81256	S100 calcium-binding protein A4 (calcium prot	40.1
424673	AA345051	Hs.294092	ES1s	39.8
416530	U62801	Hs.79361	kallikrein 6 (neurokinin, zym)	39.7
443162	T49551	Hs.3029	ESTs; Highly similar to KERATIN TYPE I CYTO	39.6
413719	BE438980	Hs.75468	small inducible cytokine subfamily A (Ony-Cys	39.2
424687	JO6070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 9)	38.9
413083	AL035737	Hs.76184	chitinase 3 like 1 (cartilage glycoprotein-3)	38.5
429441	AJ224172	Hs.204096	lipophilin D (tetraophelin family member), pro	38.1
418526	BE019030	Hs.85338	sialic acid carrier family 16 (monocarboxylic acid	37.9
415511	AF32817	Hs.152862	ES1s	37.7
409453	AI885516	Hs.55612	ES1s	37.7
445537	AJ245671	Hs.12844	EGF-like domain; multiple 6	37.3
442432	DC093589	Hs.38178	Human sapiens cDNA: FLJ23468 fs, clone HS119	37.3
402643	Y07817	Hs.624	interleukin 6	37.3
419092	JO6581	Hs.89603	myc 1, transmembrane	36.7
444172	BE147740	Hs.104568	ES1s	36.0
412115	AK001733	Hs.73239	hypothetical protein FLJ10901	35.8
423440	NM_026407	Hs.97644	mammaglobin 2	35.7
414386	XU2442	Hs.75990	hepatocellular	35.3
423225	AA852904	Hs.125359	Thy-1 cell surface antigen	35.1
404696	H13032	Hs.103378	ES1s, Weakly similar to DRP1 (Hspapins)	35.0
413278	BE653305	Hs.833	Interleukin-stimulated protein, 15 kDa	34.9
415935	AJ044248	Hs.85339	G protein-coupled receptor 39	34.8
445919	TS3519	Hs.290357	ES1s	34.7
416554	H40154	Hs.80296	Parklike cell protein 4	34.4
414186	U33446	Hs.75799	protease, serine, 8 (prosalin)	34.2
454371	AA631332		glycoprotein 1.1 NOL_CGAP_Thyl Homo sapiens cDNA	33.9
421937	AB703567	Hs.100706	Hm1 protein	33.9
449722	BE280074	Hs.23960	cyclin B1	33.8
400986			0	33.7
452203	X57522	Hs.158164	ATP-binding cassette, sub-family B (MDR/TAP),	33.5
411945	AL033627	Hs.92157	v-myc avian myelocytomatosis viral oncogene h	33.5
425811	AL039104	Hs.159557	keratin alpha 2 (KAG cohort 1, importin a	33.4
408901	AK001330	Hs.48865	hypothetical protein FLJ10468	33.3
435481	AW075486	Hs.286040	phosphoserine aminotransferase	33.3
422863	MT9141	Hs.13234	ES1s	33.3
428158	NM_001982	Hs.190907	v-erb-b2 avian erythroblastic leukemia viral	33.2
431836	AF176332	Hs.271411	beta-site APP-cleaving enzyme 2	32.6
421902	AF111858	Hs.105039	solute carrier family 34 (sodium phosphate),	32.5
431211	M88549	Hs.5559	Human sapiens connectin 26 (GJB2) mRNA, complet	32.5
426662	NM_014038	Hs.5216	HSP-0003 protein	32.5
442533	AA161224	Hs.8372	ubiquinol-cytochrome c reductase (6.4Ld) subu	32.5
405400	AA343629	Hs.104570	kallikrein 6 (neurokinin/vasin)	32.4
453363	A24461	Hs.103296	ES1s	32.4
422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	32.4
433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase like (y	32.3
441020	W9283	Hs.33962	ES1s	32.2
432201	A538613	Hs.135657	TMPSRSS3a mRNA for serine protease (ECHO1) (T	31.9
424125	M51689	Hs.1735	inhibin, beta B (activin AB beta polypeptide)	31.9
433339	AT914829	Hs.32940	defensin, beta 1	31.8
403380	AF123050	Hs.44532	dubiquitin	31.7
419329	AY007220	Hs.288996	S100-type calcium binding protein A14	31.6
459231	AA446644	Hs.692	GA733-2 epithelial glycoprotein (EGP) (KSA)	31.6
423981	DT3869	Hs.13636	Human sapiens mRNA for osteoblast specific fac	31.2
413840	AI001558	Hs.2903801	ES1s	30.8
440943	AW082298	Hs.146181	ES1s, Weakly similar to KIAA0859 protein [hs	30.8
419239	AA468183	Hs.184598	Human sapiens cDNA: FLJ23241 fs, clone COL013	30.4
410132	NM_003490	Hs.53682	Microtubule-associated glycoprotein-2	30.2
415203	Y54942	Hs.83768	CDCC2 protein kinase 2	30.1
412719	AW016910	Hs.129911	ES1s	30.0
407862	BE548267	Hs.50724	Human sapiens cDNA FLJ10934 fs, clone OVARC10	30.0
421653	AK021643	Hs.120912	ES1s	29.9
431743	AY812592	Hs.263065	ES1s	29.8
443295	AB04793	Hs.241284	ES1s	29.7
413745	AW247252	Hs.75514	nucleoside phosphorylase	29.7
441028	AU333950	Hs.17559	ES1s	29.6
442315	AI173952	Hs.7896	ES1s	29.6
425838	U59011	Hs.30743	Preferentially expressed antigen in melanoma	29.5
428479	Y00272	Hs.184572	cutl division cycle 2, G1 to S and G2 to M	29.5

WO 02/102235

PCT/US02/19297

	432280	BE440142	Ha.2943	signal recognition particle 19MD	29.4
	432155	AI791925	Ha.35549	hypothetical protein	29.3
	449033	AV652402	Ha.156145	ESTs	29.2
5	452367	U71207	Ha.29279	eyes absent (Drosophila) homolog 2	29.1
	432706	NM_013230	Ha.286124	CD24	29.0
	422163	AF027208	Ha.297332	prominin (mouse)-like 1	28.7
	447035	NM_024763	Ha.171144	short-chain dehydrogenase/reductase 1	28.6
	443958	BE241880	Ha.100209	cathelin C	28.2
	422996	BE549072	Ha.122579	ESTs	28.1
10	450377	AB033091	Ha.24936	ESTs	28.0
	447471	AF039643	Ha.16676	spandy (Drosophila) homolog 2	28.0
	444725	AW952022	Ha.234174	Homo sapiens cDNA FLJ13819 fs, clone THYRO10	27.8
	430250	NM_016529	Ha.263021	chloride intracellular channel 5	27.7
	416305	ALJ07628	Ha.79167	casackia virus and adenovirus receptor	27.6
15	416174	L25686	Ha.83656	Rho GTP dissociation inhibitor (GDI) beta	27.5
	417233	W20505	Ha.24395	small inducible cytokine like family B (Oys-X-C)	27.4
	417666	AW067903	Ha.82772	collagen, type XI, alpha 1	27.3
	427344	NM_000869	Ha.2142	5-hydroxytryptamine (serotonin) receptor 3A	27.2
	422953	BE018882	Ha.44343	ESTs	27.2
20	407137	T97307	Ha.190637	v-erb-b2 avian erythroblastic leukemia viral	27.0
	419396	AI656166	Ha.7331	ESTs	27.0
	433662	W07162	Ha.150626	CATX-8 protein	26.7
	422576	BE548555	Ha.118554	CGI-85 protein	26.4
25	423271	W47225	Ha.126750	interleukin 1, beta	26.3
	423716	AB931487	Ha.8700	cyclin E1	26.1
	420186	NM_015925	Ha.96697	liver-specific/HLH-Zip transcription factor	26.0
	419581	AW587286	Ha.31011	anterior gradient 2 (Xenopus laevis) homolog	25.9
	443672	AA323362	Ha.9367	butyrobacillin (gamma), 2-oxoglutarate dioxyge	25.8
	416849	AW293318	Ha.80356	mL-1 cell differentiation protein	25.3
30	408474	AA188823	Ha.83196	Homo sapiens cDNA: FLJ23597 fs, clone LNC152	25.3
	411825	AK000334	Ha.72289	hypothetical protein FLJ23037	25.3
	400681			0	25.2
	440394	AW445167	Ha.126036	ESTs	25.1
35	414586	AA306150	Ha.76505	lymphocyte cytosolic protein 1 (L-pistatin)	25.1
	411925	AW014588	Ha.72925	chromosome 11 open reading frame 13	25.1
	417889	BE076254	Ha.82793	proteasome (prosome, macropain) subunit, beta	25.0
	433447	U29195	Ha.3281	neuronal peroxisom 1	24.8
	420885	C18448	Ha.26887	elongation of very long chain fatty acids (FE	24.8
40	410619	BS512730	Ha.65114	keratin 18	24.6
	434094	AA305599	Ha.238205	hypothetical protein PRO2013	24.6
	421924	BE514514	Ha.109606	coronin, actin-binding protein, 1A	24.6
	446659	AW44229	Ha.16237	COX17 (yeast) homolog, cytochrome c oxidase a	24.5
	421451	AA291377	Ha.50031	ESTs	24.3
45	433629	AI375499	Ha.27379	ESTs	24.3
	438930	AW843633	Ha.81256	S100 calcium-binding protein A4 (calcium prot	24.2
	444212	AW953976	Ha.10649	basement membrane-induced gene	24.2
	441633	AW958544	Ha.110242	ESTs	24.2
	441134	W23032	Ha.7678	cellular retinoic acid-binding protein 1	24.2
	417715	AW969587	Ha.86366	ESTs	24.1
50	405361	NM_059882	Ha.54416	shio oculis homeobox (Drosophila) homolog 1	24.1
	419584	I26755	Ha.80708	diphosphate (NADH/NADP) (cytochrome b-5 reduct	24.1
	430125	U46418	Ha.233950	serine protease inhibitor, Kunitz type 1	23.9
	434078	AW880709	Ha.283633	EST	23.8
55	408559	AI493591	Ha.78148	platelet/endothelial cell adhesion molecule (23.8
	439413	AB98252	Ha.37510	ESTs	23.7
	440934	AB240449	Ha.277523	grain1ta09.x1 NCL-GAP_UH1 Homo sapiens cDNA	23.6
	420344	BE463721	Ha.97101	Putative G protein-coupled receptor GPCR150	23.6
	431243	U46455	Ha.252189	synectan 4 (amphiglycin, nystrocan)	23.6
60	417815	L24203	Ha.82237	actinin-4/betaactinin group D-associated prot	23.5
	451267	AB033694	Ha.117685	soluble carrier family 17 (apolipoprotein transpo	23.4
	450101	AW649969	Ha.24385	Human hbc57 mRNA sequence	23.4
	419683	AA133749	Ha.92323	FXD domain-containing ion transport regula	23.4
	431103	M57399	Ha.44	pleiotrophin (heparin binding growth factor 8	23.4
65	451110	AB952640	Ha.301584	ESTs	23.3
	429295	AW367293	Ha.74838	zinc finger protein 6 (ZNF61)	23.2
	446517	AA082750	Ha.42194	hypothetical protein FLJ22649 similar to sign	23.1
	424670	W61215	Ha.116651	epithelial V-alko antigen 1	23.1
	417847	AA021558	Ha.286312	Homo sapiens cDNA: FLJ22316 fs, clone HRO052	23.1
70	446027	AT127116	Ha.22860	dipeptidyl-peptidase III	23.1
	424969	AW950928	Ha.153996	oxalate kinase, mitochondrial 1 (gabiputins)	23.1
	433159	AB038986	Ha.150587	kinesin-like protein 2	23.0
	411393	AW797437	Ha.69771	B-factor, peropidin	23.0
	434915	AF155582	Ha.467444	small UDP-glucose:N-acetylglucosamine-6-p	22.8
75	427585	DS1152	Ha.179729	collagen, type X, alpha 1 (Schmid metaphyscal	22.7
	445721	H92136	Ha.13144	HSPC160 protein	22.6
	448258	BE386983	Ha.88016	ESTs, Weakly similar to MAP_HUMAN	22.6
	456644	AT264155	Ha.157361	CDP-diacylglycerol synthase (phosphatidate cy	22.6
	452686	NM_001205	Ha.301927	0	22.5
80	418693	AT750878	Ha.87409	thrombospondin 1	22.4
	414880	AW247305	Ha.119140	eukaryotic translation initiation factor 5A	22.4
	401919			0	22.4
	422496			0	22.3
	420034	AF163474	Ha.95744	DKFZP586D0823 protein, Prostate androgen-regu	22.3
	403622			0	22.2

WO 02/102235

PCT/US02/19297

434042	AI589041	Hs.8254	hypothetical protein PRO0899	22.1
415080	AW150635	Hs.18878	hypothetical protein FLJ21620	22.1
408445	AB018249	Hs.101458	small inducible cytokine subfamily A (Cys-Cys)	22.1
447362	AW176120	Hs.9091	ESTs	22.0
429547	AW008166	Hs.99376	ESTs	22.0
427954	J03060	Hs.247551	meskin 1	21.9
423161	ALJ45227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (from c	21.9
428392	F10233	Hs.2255	secretory granule, neuronendocrine protein 1 (21.8
444107	T46839	Hs.10319	UDP-glucose-4-epimerase 2 family, polypeptide	21.7
414421	AI521130	Hs.155567	ESTs, Weakly similar to LAK-4p [L-sapiens]	21.5
412589	TC0660	Hs.24305	ESTs	21.5
446525	AW967059	Hs.211556	Homo sapiens cDNA: FLJ23378, clone HEP162	21.5
416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like docking	21.5
438972	AA284679	Hs.25540	claudin 3	21.5
428688	AA652773	Hs.297939	ESTs; Weakly similar to oncostatin [H.sapiens]	21.5
421340	F07783	Hs.1389	decay accelerating factor for complement (CD5	21.4
413966	AA133335	Hs.173704	ESTs	21.4
448243	AW369771	Hs.77496	ESTs	21.3
421928	AF013758	Hs.109643	polyclonocyte binding protein-interacting pro	21.3
403398			0	21.3
435793	AB037734	Hs.4993	ESTs	21.3
432629	AW860548	Hs.280558	ESTs	21.2
449057	AB037794	Hs.22941	ESTs	21.2
437575	AW954355	Hs.36529	ESTs	21.2
401131			0	21.0
407207	TC3661	Hs.179661	lutealin, beta polypeptide	20.8
444783	AK001468	Hs.62180	ESTs	20.8
428230	AA367019	Hs.241395	protease, serine, 1 (thymosin 1)	20.8
447343	AA256641	Hs.236894	ESTs; Highly similar to LOW-DENSITY LIPOPROTE	20.7
409041	AB033025	Hs.50081	KMA1159 protein	20.6
421305	BE307354	Hs.289721	diphtheria toxin resistance protein required f	20.6
411704	AA99220	Hs.17573	hypothetical protein FLJ10074	20.5
407016	M16038	Hs.80867	v-yes-1 Y-maguchi sarcoma viral related oncog	20.5
423827	Z88128	Hs.3109	Rho GTPase activating protein 4	20.4
410174	AA306007	Hs.59461	DKFZP434C245 protein	20.4
425184	BE278288	Hs.155048	Lutheran blood group (Aubergin b antigen incl	20.4
452322	BE566543	Hs.28588	glutaredoxin (thioltransferase)	20.3
447626	AL046793	Hs.340	small inducible cytokine A2 (monocyte chemot	20.2
447335	BE617635	Hs.286192	protein phosphatase 1, regulatory (inhibitor)	20.2
424867	U024860	Hs.153591	Not5f (D. melanogaster)-like protein	20.1
410275	U05658	Hs.51795	transcription factor AP-2 gamma (activating o	20.1
425043	Y93387	Hs.227817	BCL2-related protein A1	20.0
410173	AA708017	Hs.118944	ESTs	19.8
433047	M66135	Hs.275946	methionine-tRNA synthetase	19.8
419088	AI538323	Hs.77496	ESTs	19.7
403381			0	19.6
409162	H25530	Hs.50868	solo carrier family 22 (organic cation tran	19.5
426150	NM_003658	Hs.167218	Barf4-like homeobox 2	19.4
449292	AI990292	Hs.225457	ESTs	19.4
425207	AB014681	Hs.155120	rhoGAP guanine nucleotide exchange factor (G	19.4
413950	AK001645	Hs.33871	hypothetical protein FLJ10783	19.3
434641	AA378937	Hs.51590	HSPC150 protein similar to ubiquitin-conjugat	19.3
445930	AF055009	Hs.13456	Homo sapiens clone 24747 mRNA sequence	19.2
446608	N75217	Hs.257846	ESTs	19.1
425222	M85430	Hs.155191	vlim 2 (zein)	19.1
428309	M67815	Hs.16350	cellular retinoic acid-binding protein 2	19.1
420005	AW271106	Hs.133294	ESTs	19.1
406982	AB018305	Hs.5378	spondin 1, (spondin) extracellular matrix p	19.0
407142	AA412635	Hs.55235	sphingomyelin phosphodiesterase 2, neutral me	19.0
430122	NM_013342	Hs.233785	CFP3 (E2A) fusion partner (in childhood Leuk	18.9
446293	AA020213	Hs.149722	ESTs	18.9
444825	AW167613	Hs.248	mitogen-activated protein kinase kinase kinas	18.9
407634	AW015599	Hs.301280	UDP-GlcNAc:beta-Gal beta-1,3-N-acetylglucosami	18.9
445200	AA084480	Hs.12409	somatomedin	18.8
418917	X02954	Hs.1217	adenosine deaminase	18.8
435777	AW415202	Hs.286192	protein phosphatase 1, regulatory (inhibitor)	18.8
431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to gene	18.7
426427	M66599	Hs.1619840	TK protein kinase	18.7
436261	AW111154	Hs.1220051	ESTs	18.6
425907	AA365752	Hs.155965	ESTs	18.6
459720			ESTs	18.5
421242	AW161306	Hs.13561	ESTs, Weakly similar to DJ37E16.5 [H.sapiens]	18.5
457715	AA624202	Hs.59142	ESTs	18.5
451668	Z33948	Hs.28789	ASPC (acidic secreted protein in cartilage)A	18.4
437142	AT791617	Hs.145068	ESTs	18.4
418588	BE387040	Hs.162476	ESTs, Weakly similar to similar to alpha-beta	18.3
433068	NM_006456	Hs.286215	sialyltransferase	18.3
419854	AW054873	Hs.87835	Homo sapiens P4C clone RP5-1087M19 from 7q11.	18.3
444726	NM_005147	Hs.11801	interleukin regulatory factor 6	18.3
423011	NM_000683	Hs.299847	ESTs, Highly similar to A2AD_HUMAN ALPHA-2C-2	18.2
451428	AW083354	Hs.11067	ESTs, Weakly similar to K02E10.2 [C.elegans]	18.2
424865	AF011333	Hs.153563	lymphocyte antigen 75	18.2
418742	AW461197	Hs.153116	ESTs	18.1
446827	AW73016	Hs.15725	ESTs; hypothetical protein SB948	18.1

WO 02/102235

PCT/US02/19297

	424885	A0333771	Hs.82204	ESTs	18.1
	462926			0	18.0
	488452			0	18.0
5	428641	AA431367	Hs.23456	GMPF2 for guanosine monophosphate reductase i	18.0
	454390	A0020713	Hs.58966	KIAA0906 protein	18.0
	441784	AB22132	Hs.28700	ESTs	17.8
	418756	AB088311	Hs.87078	ESTs	17.8
	408521	AB70572	Hs.46528	chromosome 11 open reading frame 8; fetal br	17.9
	426201	AW182614	Hs.128499	ESTs	17.8
10	410442	X73424	Hs.63768	propionyl Coenzyme A carboxylase, beta polype	17.8
	455623	AW748920		gtaCAG-570306-171199-034-gc2 570306 Homo sapi	17.8
	422857	L32137	Hs.1584	cartilage oligomeric matrix protein	17.8
	448110	AA626937	Hs.181551	ESTs	17.7
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	17.7
15	405224			0	17.7
	447630	A1660148	Hs.44865	lymphoid enhancer-binding factor 1	17.7
	407663	NM_016429	Hs.37492	COP22 for nonclathrin coat protein zeta-COP	17.7
	427400	Z95152	Hs.178656	mitogen-activated protein kinase 13	17.6
	414812	X72755	Hs.77367	monokine induced by gamma interferon	17.6
20	427681	AW154426	Hs.20726	ESTs	17.6
	420050	AA455706	Hs.44581	heat shock protein hsp70-related protein	17.5
	439841	AF038961	Hs.6710	mannose-6-phosphate utilization defect 1	17.5
	425810	A0023627	Hs.31903	ESTs	17.5
25	425387	J04088	Hs.156346	topoisomerase (DNA) II alpha (170K)	17.5
	426956	AW747800	Hs.55516	hypothetical protein FLJ21535	17.4
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	17.4
	410361	BE391804	Hs.62961	guanylate binding protein 1, interferon-induc	17.4
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21KD, brain)	17.4
	411734	AW374954	Hs.71779	Homo sapiens DNA from chromosome 19, cosmid F	17.3
30	405295			0	17.3
	408340	A0037762	Hs.44208	myelin gene expression factor: 2	17.3
	456068	A1677897	Hs.76640	RGC32 protein	17.3
	446571	AA482794	Hs.06915	ESTs, Weakly similar to 16.7kd protein [Hsap	17.2
	441829	AL117482	Hs.7978	DMP7P434G131 protein	17.2
35	418004	U37519	Hs.87539	aldehyde dehydrogenase 8	17.2
	412078	X68699	Hs.73149	paired box gene 8	17.2
	414658	X68528	Hs.76781	ATP-binding cassette, sub-family D (ALD), mem	17.1
	418478	U36045	Hs.11714	cyclic-dependent kinase inhibitor 2A (melanom	17.0
40	429605	AB035245	Hs.172506	myosin VI	17.0
	410247	AF181721	Hs.61345	RU2S	17.0
	434516	AA807814	Hs.70582	ESTs, Moderately similar to AF144056 1 apolpo	16.9
	428153	AW513143	Hs.58367	hypothetical protein FLJ22252 similar to SRY-	16.9
	417793	AW435434	Hs.82575	small nuclear ribonucleoprotein polypeptide B	16.9
	454163	AW175937		gbc-QV0-B10078-190899-005-E02 570078 Homo sapi	16.9
45	415402	AA164667	Hs.297889	ESTs	16.9
	420309	AW043637	Hs.21766	ESTs	16.9
	413201	M22224	Hs.12250	alanyl (membrane) aminooxidase (aminopeptid	16.9
	444391	AL137597	Hs.11114	hypothetical protein dJ11811N3.1	16.9
50	457705	AW974668	Hs.1295	gb:EST396757 MAGE resequences, MAGM Homo sapi	16.8
	412223	AA648469	Hs.179912	ESTs	16.8
	435774	R88066	Hs.4952	tumor suppressing nontransferable candidate 1	16.8
	428783	AS331192	Hs.47438	SPQ domain binding glutamic acid-rich protein	16.8
	447783	AF054178	Hs.13561	NADH dehydrogenase (ubiquinone) 1 alpha subco	16.8
	418085	R40328	Hs.258822	ESTs	16.7
55	424242	AW067300	Hs.294142	ESTs, Weakly similar to SP42_HUMAN SPLICEOSOM	16.7
	402112	BE243971	Hs.50960	quinoxaline oxidoreductase homolog	16.7
	410250	A0082777	Hs.61334	KIAA1445 protein	16.7
	446219	A1287344	Hs.149327	ESTs	16.6
	428928	BE406838	Hs.194067	cecherin 1, type 1, E-cadherin (epithelial)	16.6
60	425812	AA364126	Hs.245933	ESTs	16.6
	411742	AW247593	Hs.71618	eukaryotic translation initiation factor 4E b	16.6
	415076	NM_000857	Hs.77780	guanylate cyclase 1, soluble, beta 3	16.6
	416209	AA236776	Hs.79378	MAO2 (mitotic arrest deficient, yeast, homolog	16.6
	440687	BE017689	Hs.7337	hypothetical protein FLJ10536	16.6
65	430375	AK071046	Hs.93758	H4 histone family, member H1	16.6
	419607	RS2557	Hs.91570	Homo sapiens clone 23783 mRNA sequence	16.6
	410328	BE080190	Hs.62275	C3H-141 protein	16.6
	405426			0	16.5
70	423556	AA340664	Hs.276562	clauzin 7	16.5
	434726	AK000796	Hs.4104	hypothetical protein	16.5
	414683	S76299	Hs.76868	interleukin neuronal intermediate filament pro	16.5
	429500	X78565	Hs.289114	hexabrachion (kennasin C, cytolactin)	16.5
	440844	AF290512	Hs.56215	Homo sapiens (h)olefin mRNA, partial cds	16.4
	400696			0	16.4
75	421536	BE250990	Hs.105509	CTL2 gene	16.4
	426032	AA150797	Hs.109276	lactenin protein	16.4
	418186	A745640	Hs.26540	ESTs, Weakly similar to 100066 hypothetical p	16.4
	452323	W44358	Hs.252812	ESTs, Weakly similar to C49H6.1 (C49H6)	16.4
	407690	AA825974	Hs.33846	Homo sapiens cDNA, FLJ21501 f1s, clone HEP034	16.4
80	414817	A133950	Hs.20524	ESTs, Moderately similar to hexokinase 1 [Hs	16.3
	406204	AA454501	Hs.43366	protein tyrosine phosphatase type IVA, member	16.3
	452560	AW270150	Hs.254516	ESTs	16.3
	432905	BE285489	Hs.31223	lethal giant larvae (Drosophila) homolog 2	16.3
	402406			0	16.3

WO 02/102235

PCT/US02/19297

	408605	H69012	Hs.48269	vaccinia related kinase 1	16.3
	447155	AA100605	Hs.121557	ESTs, Weakly similar to AF251041.1 SGC32445 p	16.3
	409599			0	16.2
5	406893	M22406		gb human intestinal mucin mRNA, partial cds,	16.2
	118629	BE247550	Hs.66859	growth factor receptor-bound protein 7 (GRB7)	16.2
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	16.2
	424243	AB049359	Hs.301637	ESTs, Highly similar to cdc Gcd1 localized c	16.2
	118462	BE001596	Hs.65266	inhibitor, beta 4	16.1
10	457205	A1905780	Hs.198272	NADH dehydrogenase (ubiquinone) 1 beta subcom	16.1
	428186	M68447	Hs.2222	transglutaminase 1 (K) polypeptide epidermal t	16.1
	419845	AW971183	Hs.600504	ESTs	16.1
	409429			0	16.1
	407375	AA091354	Hs.171380	gb B015.scq.F Human fetal heart, Lambda ZAP	16.1
15	448377	AA484514	Hs.171380	ESTs	16.1
	411156	NM_002220	Hs.2722	inositol 1,4,5-trisphosphate 3-kinase A	16.0
	453043	AA885699	Hs.24332	CG-26 protein	16.0
	403121			0	16.0
	400214			0	15.9
20	453252	R02436	Hs.215725	ESTs	15.9
	451734	NM_006176	Hs.26344	neurogranin (protein kinase C substrate, RC3)	15.9
	118655	AA106763	Hs.36793	Homo sapiens cDNA; FLJ23168 fs, clone UNG120	15.9
	424474	AA308883	Hs.148580	calcyon: D1 dopamine receptor-interacting pro	15.9
	423885	BE350484	Hs.49753	Homo sapiens mRNA for KIAA1551 protein, parti	15.9
25	428187	A0871303	Hs.285529	ESTs	15.9
	433617	A023799	Hs.163242	ESTs	15.9
	425952	D09041	Hs.155956	NAT1; acylamine N-acyltransferase	15.9
	421674	T10707	Hs.298355	neuronal PAS domain protein 2	15.9
	439999	AA115811	Hs.6638	ras homolog gene family, member E	15.9
	411351	W02919	Hs.283476	peroxisomal acyl-CoA thioesterase 1	15.9
30	413207	NM_002085	Hs.75151	RAP1, GTPase activating protein 1	15.9
	453684	AA355925	Hs.36232	KIAA0185 gene product	15.8
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase C-beta	15.8
	422748	AA316266	Hs.129349	ESTs	15.8
	414581	AB684903	Hs.52692	ESTs	15.8
35	421877	AW250390	Hs.109059	mitochondrial ribosomal protein L12	15.8
	404780			0	15.8
	401192			0	15.8
	447519	UA6258	Hs.23448	ESTs	15.8
40	434292	AF121858	Hs.12189	sorting nexin 8	15.7
	451263	H48299	Hs.26128	claudin 10	15.7
	435499	R89344	Hs.14148	ESTs	15.7
	424244	AF185431	Hs.116577	prostate differentiation factor, placental ho	15.7
	424834	AK001432	Hs.153436	Homo sapiens cDNA; FLJ10570 fs, clone NT2RP20	15.7
45	424562	AA020859	Hs.150557	basic transcription element binding protein 1	15.7
	432427	BE1614387	Hs.47378	ESTs	15.7
	430686	AA531276	Hs.59509	ESTs	15.6
	437044	AL035684	Hs.65517	ESTs, highly similar to differentially expres	15.6
50	428237	AF173206	Hs.163325	killer cell lectin-like receptor F1	15.6
	440048	AA897461	Hs.158489	ESTs, Weakly similar to envelope protein (Hs	15.6
	414922	D00723	Hs.77631	glycine cleavage system protein H (aminomethyl	15.6
	422030	X51416	Hs.110849	estrogen-related receptor alpha	15.6
	402716	AB567339	Hs.157114	ESTs	15.5
	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-bisphosp	15.5
55	410530	M25809	Hs.64173	ESTs, Highly similar to VAB1_HUMAN VACUOLAR A	15.5
	447072	BE1594	Hs.17279	tyrosyl-protein sulfotransferase 1	15.5
	420615	BE368387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S protein	15.5
	447549	AK71120	Hs.231285	ESTs	15.5
	449704	AK007033	Hs.23990	GTPase activating protein	15.4
60	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIIb, recept	15.4
	421630	NM_001956	Hs.1407	endothelin 2	15.4
	433018	AB697603	Hs.184881	ESTs	15.4
	422938	NM_001809	Hs.1594	centromere protein A (TPX1)	15.3
	407014	U38268		gb human cytochrome b pseudogene, partial cds	15.2
65	429311	AF080157	Hs.196996	conserved helix-loop-helix ubiquitous kinase	15.2
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carcinoma,	15.2
	406907	Z25427		gb caspase protein-caspase/threonine kinase	15.2
	456495	A020029	Hs.148693	ESTs	15.2
	420561	AL137692	Hs.96790	Homo sapiens mRNA; cDNA DKFZp434P182 (from d	15.1
70	446443	AW167128	Hs.231934	ESTs	15.1
	443646	A065198	Hs.268899	ESTs	15.1
	431538	AL137547	Hs.269619	Homo sapiens mRNA; cDNA DKFZp434B1120 (from c	15.1
	436687	AA688643	Hs.120461	ESTs	15.1
	420917	AW135716	Hs.117330	ESTs	15.0
75	428575	M19684	Hs.184829	serine (or cysteine) proteinase inhibitor, cl	15.0
	403482			0	15.0
	421499	AJ271438	Hs.105022	Homo sapiens PAC clone RP4-7016 to from 7a33-q	15.0
	401047			0	14.9
	417749	U09196	Hs.82520	polymetase (DNA-directed), delta 4	14.9
80	416893	A373204	Hs.79531	Homo sapiens TTF-4 interacting peptide 20 mRNA	14.9
	428474	A0023182	Hs.164523	KIAA0965 protein	14.9
	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9 (campome	14.9
	402721	T06199	Hs.237506	heat shock cognate 40	14.9
	414328	Z21666	Hs.75900	acetylase 2, mitochondrial	14.9
	415314	N68802	Hs.5422	glycoprotein M6B	14.8

WO 02/102235

PCT/US02/19297

	453735	AI066629	Hs.125073	ESTs	14.8
	424345	AK001380	Hs.145479	Home sapiens cDNA FLJ10516 fs, clone NT2RP20	14.8
	423575	C18863	Hs.163443	ESTs	14.8
	433081	I48546	Hs.298964	ESTs	14.8
5	403485			0	14.8
	452114	N22687	Hs.8236	ESTs	14.8
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system 4	14.8
	412669	AA290712	Hs.82407	Homo sapiens HSPC296 mRNA, partial cds	14.8
10	452101	T60286		gryb6/MT2.r1 Stratagene liver (57224) Homo	14.7
	420505	AW967894	Hs.291612	ESTs	14.7
	424125	X97241	Hs.168594	FAT tumor suppressor (Drosophila) homolog	14.7
	433336	AF017896	Hs.31396	ESTs; Highly similar to FRIZZLED PROTEIN PRE	14.7
	428977	AK001404	Hs.194698	cystin B2	14.7
15	429785	H82114	Hs.301769	ESTs	14.7
	424242			0	14.7
	424971	AA479005	Hs.154036	tumor suppressing subtransferrable candidate 3	14.7
	433037	NM_014166	Hs.279638	HSPC067 protein	14.6
	421670	BE207318	Hs.106674	BRCA1 associated protein-1 (ubiquitin carboxy	14.6
20	438598	AB005943	Hs.5723	Home sapiens cDNA: FLJ23439 fs, clone HS01001	14.6
	453370	IA70623	Hs.152348	ESTs; Moderately similar to translation initiation	14.6
	410561	BE540255	Hs.6994	Home sapiens cDNA: FLJ22044 fs, clone HEP091	14.6
	422287			0	14.6
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	14.6
25	420247	AA674598	Hs.153324	ESTs	14.6
	426882	BE336989	Hs.165665	BONE protein	14.6
	440006	AK000517	Hs.6844	hypothetical protein: FLJ20510	14.6
	406851	AA609784	Hs.180285	major histocompatibility complex, class II, D	14.6
	457316	AI123657	Hs.127264	ESTs	14.6
	424453	AL157500	Hs.57940	Home sapiens mRNA: cDNA DKFZ434G015 (from cl	14.6
30	436406	AW106723	Hs.125346	ESTs	14.6
	420736	AI263022	Hs.82204	ESTs	14.6
	419743	AW404762	Hs.127478	ESTs	14.6
	429113	C26235	Hs.195304	Prostaglandin-endoperoxide synthase 2 (COX-2)	14.6
	452266	AA248087	Hs.24724	MT4-amplified sequences with leucine-rich tm	14.6
35	424906	AI566066	Hs.153716	Home sapiens mRNA for Hmnb33 protein, 3' unt	14.6
	427414	F11750	Hs.6647	Home sapiens cDNA FLJ13086 fs, clone NT2RP30	14.6
	419839	U28477	Hs.93304	phospholipase A2, group VII (platelet-activat	14.6
	416736	AF038633	Hs.6562	scute carrier family 7, member 11	14.3
40	429414	AT783656	Hs.200265	empty spiracles (Drosophila) homolog 2	14.3
	424669	AA417181	Hs.120858	Home sapiens cDNA FLJ13945 fs, clone Y79AA10	14.3
	408989	AW361666	Hs.48500	KIAA0746 protein	14.3
	405788	AB115641	Hs.5164	TH1 drosophila homolog	14.3
	417681	AA334551	Hs.82767	sperm specific antigen 2	14.3
45	402104			0	14.3
	416368	R88849		gbyrn95a05.r1 Soares adult brain N2b4/B65Y Ho	14.2
	405802			0	14.2
	448357	N20169	Hs.106623	ESTs	14.2
	444261	AA298958	Hs.10724	MD5023 protein	14.2
50	407846	AA426202	Hs.40403	Ctbp3/300-interacting transactivator, with Gu	14.2
	425183	D10040	Hs.154830	fatty-acid-Coenzyme A ligase, long-chain 2	14.1
	402520			0	14.1
	429507	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	14.1
	430044	AA464510	Hs.152812	EST cluster (not in UniGene)	14.1
55	429663	M68874	Hs.211587	Human phosphatidylcholine 2-acylhydrolase (cP	14.1
	427036	AA393626	Hs.163913	ESTs	14.1
	444381	BE387335	Hs.263713	ESTs	14.1
	432090	AW972655	Hs.29263	ESTs	14.0
	406778	H62273	Hs.101651	Home sapiens mRNA: cDNA DKFZp434C107 (from d	14.0
60	404361	AW972155	Hs.284236	alko-keto reductase family 7, member A3 (afa	14.0
	452313	Y05466	Hs.28914	adrenine phosphoribosyltransferase homolog	14.0
	452355	NS4026	Hs.25202	G protein-coupled receptor 34	14.0
	429942	BC138993	Hs.134535	ESTs	14.0
	403165			0	13.9
	442150	AI368155	Hs.128664	ESTs	13.9
65	439709	AW401433	Hs.65649	hypothetical protein FLJ20128	13.9
	456799	AC004923	Hs.135187	Home sapiens clone CDABP0025 mRNA sequence	13.9
	427356	AW023482	Hs.597849	ESTs	13.9
	445862	AI638164	Hs.225520	ESTs	13.9
	432025	BE407152	Hs.111286	hypothetical protein FLJ22512	13.8
70	427505	AA361562	Hs.178151	26S proteasome-associated psd1 homolog	13.8
	402965			0	13.8
	418501	AA279490	Hs.65368	calmagin	13.8
	436954	AA740151	Hs.130425	ESTs	13.8
	405024			0	13.8
75	453976	BE463830	Hs.163714	ESTs	13.8
	431921	NA4646	Hs.58879	ESTs	13.8
	401735			0	13.8
	445496	AB007860	Hs.12802	development and differentiation enhancing fac	13.8
80	426007	AA456483	Hs.172081	phosphodiesterase 4D, cAMP-specific (dunce) (D	13.7
	409463	AI458165	Hs.17296	ESTs	13.7
	430193	AB286653	Hs.102528	Home sapiens cDNA FLJ13479 fs, clone PLACE10	13.7
	455889	AB373034	Hs.224678	ESTs	13.7
	426789	AA075596	Hs.172153	phthalane peroxidase 3 (ptaloan)	13.7
	419661	AA634543	Hs.79440	IGF-3 mRNA-binding protein 3	13.7

WO 02/102235

PCT/US02/19297

5	439901	N73865	Hs.124189	ESTs	13.7
	431374	DE268532	Hs.251871	CTP synthase	13.7
	432891	AAS39426	Hs.275933	HSPC171 protein	13.7
	441172	AIZ79652	Hs.132879	ESTs	13.7
	410001	AD041035	Hs.57771	kallistatin 11; serine protease (TLSP)	13.7
	430815	NM_004293	Hs.239147	guanine deaminase	13.6
	422769	AAS38905	Hs.289112	CO-43 protein	13.6
	402389			0	13.6
10	448977	X31809	Hs.22698	regulator of G-protein signalling 19	13.6
	459648			gbrL3-C10220-150200-070-B02 CT0220 Homo sapi	13.6
	452972	IG21732	Hs.31210	B-cell CLL/lymphoma 3	13.6
	411441	UR1961	Hs.2754	sodium channel, nonvoltage-gated 1 alpha	13.6
	448685	AB020676	Hs.21543	KIA0069 protein	13.6
15	428385	AF112213	Hs.184052	putative Rab5-interacting protein	13.6
	434899	AAS43887	Hs.154525	Homo sapiens cDNA FLJ11980 fs, clone HEMB610	13.6
	447288	AW551676	Hs.158664	ESTs	13.5
	437108	AA434054	Hs.80524	Homo sapiens cDNA:FLJ23442 fs, clone H51009	13.6
	425749	AW326587	Hs.159448	serfot 2	13.5
20	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	13.5
	413153	U17760	Hs.201103	Laminin, beta 3 (lamin 125KD), kallitricin (140	13.5
	410034	NM_002110	Hs.85555	hemopoietic cell kinase	13.5
	448361	H82028	Hs.238707	Homo sapiens cDNA:FLJ22457 fs, clone HRC099	13.5
	412754	AW160375	Hs.74555	amyloid beta (A4) precursor-like protein 1	13.5
	419081	AI798463	Hs.87191	ESTs	13.5
25	407732	AW138639	Hs.24210	ESTs	13.5
	423329	AF054510	Hs.127111	teklin 2 (testicular)	13.5
	428227	DE336857	Hs.118787	transforming growth factor, beta-induced, 68k	13.4
	439636	AF089467		gb-Homo sapiens full length insert cDNA clone	13.4
30	417605	AF005606	Hs.82294	regulator of G-protein signalling 3	13.4
	445981	DE293423	Hs.11690	single Ig IL-1R-related molecule	13.4
	447350	AJ375572	Hs.172534	ESTs; HER4 (c-erb-B4)	13.4
	451807	Y52854	Hs.27099	DKFZP554J0863 protein	13.4
	421515	U11336	Hs.105332	GaINac alpha-2, 6-sialyltransferase 1, long f	13.4
35	422443	NM_014707	Hs.116735	histone deacetylase 70	13.4
	412504	Z44495	Hs.25039	Homo sapiens cDNA FLJ13637 fs, clone Y76AA10	13.4
	453344	DE346075	Hs.44571	ESTs	13.4
	402895			0	13.4
	436712	AW978161	Hs.159877	ESTs	13.4
40	421774	AL050374	Hs.108169	DKFZP596C1619 protein	13.3
	429638	NM_012337	Hs.158450	nasopharyngeal epithelium specific protein 1	13.3
	401687			0	13.3
	429601	AW028455	Hs.263352	ESTs	13.3
	450779	AW024145	Hs.155244	ESTs	13.3
45	444558	AI199738	Hs.208275	ESTs, Weakly similar to unnamed protein produ	13.3
	442619	AA447462	Hs.201183	ESTs, Weakly similar to AF154753 1 protein.x	13.3
	443263	IG4585	Hs.44548	ESTs	13.3
	426059	DE292542	Hs.166129	interferon regulatory factor 7	13.3
	407467	DE5538		gbrHuman: B-cell PABL (pseudoautosomal boundar	13.3
50	412560	R24501	Hs.108300	CCR4-NOT transcription complex, subunit 3	13.2
	442946	AB029590	Hs.265520	ESTs	13.2
	420317	AB002958	Hs.86495	KIA00290 protein	13.2
	443211	AI128360	Hs.143655	ESTs	13.2
	434361	AF126755	Hs.117772	ESTs	13.2
55	423463	AI819085	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homologue	13.2
	414183	AW657446	Hs.301711	ESTs	13.2
	447776	DE330392	Hs.71190	ESTs	13.2
	435106	AA100847	Hs.163360	ESTs, Highly similar to AF174600 1 F-box prot	13.1
	436490	AW249157	Hs.100043	ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIA	13.1
	406806	AW444584	Hs.2387	transglutaminase 4 (prostate)	13.1
60	421308	AA681222	Hs.162843	ESTs	13.1
	414650	C15407		gbrC15407 Clontech human aorta poly(A+) mRNA [6	13.1
	418783	AA206166	Hs.79889	monocyte to macrophage differentiation-asso	13.1
	415927	AL120158	Hs.78919	Kell blood group precursor (McLeod phenotype)	13.1
	422005	U19545	Hs.116696	Human clone 23756 mRNA, partial cds	13.0
65	438427	AA296701	Hs.241433	oplin	13.0
	424820	AA101043	Hs.151254	kallistatin 7 (clonotrophic; stratum corneum)	13.0
	421563	X71490	Hs.109876	ATPase, H+ transporting, lysosomal (vacuolar	13.0
	407727	AW411148	Hs.38044	DKFZP646M082 protein	13.0
	421706	AW971225	Hs.293803	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	13.0
70	405709	AB35751	Hs.242463	keratin 8	13.0
	405353			0	13.0
	453060	AW294092	Hs.21594	ESTs	13.0
	459299	BE784261	Hs.159551	hepatocyte nuclear factor 3, beta	13.0
75	441843	AW337186	Hs.224891	ESTs	13.0
	445575	AW59477	Hs.51820	ESTs, Moderately similar to ALU1_HUMAN ALU SU	13.0
	449700	L02897	Hs.78358	ESTs	13.0
	438476	AA326108	Hs.53631	ESTs	13.0
	423532	AW008469	Hs.162246	ESTs	13.0
80	408405	AW001332	Hs.44672	hypothetical protein FLJ10470	13.0
	432673	AB026859	Hs.278505	ER-associated DNAI3; ER-associated 1 bp40 co-ch	12.9
	414584	AW350323	Hs.76893	3-hydroxybutyrate dehydrogenase (heart, mito	12.9
	447210	AF035269	Hs.17752	phosphatidylinositol-specific phospholipase A1a	12.9
	427943	AF074307	Hs.268384	Fc gamma 1 protein	12.9
	437395	AL355408	Hs.10632	hypothetical protein DKFZp62M136	12.9

WO 02/102235

PCT/US02/19297

	441627	AA047552	Hs.58086	ESTs	12.9
	419084	AA065338	Hs.179902	transporter-like protein	12.9
	429357	AA321365	Hs.266401	ESTs	12.9
5	423070	R56977	Hs.156559	ESTs	12.8
	441344	BE250144	Hs.41514	ESTs	12.8
	423527	AJ026905	Hs.103681	Human sapiens cDNA FLJ18624 f1, clone THYRO10	12.8
	417005	AW671050	Hs.807198	aspartyl-ATPase synthetase	12.8
	435352	ALD41941	Hs.154729	3-phosphoinositide dependent protein kinase-1	12.8
10	435857	W23237	Hs.296152	ESTs	12.8
	434414	AF358376	Hs.26329	gb354007.x1 NC1_CGAP_Ov23 Homo sapiens cDNA	12.7
	435051	T63236	Hs.14248	hypothetical protein FLJ20608	12.7
	451559	BE379751	Hs.14248	ESTs, Weakly similar to ALUB_HUMAN ALU SURFAM	12.7
	418216	AA652240	Hs.263099	AF15q14 protein	12.7
15	423281	AA271684	Hs.126355	C-type (calcium dependent), carbohydrate-recog	12.7
	424275	AW675173	Hs.144505	DNFZP566F0546 protein	12.7
	440652	AB30918	Hs.126692	ESTs	12.7
	444371	BE540274	Hs.239	Forhead box M1	12.7
	412520	AA442324	Hs.735	H2A histone family, member O	12.7
20	413349	BE095632	Hs.146078	gbQV1-B10678-130400-156-g07 B10678 Homo sapi	12.7
	414590	W24067	Hs.76245	DNFZP564D167 protein	12.6
	429251	AWY75254	Hs.143475	ESTs	12.6
	402238		0		12.6
	400280		0		12.6
25	421246	AW582952	Hs.300951	ESTs, Highly similar to AF151805 1 CG4-47 pro	12.6
	422229	AW956606	Hs.14456	neural precursor cell expressed, developmenta	12.6
	435502	L13266	Hs.105	glutamate receptor, ionotropic, N-methyl-D-as	12.6
	409954	AK368226	Hs.67928	ESTs	12.6
	418783	AW362367	Hs.88474	prostaglandin-endoperoxide synthase 1 (prosta	12.5
30	452117	AA21780	Hs.77370	Human sapiens cDNA FLJ12750 f1, clone NT2PFP20	12.5
	448074	BE621355	Hs.27160	ESTs	12.5
	442655	AW027457	Hs.30323	ESTs	12.5
	409928	AL137163	Hs.75749	hypothetical protein dH73B4	12.5
	402400		0		12.5
35	413348	MR3221	Hs.75182	mucrose receptor, C type 1	12.5
	425215	AW963419	Hs.155223	ESTs	12.5
	430024	AA080760	Hs.227730	Integrin, alpha 6	12.5
	445555	AA873930	Hs.157746	B cell linker protein	12.5
	41041	X59654	Hs.33837	phosphatidylethanol transfer protein, membra	12.5
40	432620	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (soluble)	12.5
	427787	AB79283	Hs.180174	cytochrome c oxidase subunit VIa polypeptide	12.4
	450243	AW119084	Hs.201037	ESTs	12.4
	406530	AA146721	Hs.49005	hypothetical protein	12.4
45	416753	TF1394	Hs.1872	shgsh1d_151TV Outward Alu primed hncDNA lib	12.4
	452096	BE394901	Hs.226785	ESTs	12.4
	424613	BE385864	Hs.149894	mitochondrial translational initiation factor	12.4
	422306	BE544325	Hs.227260	Human sapiens mRNA for LsmE protein	12.4
	409031	AA379835	Hs.76728	ESTs	12.4
	435515	N40060	Hs.6879	DC13 protein	12.4
50	429583	NM_006412	Hs.209119	1-acetylglucosyl-3-phosphate O-acetyltransferase	12.3
	449643	R0589	Hs.19603	ESTs	12.3
	440313	AL050060	Hs.7150	DNFZP566H073 protein	12.3
	426553	AA278921	Hs.1908	polysaccharide 1, secretory granule	12.3
	447357	AJ378922	Hs.159387	ESTs	12.3
	405089		0		12.3
55	414872	BE263762	Hs.77695	KAA04008 gene product	12.3
	435339	AW043921	Hs.138526	ESTs	12.3
	447033	AB357412	Hs.157601	EST - not in UniGene	12.3
	427521	AW973352	Hs.299056	ESTs	12.3
60	406377	AA300274	Hs.115659	Human sapiens cDNA: FLJ23461 f1, clone HS0707	12.3
	403116		0		12.3
	445806	AL137516	Hs.13323	hypothetical protein FLJ22059	12.2
	457817	AA247751	Hs.78572	cathopon D (lysosomal aspartyl protease)	12.2
	442410	AW996503	Hs.197680	ESTs	12.2
65	445404	AB251697	Hs.145541	ESTs, Weakly similar to J04574 sodium iodide	12.2
	403372	AW069152	Hs.44017	SRF2 (short reading frame information regulat	12.2
	427082	AB037858	Hs.173484	hypothetical protein FLJ10337	12.2
	433764	AW753676	Hs.393682	ESTs	12.2
	400266		0		12.2
70	433190	W25991	Hs.3210	renin	12.2
	444953	AW684082	Hs.301323	ESTs	12.2
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, subfam	12.2
	461345	NM_006338	Hs.25312	glioma amplified on chromosome 1 protein (neu	12.2
	430582	AA216760	Hs.231723	N-acetylglucosaminyl-phosphatase	12.2
75	424711	AB111238	Hs.104475	ESTs	12.1
	426773	NM_015556	Hs.172180	KAA04040 protein	12.1
	409178	BE303948	Hs.50915	kallikrein 5	12.1
	400260		0		12.1
	428450	NM_014791	Hs.184339	KAA0175 gene product	12.1
80	414531	T63587	Hs.76304	allograft inflammatory factor 1	12.1
	448210	AW247775	Hs.7393	hypothetical protein from EUROMAGE 1987170	12.1
	440081	AA083389	Hs.135943	ESTs	12.1
	413179	N99852	Hs.73227	NADH dehydrogenase (ubiquinone) 1 alpha subco	12.1
	447551	BE035634	Hs.929	myosin, heavy polypeptide 7, cardiac muscle,	12.1
	400517	AF242388	Hs.149585	keratin	12.1

WO 02/102235

PCT/US02/19297

	401610		0	12.0	
	454381	A835093	Hs.193428	ESTs	12.0
	443997	AW081465	Hs.295644	ESTs	12.0
	402544			0	12.0
5	430537	BE190081	Hs.250290	S100 calcium-binding protein A11 (calgizarin)	12.0
	415059	AI492170	Hs.77917	ubiquitin carboxyl-terminal esterase L3 (ubiq)	12.0
	445422	AV653721	Hs.262829	ESTs	12.0
	419957	AK000525	Hs.79467	hypothetical protein FLJ20519	12.0
	442611	BE077155	Hs.177537	ESTs	12.0
10	443271	BE588598	Hs.195704	ESTs	12.0
	415120	N84464	Hs.34950	ESTs	12.0
	435574	AA681788	Hs.165150	ESTs	12.0
	405804			0	12.0
15	412519	AA195241	Hs.73380	troponin T1, skeletal, slow	12.0
	414135	NM_004419	Hs.2128	dist specific phosphatase 5	12.0
	447075	AV650397	Hs.124740	ESTs	12.0
	416841	NS3878	Hs.249456	heterogeneous nuclear ribonucleoprotein A1	12.0
	402943			0	11.9
20	418933	BE561850	Hs.80509	small nuclear ribonucleoprotein polypeptide A	11.9
	435744	AL389994	Hs.301272	ESTs, Weakly similar to homologue of Drosophila	11.9
	405782			0	11.9
	408983	NM_000492	Hs.663	cystic fibrosis transmembrane conductance reg	11.9
	455102	BE005495	Hs.301272	gbc:CM1-BN0117-110400-183-b09 BN0117 Homo sapi	11.9
	402840			0	11.9
25	449193	AW445022	Hs.195985	Homo sapiens cDNA: FLJ21135 fs, clone CAS072	11.9
	435273	AW138099	Hs.289701	ESTs	11.9
	450484	BE220675	Hs.12701	gbc:ts8811.x1 NCL_CGAP_Lu24 Homo sapiens cDNA	11.9
	445431	AF137336	Hs.12701	plasmalogen	11.9
	401888			0	11.9
30	426037	AW160790	Hs.166071	cyclin-dependent kinase 5	11.9
	416742	R38544	Hs.248420	ESTs	11.9
	418324	AW245273	Hs.84131	threonyl-HRNA synthetase	11.8
	412870	N27398	Hs.62407	Homo sapiens HSPC299 mRNA, partial cds	11.8
35	432880	T47364	Hs.278813	interferon, alpha-inducible protein 27	11.8
	421478	A1883243	Hs.97258	ESTs	11.8
	426635	BE386109	Hs.125327	ESTs	11.8
	420523	AA262959	Hs.42788	ESTs	11.8
	426227	U67055	Hs.185102	Human proteinase activated receptor 3 mRNA; 3	11.8
	419958	U03272	Hs.75432	fibrillin 2 (congenital contractural arachnoid)	11.8
40	441816	AI401807	Hs.149997	ESTs	11.8
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	11.8
	408640			0	11.8
	446135	AA723157	Hs.73769	folate receptor 1 (adult)	11.8
	401532			0	11.8
45	40181			0	11.8
	442556	AL137751	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (from c	11.7
	451002	AA013299	Hs.5016	ESTs, Weakly similar to ALU3_HUMAN ALU SUBFAM	11.7
	401879			0	11.7
50	415989	AI267700	Hs.111126	ESTs	11.7
	416434	AW163045	Hs.78334	nuclear factor, interleukin 3 regulated	11.7
	410816	AW873401	Hs.273593	ESTs	11.7
	449239	T34653	Hs.23360	likely ortholog of yeast ARV1	11.7
	447689	AL049665	Hs.19180	Homo sapiens mRNA; cDNA DKFZp586E122 (from d	11.7
55	438877	AA531484	Hs.121255	ESTs, Weakly similar to cDNA EST EMBL-D67419	11.7
	434580	R13052	Hs.3964	Homo sapiens clone Z4877 mRNA sequence	11.7
	448105	AW991433	Hs.170675	ESTs, Weakly similar to TM52_HUMAN TRANSMEMBR	11.7
	402079			0	11.6
	404597	AA887265	Hs.144979	ESTs	11.6
60	451260	AW750773	Hs.127714	gbc:CM4-CHN004-260100-164-b03 CHN004 Homo sapi	11.6
	425175	AB553940	Hs.127714	ESTs, Moderately similar to SOX30 protein [H	11.6
	403209	NM_004454	Hs.43957	etc variant gene 5 (etc-related molecule)	11.6
	428856	AA438735	Hs.183171	Homo sapiens cDNA: FLJ22002 fs, clone HEP006	11.6
	420153	N22120	Hs.75277	hypothetical protein FLJ13910	11.6
	428780	A051469	Hs.152358	ESTs	11.6
65	421401	AW419478	Hs.104015	ion-forming, acidic coiled-coil containing p	11.6
	404502			0	11.6
	430423	AI190548	Hs.143479	ESTs, Weakly similar to hypothetical protein	11.6
	405182			0	11.6
70	435682	AA630149	Hs.127714	gbc:CM4-CHN004-260100-164-b03 CHN004 Homo sapi	11.6
	407174			0	11.6
	439335	AA742997	Hs.82462	ESTs, Weakly similar to S58855 collagen alpha	11.5
	405082	S47833	Hs.82527	adenosine monophosphate deaminase 2 (isoform	11.5
	401010			0	11.5
75	412140	AA215651	Hs.73625	RAB5 interacting, kinesin-like (rakkinosin)	11.5
	409339	AB020686	Hs.54037	ectonucleotide pyrophosphatase/hydrolase	11.5
	459884			0	11.5
	451061	BE294309	Hs.125262	DKF_ZP586G1624 protein	11.5
	453233	BE283532	Hs.949	neutrophil cytosolic factor 2 (NSC4)	11.5
80	421053	R05734	Hs.127714	gbc:CM4-CHN004-260100-164-b03 CHN004 Homo sapi	11.5
	427256	AL042435	Hs.97723	ESTs	11.5
	406708	AE282759	Hs.242463	keratin 8	11.5
	457644	AA770800	Hs.144652	ESTs, Moderately similar to 163935 ubiquitin	11.4
	422848	Z25884	Hs.171453	chloride channel 1, skeletal muscle (Thomsen	11.4
	424134	AF070637	Hs.140950	hypothetical protein	11.4

WO 02/102235

PCT/US02/19297

	403398		0	10.9
	401406		0	10.9
	402570		0	10.9
5	421240	R72730	Hs.29283	ESTs, Weakly similar to PLK_HUMAN PROTEOLYCA
	403849			0
	447824	BE520820		gb:50146337911 NIH_MGC_66 Homo sapiens cDNA c
	450335	BE514743	Hs.25664	ioner suppressor deleted in oral cancer-retal
	430853	AL119566	Hs.6721	lymphoproliferative-like
	451852	RS1928		gby/71c65.r1 Soares breast 2NblHst Homo sapi
10	431218	NM_002145	Hs.2733	homco box E2
	467194	AA688292	Hs.246560	ESTs
	444374	AA008941	Hs.11039	Homo sapiens cDNA FLJ12795 5s, clone NT2RP20
	455696	AW235317	Hs.29214	ESTs
	405552			0
15	439436	BE140845	Hs.57868	ESTs
	435110	AA706975	Hs.165536	Rhesus blood group-associated glycoprotein
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide
	415807	H03139	Hs.24683	ESTs
	409430	R21945	Hs.166975	splicing factor, arginine/serine-rich 5
20	417033	H83784	Hs.40532	ESTs, Weakly similar to PERP_MOUSE PNACSPHATID
	419464	R07380		ghym5N07.r1 Soares adult brain N2MHB55Y Ho
	404567			0
	418384	AW149266	Hs.25130	ESTs
	421071	U63127	Hs.110121	SEC7 homolog
25	425769	AW207175	Hs.106771	ESTs
	459104	R19238	Hs.232057	ESTs
	410696	AW809337		gb:MRA-ST0124-261059-015-b07 ST0124 Homo sapi
	416969	AB15443	Hs.283404	organic cation transporter
	408796	AA688292	Hs.118553	ESTs
30	425296	AW065056	Hs.111523	ESTs
	421596	AB014520	Hs.105998	Homo sapiens cDNA: FLJ22735 5s, clone HUV001
	406007	AW135966	Hs.246783	ESTs
	400167			0
	445243	A1217430	Hs.100954	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM
35	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (patchdo
	412241	AW948343		gb:RCO-MT0015-130400-031-c01 MT0015 Homo sapi
	425827	W28316		gb:4865 Human retina cDNA randomly primed sub
	446759	NM_007269	Hs.1296	membrane metallo-endopeptidase (neutral endop
	430891	U22492	Hs.248118	G protein-coupled receptor 5
40	402883			0
	423811	AW295696	Hs.50595	homeo box C4
	447078	AW685727	Hs.305710	ESTs
	414343	AL030166	Hs.75914	coated vesicle membrane protein
45	446913	AA430653	Hs.16529	transmembrane 4 superfamily member (tetrasp
	452279	AA266944	Hs.51260	hypothetical protein FLJ13164
	401220			0
	459259	AJ003294		gbcAJ003294 Selected chromosome 21 cDNA libra
	414771	AA360320	Hs.865	RAP1A, member of RAS oncogene family
	446449	BE314967	Hs.211440	ESTs
50	428670	L01087	Hs.211593	protein kinase C, beta
	446759	RS1463	Hs.16165	expressed in activated TLAK lymphocytes
	400776			0
	428093	AW594506	Hs.104830	ESTs
	412801	AA121055		ghzm2201.r1 Stralagene pancreas (937208) Ho
55	440845	AW163201	Hs.190569	ESTs
	434540	NM_016945	Hs.5164	TH1 desoglyla homolog
	414273	BE250957		gb:601184231F1 NIH_MGC_8 Homo sapiens cDNA cl
	401617			0
	410423	AW402432	Hs.63439	protein tyrosine phosphatase, non-receptor ty
60	430590	AW383947	Hs.245381	CD68 antigen
	426680	AA320160	Hs.171611	adenylate kinase 2
	445413	AA151342	Hs.12677	CG-147 protein
	402947			0
	457426	AW971119		gb:EST35205 MAGE resequences, MAGL Homo sapi
65	421458	BE342274	Hs.1741	integrin, beta 7
	404944			0
	405421			0
	416772	A1733872	Hs.79769	protocadherin 1 (cadherin-like 1)
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (offn)
70	457588	A571225	Hs.284711	RNAI555 protein
	405038	Y14443	Hs.88219	zinc finger protein 200
	404790			0
	418922	AW056590	Hs.42699	Thrombospondin-1 (Hs.87409)
	425940	AB023164	Hs.163990	KIA00671 protein
75	445749	AW059679	Hs.21802	Homo sapiens clone 25237 mRNA sequence
	418870	AF147204	Hs.89414	CXCR4; chemokine CXCR receptor 4 (hesin)
	417933	X02308	Hs.82962	thymidylate synthase
	455238	AW297396	Hs.227052	ESTs
	427928	AA417862	Hs.118217	ESTs
80	432721	AL121478	Hs.3132	steroidogenic acute regulatory protein
	428267	AA299290	Hs.246857	ESTs, Highly similar to S71100 protein kinase
	439190	AW078603	Hs.293811	ESTs
	408975	AW058693	Hs.40391	hypothetical protein LOC54149
	415130	W85893	Hs.248967	ESTs

WO 02/102235

PCT/US02/19297

	426738	H25630	Hs.159408	Homo sapiens clone 24420 mRNA sequence	10.5
	440232	AJ766925	Hs.112554	ESTs	10.5
	423565	AA371905	Hs.294130	ESTs, Moderately similar to KIA0544 protein	10.5
	420829	AW656512	Hs.221988	ESTs	10.5
5	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	10.5
	407771	AL138272	Hs.62713	ESTs	10.5
	444611	AF002180	Hs.11449	DNFZP554C123 protein	10.5
	444665	BE511125	Hs.47783	ESTs, Weakly similar to T12540 hypothetical p	10.5
10	446030	N30714	Hs.20151	HDCME31P protein	10.5
	439882	AW576101	Hs.261580	ESTs	10.5
	445224	AW450551	Hs.13308	ESTs	10.5
	405105			0	10.5
	438233	W52446	Hs.55147	ESTs	10.5
	401799			0	10.5
15	454038	X06374	Hs.37040	platelet-derived growth factor alpha polypept	10.5
	414222	AL135173	Hs.878	aspartyl dehydrogenase	10.5
	424328	AW811965	Hs.289109	dimethylarginine dimethylaminohydrolase 1	10.5
	422525	AA344632	Hs.118786	metallothionein 2A	10.5
	449281	AB371992	Hs.224658	ESTs	10.4
20	415218	R21459	Hs.23213	ESTs	10.4
	487846	Y02524	Hs.125602	ESTs, Weakly similar to C2092.2 [C.elegans]	10.4
	442577	AA252998	Hs.163900	ESTs	10.4
	406505	AF015272	Hs.115418	cathepsin 15, KSP-cathepsin	10.4
25	412258	AA375708	Hs.288677	Homo sapiens cDNA: FLJ22622 fs, clone HS065	10.4
	423624	AB065790	Hs.195272	NADH dehydrogenase (ubiquinone) 1 beta subcom	10.4
	447774	BE318118	Hs.19554	chromosome 1 open reading frame 2	10.4
	403914			0	10.4
	406329			0	10.4
	424223			0	10.4
30	431986	AA536130	Hs.146018	ESTs	10.4
	423145	BE264548	Hs.222190	ESTs, Weakly similar to secretory carrier mem	10.4
	414402	BE294196		gb:011725565.1 N1H_MGC_17 Homo sapiens cDNA c	10.4
	417079	U05590	Hs.81134	interleukin 1 receptor antagonist	10.4
35	426595	AB278223	Hs.89685	ESTs	10.4
	434577	R37316	Hs.176789	Homo sapiens cDNA: FLJ22487 fs, clone HRC109	10.4
	442415	AI005101	Hs.125590	ESTs	10.3
	421506	BE302796	Hs.106067	thymidine kinase 1, soluble	10.3
	435084	D17518	Hs.301957	acrylate cyclase activating polypeptide 1 (p	10.3
40	431724	AA514635	Hs.283704	ESTs	10.3
	466798	AJ006422	Hs.135183	centaurin-alpha	10.3
	417370	T28651	Hs.82030	lyso-phosphatidyl-RNA synthetase	10.3
	422586	AF068311	Hs.118633	Z-Specific acyltransferase synthetase-like	10.3
	432226	A2486538	Hs.271015	ESTs	10.3
45	433152	AB049860	Hs.225654	ESTs, Moderately similar to KIAA1447 protein	10.3
	419879	Z17805	Hs.63554	Homer, neuronal immediate early gene, 2	10.3
	416228	AW605160	Hs.70068	sema domain, immunoglobulin domain (Ig), tran	10.3
	453403	BE486538	Hs.61778	Homo sapiens cDNA FLJ13561 fs, clone PLACE10	10.3
	447905	AL063593	Hs.19595	DNFZP559K023 protein	10.3
50	401782	NM_012434	Hs.117665	solute carrier family 17 (anion/cation transpo	10.3
	453927	AA082455	Hs.301751	ESTs, Weakly similar to prediction	10.3
	450737	AW007152	Hs.203330	ESTs	10.3
	421633	AF121800	Hs.106260	sorting nexin 10	10.3
	429881	AF136799	Hs.200630	ESTs	10.3
55	432883	U48635	Hs.3112	sodium channel, nonvoltage-gated 1, gamma	10.3
	443095	AL380058	Hs.56505	DNFZP554G202 protein	10.3
60	416024	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi polype	10.3
	401635			0	10.3
	408895	AI510447	Hs.48778	ribon protein	10.3
	443120	AW402677	Hs.260801	ESTs	10.3
	403028			0	10.2
65	415508	AA333550	Hs.80424	coagulation factor XIII, A1 polypeptide	10.2
	400195			0	10.2
	434642	W25735	Hs.135287	ESTs	10.2
	424837	BE270113	Hs.153436	N-acetyltransferase, homolog of S. cerevisiae	10.2
	435076	RS1054	Hs.12408	ESTs	10.2
	422612	AL187629	Hs.152189	serine/threonine kinase with Dbl- and pleckst	10.2
	435090	AB311760	Hs.155111	ESTs	10.2
	414998	NM_002543	Hs.77729	oxidized low density lipoprotein (oxLDL)-like	10.2
70	401020	T85135	Hs.7278	ribonuclease, RNase A family, 2 (beta, eosin	10.2
	411410	R20583	Hs.69854	laminin, gamma 3	10.2
	460294	H42587	Hs.238730	ESTs	10.2
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14209 fs, clone PLACE10	10.2
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	10.2
	406812			0	10.2
75	425843	BE313290	Hs.159527	death associated protein 3	10.2
	449392	Z41598	Hs.26239	Homo sapiens cDNA FLJ13937 fs, clone Y79AA10	10.2
	406089	NM_014781	Hs.550421	KIAA0203 gene product	10.2
	401383			0	10.2
	468855	AF035238	Hs.153953	MAD (mothers against decapentaplegic, Drosoph	10.2
80	424912	AI008000	Hs.131450	ESTs	10.2
	400954	D25989	Hs.75325	Homo sapiens cDNA: FLJ23125 fs, clone LING082	10.2
	401029	BE382701	Hs.25850	v-myc avian myelocytomatosis viral related on	10.2
	416862	NM_005159	Hs.75389	nal (chicken)-like 2	10.2
	421905	AI550247	Hs.32399	ESTs, Weakly similar to UV-1 protein [H.sapi	10.2

WO 02/102235

PCT/US02/19297

	405054		0	10.2	
	450832	AW570022	Hs.105421	ESTs	10.2
	440076	R32052	Hs.179617	ESTs, Weakly similar to AF151940.1 C3-82 pro	10.2
	447563	BE536115	Hs.160663	ESTs	10.2
5	421238	AB033101	Hs.102796	KIAA1275 protein	10.2
	404882		0	10.2	
	415738	BE533057	Hs.265953	ESTs, Weakly similar to AF220045.1 uncharacter	10.1
	445464	AW172369	Hs.240959	ESTs	10.1
	456042	AW272056	Hs.210338	ESTs	10.1
10	414469	R51952	Hs.32587	steroid receptor RNA activator 1 (complexes w	10.1
	434732	A376443	Hs.174424	class25g95.x1 Scn5a, fctn, fctn, cpln, HNF1S	10.1
	441030	AW204139	Hs.174424	ESTs, Weakly similar to p140nctn [Mus musculus]	10.1
	446855	BE516757	Hs.16269	B-cell CLL/lymphoma 7B	10.1
15	456766	AF151074	Hs.132744	hypothetical protein	10.1
	404182		0	10.1	
	410386	AW675168	Hs.13337	ESTs, Weakly similar to unnamed protein produ	10.1
	430356	NM_006219	Hs.239816	phosphoinositide-3-kinase, catalytic, beta po	10.1
	442152	R35246	Hs.239966	Homo sapiens cDNA FLJ13495.5s, clone PLACE10	10.1
20	438354	AB79252	Hs.5151	Homo sapiens mRNA; cDNA, DKF-ZP564C2163 (from c	10.1
	425711	AA383471	Hs.185669	conserved gene amplified in osteosarcoma	10.1
	450599	AA460865	Hs.48516	ESTs	10.1
	454393	BE153288		gb:PMO:HT0335-180400-008-c08 HT0335 Homo sapi	10.1
	403383		0	10.1	
25	415947	U04045	Hs.78334	matS (E. coli) homolog 2 (colon cancer, nopo	10.1
	417772	NM_005769	Hs.72028	protease, serine, 21 (testis)	10.1
	412146	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymphocyte	10.1
	413808	J00287	Hs.182183	caldesmon 1	10.0
	458872	U223423	Hs.292794	ESTs	10.0
	403255		0	10.0	
30	403910		0	10.0	
	453400	A1991901	Hs.82990	ESTs, Moderately similar to ALUT_HUMAN ALU SU	10.0
	406502		0	10.0	
	404743		0	10.0	
35	412517	BE271584		gb:BC114106SF1 NIH_MGC_5 Homo sapiens cDNA cl	10.0
	402679		0	10.0	
	456864	BE148970		gb:CMO:HT0245-031199-085-h05 HT0245 Homo sapi	10.0
	425734	AF595203	Hs.155336	peptidyltyrosine alpha-amidating monooxygenase	10.0
	415260	W07505	Hs.283325	Homo sapiens cDNA FLJ12527.1s, clone HT2PM40	10.0
40	443503	AV545438	Hs.282927	ESTs	10.0
	423165	A1537547	Hs.124915	Human DNA sequence from clone 380A1 on chromo	10.0
	450206	A1799450	Hs.201600	ESTs	10.0
	459052	AA239812	Hs.38539	ESTs	10.0
	456246	AL397586	Hs.82426	actin related protein 2/3 complex, subunit 5	10.0
	428438	NM_001955	Hs.2271	Endothelin 1	10.0
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgranulin	10.0
	426127	L39683	Hs.167013	dynamic 2	10.0
TABLE 13B:					
Pkey: Unique EST probe/identifier number					
CAT number: Gene cluster number					
Accession: Genbank accession numbers					
	Pkey	CAT number	Accession		
50	110896	122653	AW582637 AW580977 AW105544 AW809707 AW809885 AW810000 AW10006 AW809742 AW809816 AW809749 AW809639 AW809722		
	122653		AW809836 AW809877 AW100023 AW810013 AW809613 AW809660 AW809678 AW809698 AW809691 AW809657 AW809654		
	412153	1279701_1	R87934 AW898205 AW896020 AW896035		
	412241	1248481_1	AW945343 AW1948341 AW193025 AW1954737		
	412201	130281_1	BE271584 AA116311		
	412817	132625_1	AA110556 A339917		
60	413349	1363558_1	BE586952 BE080777 BE087072		
	414273	1431911_1	BE285027 BE513434 BE359654		
	414402	1443240_1	BE258186 BE278075		
	414552	1509777_1	C15477 DB1195 DB1133		
65	415789	1555357_1	H11811 H12850 R69606 H13063		
	416388	1591066_1	R88849 R84573 H53590		
	418454	1759308_2	R67580		
	418783	1789701_1	T41388 T41366 T41294		
	424627	241724_1	AA344555 AA344312 AW963070		
	425827	255834_1	VZ82136 VZ8136 AA34334		
70	434531	34838_1	AA513572 AA83136		
	434414	35585_1	AW815640 AW811617 AW811616 W00557 BE142245 AW558222 AW801851 AW593362 AA222351 AA218561 AA055556 AW558231		
			AW587541 AW814172 H65214 AW814356 AF134164 AA243093 AA13345 AA155942 AA223384 AA227052 AA227080 T12975 AA052174		
			T61139 AW145776 AW595829 AW875188 AW813567 AW613538 A1267168 AA1557719 AA100472 AA100774 AA130786 AA151705		
			AA157730 AW150715 AA055246 AW1845901 AW656666 C8C254 AW882836 T57637 AW812671 AA205853 AA205204 AW158905 AW812662		
			AW825036 AW819167 AW85951 AA527314 H55216 AA045564 AW642656 AW642656 AW642656 AW642656 AW642656 AW642656 AW642656		
75			AW811705 AW811703 AW811705 BE081553 H159570		
			AW818443 AA648102 NT65577 AW974381		
			AA501480 AW157640 AW595933 AW503637		
			AF084657 WB1444 WB1445		
80	447824	73891_1	BF520600		
	450484	83645_1	BE220675 AA345621 AA009992		
	452189	853912_1	AW150773 AW781514		
	451852	883352_1	BE1620 AW820958 RW830 AW820964		
	451201	888742_1	T60C26 A85827 T69567 T67534 T611224 T71537 T68933		

	454163	1048369_1	AW175997 AW176000 AW175999 AW175994 AW176004 AW175989
	454393	115888_1	BE153288 BE153161 BE152905 AA078302
	455102	1253524_1	BE005496 BE005094 AA665324 AA090199
5	455864	1377038_1	BE148970 BE148976 BE148967 BE148937
	455988	1397521_1	BE177736 BE177735 BE177734
	456423	187241_1	AW748920 AA687506 AA248914 AA750494
	457426	336188_1	AW571159 AA574256 AA532359
	457484	324113_1	H57645 T59302 AA527038 Z24851 H83171
	457795	385383_1	AJ05974658 AA651599 AA645572 AA640401 AA640402
10	458259	966289_1	AJ003294 AJ003315 AJ003293

TABLE 13C.

Play: Unique number corresponding to an Exon probe

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Durham I. et al." refers to the publication entitled "The DNA sequence of

human chromosome 22" Durham, et al. (1999) Nature 402:465-495

Strand: Indicates DNA strand from which exons were predicted

N1_position: Indicates nucleotide positions of predicted exons

	Play	Ref	Strand	N1_position
20	406640	8117676	Plus	145324-144429
	406646	8116496	Plus	17982-18115,20297-20456
	406776	8131561	Plus	103576-103720
	406812	8568711	Plus	71708-72153
25	406881	2842777	Minus	81446-81903,92123-92265
	406882	2842777	Minus	110431-111708
	406965	7770576	Minus	173043-173564
	401010	8117301	Minus	83967-84180
	401020	8117458	Minus	59065-60227
	401025	8117576	Minus	175267-179483,181044-181166,181844-182039
30	401047	8709805	Minus	4804-5035,5133-5314
	401131	8699612	Minus	94802-94957,95904-95987,96323-96487,97596-97825
	401192	9719502	Minus	69559-70101
	401220	9929324	Minus	48079-48279
35	401383	6721135	Minus	155543-157381
	401405	7798126	Minus	69276-69452,69545-69568
	401519	6649315	Plus	157315-157950
	401532	7798785	Plus	124414-124560,125050-125418
	401610	7706541	Minus	16821-15955
40	401714	9715702	Plus	86484-86881
	401735	3252819	Plus	217235-217356,217521-217873
	401799	7331447	Plus	147802-145251
	401817	7417650	Minus	45868-45335
	401835	7139700	Plus	142257-142742
	401879	8099914	Minus	101064-102827
45	401888	8510069	Minus	189498-190514
	401897	8998218	Plus	604-767
	402066	6640289	Plus	135543-139031
	402077	8117414	Plus	85014-66195
50	402104	8119072	Plus	122408-122900
	402238	7890126	Plus	24726-24880,26791-27021
	402267	4589317	Plus	40811-42447
	402389	9805989	Minus	7714972,15714-1683
	402408	9796239	Minus	110326-110491
55	402423	9796344	Minus	62487-62864
	402424	9796344	Minus	64928-65073
	402466	9797789	Minus	9515-9103
	402520	7959999	Minus	171781-171996
	402679	8113438	Plus	132079-132216
60	402840	6369121	Minus	57118-67306
	402863	9026562	Plus	38656-38673,38685-39019,39097-39231,39308-39445
	402895	8926751	Plus	71919-72049
	402926	8217647	Minus	41281-41443
	402927	8217647	Minus	47247-47396
	402943	6456831	Plus	36467-36098
65	402944	6368423	Plus	110411-110748,111173-111640
	402947	6368458	Minus	101528-101991
	402965	9581599	Minus	46955-46941,47032-47148
	403022	3132351	Plus	92097-92864
70	403121	9180223	Plus	4059-4286
	403145	9830958	Minus	90695-91648
	403295	8096528	Plus	22385-22708
	403381	9438267	Minus	25009-26178
	403383	9438267	Minus	119637-121197
75	403398	6862689	Plus	13565-14659
	403399	6864178	Plus	61841-62145,62367-62765
	403482	9966050	Plus	196804-197135
	403485	9966528	Plus	2889-3001,3198-3532,3655-4117
	403649	8705159	Minus	27141-27247
80	403810	7710710	Minus	5761-6188
	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
	403914	7417588	Minus	7431-8472
	404162	4775644	Plus	18163-18444
	404802	7228863	Minus	66277-66819
	404867	7249169	Minus	101320-101501

WO 02/102235

PCT/US02/19297

	404678	9797204	Plus	115196-115448
	404743	8894169	Minus	120556-120999
	404780	9887810	Minus	175708-175971
5	404790	7230958	Plus	38811-38761
	404931	7342203	Plus	44226-44362
	404944	6899705	Plus	4256-4581
	405024	7107127	Plus	88580-88697
	405089	8072523	Plus	103182-103593
10	405094	8072579	Plus	135387-136758
	405108	7107890	Minus	135020-135472
	405145	9438278	Plus	37863-38152,38138-38332
	405192	7230700	Plus	115529-116071
	405224	6731245	Minus	14413-15579
15	405295	3818412	Plus	56933-57099
	405353	2811095	Plus	118525-118892
	405358	2341077	Minus	18016-18115
	405421	7243869	Minus	97411-57687
	405426	7243900	Minus	37640-37817
20	405452	7656638	Minus	93876-94275
	405484	5922025	Plus	199214-199579,199572-199520,20062-200495
	405532	1525206	Plus	45160-45647
	405570	2808656	Plus	98208-98331
	405626	4508116	Minus	89275-89384,92450-92629,97091-97279,98546-98666
	405699	4168331	Plus	100727-100859
25	405762	5331535	Plus	165502-161130
	405802	5924004	Minus	27145-26264
	405804	7274891	Minus	122557-123551
	406329	6982072	Minus	607903-608271
30	406429	5284476	Minus	83206-83365,94051-94193
	406502	7711350	Minus	53435-53602

Table 14A lists about 595 genes up-regulated in ovarian cancer compared to normal adult tissues. These were selected from 59600 probesets on the Affymetrix/Exon H10 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 4.0. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 14A: ABOUT 595 UP-REGULATED GENES, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Play: Primerkey

Ex. Accon: Exemplar Accession

UG ID: UniGene ID

Title: UniGene Title

ratio: ratio of tumor vs. normal tissues

	Play	Ex. Accon	UG ID	Title	ratio
45	452838	U65111	Hs.30743	Preferentially expressed antigen in melanoma	70.4
	49817	A023799	Hs.163242	ESTs	62.8
50	432938	TZ7013	Hs.3132	steroidogenic acute regulatory protein	57.8
	421478	A083243	Hs.97258	ESTs	45.7
	415989	A261700	Hs.111128	ESTs	42.7
	418179	X51530	Hs.1145	Wilms tumor 1	36.0
	449034	A624049		gb3s41a05.x1 NC1_CGAP_U81 Homo sapiens cDNA clone	34.0
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	30.5
55	428153	A0513143	Hs.98367	hypothetical protein FLJ22252 similar to SRY-box c	30.1
	435982	A0516336	Hs.5378	spondin 1, (spondin) extracellular matrix protein	29.4
	427865	C01152	Hs.179229	collagen, type X, alpha 1 (Schmid metaphysal chon	27.0
	435084	A560129	Hs.277523	EST	26.2
	435691	C14187	Hs.103538	ESTs	26.2
60	435491	AL109791	Hs.241559	Homo sapiens miRNA full length insert cDNA clone EU	25.1
	416511	A702917	Hs.182962	ESTs	24.8
	448243	A0369771	Hs.77496	ESTs	24.7
	428187	A687303	Hs.286529	ESTs	23.9
	406801	A0451597	Hs.167409	ESTs	21.9
65	413007	M13529	Hs.83169	Medin metalloproteinase 1 (interstitial collagenase	20.6
	403022	A250737	Hs.72472	BMPRII, type II, bone morphogenetic protein receptor, ty	20.6
	422956	BE545072	Hs.122579	ESTs	20.0
	413335	A0513318	Hs.48442	ESTs	19.9
	423739	A0398155	Hs.97600	ESTs	18.9
70	411529	H47233	Hs.30543	ESTs	18.5
	424086	A051010	Hs.102267	lysyl oxidase	17.7
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase 2	17.4
	427356	A0623482	Hs.97849	ESTs	17.4
	407166	R65175		glycyl-400/Ls1 Soars Infant brain 1N8 Homo sapien	17.1
75	407538	AJ404872	Hs.288693	EST	17.1
	427499	AA403084	Hs.289347	ESTs	17.0
	438993	A4828995		integrin, beta 8	16.7
	428654	AK001666	Hs.169595	similar to SAL1.1 (sal (Drosophila)-like	16.5
80	438630	AL390204	Hs.263543	Homo sapiens miRNA full length insert cDNA clone EU	16.5
	421155	H07879	Hs.102267	lysyl oxidase	16.1
	428635	BE395109	Hs.125327	ESTs	15.9
	431989	A0607207	Hs.291089	ESTs	15.9
	422805	AA-436989	Hs.121017	HDA Histone family, member A	15.9
	444783	AK001488	Hs.621180	ESTs	15.8

WO 02/102235

PCT/US02/19297

	424581	M62062	Hs150917	catenin (cadherin-associated protein), alpha 2	15.7
	431917	AF116269	Hs100657	ETS3, Weakly similar to ALL1, HUMAN AL1 SUBF. AM1	15.7
	458325	AW083869	Hs287184	ESTs	15.7
	426876	AF013724	Hs146459	ETS1, human germ cell family, member 1	15.7
5	416209	AC238776	Hs79578	MDM2 (mouse aurist deficient, yeast), homolog-1	15.7
	408660	AA525775	Hs252523	ETS2	15.0
	410247	AF171821	Hs61345	RUS2	15.0
	416730	AA353553	Hs6682	solute carrier family 7, member 11	15.0
	466683	AF001673		gfp1L-ET12-480339-504 ET122 Homo sapiens cDNA, mR	15.0
	413623	AC282721	Hs246673	ETS3	14.8
	437006	AW872527	Hs56761	ETS1	14.7
	456041	AB303305	Hs50081	KIAA1199 protein	14.7
	411110	AF555400	Hs301634	ETS3	14.7
	435775	AA731111	Hs201951	ETS1	14.3
	442311	AF112838	Hs143555	ETS1	14.3
	425238	AB93351	Hs47613	ETS1	14.3
	427350	AF15572	Hs172353	ETS1; HERA (c-erb-B)	14.3
	428227	AC121646	Hs2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	14.3
	433392	U23752	Hs32064	SRY (sex determining region Y-box 1)	13.7
	447033	AF531412	Hs15760	EST - not in UniGene	13.7
	428111	AW056938	Hs10000	homoec box CA	13.7
	452461	H78223	Hs108105	transcription factor	13.7
	451106	BE382701	Hs25960	N-myc	13.7
	416208	AW261168	Hs41295	ETS6	13.7
	428246	BC350412	Hs615262	ETS2	13.7
25	452055	AF174731	Hs263772	ETS1	13.7
	430243	AA553254	Hs191340	ETS1	13.7
	420149	AA255520	Hs88055	ETS6	13.7
	425125	AA446854	Hs271490	ETS1	13.7
	413587	AW302885	Hs117183	ETS1	13.7
	416566	NA_003914	Hs79378	cyclin A1	13.7
	424238	AA559568		glox2603.31 NCL_OGAP_Kid Homo sapiens cDNA clone	13.7
	407170	AW022727	Hs23618	ETS1	13.7
	416681	AC134543	Hs70440	QIP-1 mRNA-binding protein	13.7
	428392	H10233	Hs2265	serotransferrin, neonatodescent protein 1 (762 p	13.7
	411725	W57574	Hs50724	Norie disease (pseudoglycemia)	13.7
	447700	AA201163	Hs177077	ETS1, Weakly similar to 25S(r25.1) fusion g	13.7
	416554	L49054	Hs85195	ETS1, Highly similar to c35(g25.1) fusion g	13.7
	408460	AA054726	Hs285574	short-chain alcohol dehydrogenase family member	13.7
	424735	U51675	Hs152577	ETS1	13.7
	415253	AA548033	Hs138555	ETS1	13.7
	400258	AC232776	Hs61635	STEAP1	13.7
	452056	BE334901	Hs226781	ETS1	13.7
	421451	AA251377	Hs50136	ETS1	13.7
	435456	AW040171	Hs265338	ETS1, Weakly similar to transformation-related pr	13.7
	423715	AF531197	Hs5790	tyr-oxin E1	13.7
	402606	W040AT			13.7
	435654	AA740151	Hs130425	ETS1	13.7
	417472	BE428170	Hs75379	solute carrier family 1 (glut high affinity glut)	13.7
	434539	BE245838	Hs277577	ETS1	13.7
	408562	AA363323	Hs31141	Homo sapiens mRNA for KIAA1555 protein, partial d	13.7
	452030	AL135758	Hs27807	Homo sapiens mRNA; cDNA DKFZ596426.46 (from don	13.7
	423253	BE376564	Hs49136	ETS1	13.7
	NA_000869		Hs212142	serotransferrin (serotransferrin) receptor 3A	13.7
	425363	AA523307	Hs142228	ETS1	13.7
	428427	M66699	Hs105840	TTK protein kinase	13.7
	449433	AF162096	Hs9012	ETS1	13.7
	412723	AA649459	Hs175912	ETS1	13.7
	400250			0	13.7
60	419752	AA245673	Hs152616	ETS1	13.7
	438167	R26363	Hs24298	ETS1	13.7
	434539	AF474078	Hs214450	ETS1	13.7
	429518	AW673666	Hs118358	ETS1	13.7
	400375	AA050647	Hs8850	a disintegrin and metalloprotease domain 12 (mol	13.7
	400375	X07620	Hs2258	Melanopsin (melanopsin 1) (Stronyam2) g	13.7
	420630	ALJ45633	Hs44226	ETS1	13.7
	427558	AA433088	Hs98192	Homo sapiens cDNA FLJ14303.6, clone PLACE2300132	13.7
	451412	AF154683	Hs145958	ETS	13.7
	421285	NA_000212	Hs1363	cyclohexan-P450, subfamily Y10 (xretrod 17-alpha-	13.7
	433656	AF064254	Hs49765	LONG-CHAIN ACYL-CoA SYNTHETASE	13.7
	416836	AA050430	Hs85136	protein coupled receptor 36	13.7
	433447	U21595	Hs3281	neuronal protein 18	13.7
	421818	AW554552	Hs142634	zinc finger protein	13.7
	416241	BE184072	Hs75850	WAS protein family, member 1	13.7
	425462	U05111	Hs165053	chromium sulphate protein complex	13.7
	412805	AC127940	Hs86368	calmagin	13.7
	444170	AW61387	Hs102408	ETS1	13.7
	453616	NA_002462	Hs33846	cyt6a, axonemal, light intermediate polypeptide	13.7
	407371	AC292524	Hs26273	glox111752 Homo sapiens cDNA S.9 and simle	13.7
	440091	AA509336	Hs128612	ETS1	13.7
	407366	AF026842		glo23a sapiens clog33 mRNA, partial sequence,	13.7
	415527	NA061113	Hs72402	ETS1	13.7
	435763	AA576553	Hs22673	glox111752 Homo sapiens cDNA S.9 and simle	13.7
	450480	X52129	Hs25040	zinc finger protein 239	13.7

WO 02/102235

PCT/US02/19297

	419088	A053823	Ha.77466	ESTs	10.0
	453922	AF053396	Ha.36708	binding uninhibited by benzimidazoles 1 (yeast hom	9.9
	422525	AL133940	Ha.183282	Homo sapiens mRNA; cDNA DKF7p056C1021 (from clone	9.8
5	426471	M22440	Ha.170009	transforming growth factor, alpha	9.8
	407881	AW072003	Ha.40968	heparan sulfate (glucosaminase) 3-O-sulfotransferase	9.7
	452291	AF015592	Ha.28853	CDC7 (cell division cycle 7, S. cerevisiae, homolo	9.7
	445337	AJ249671	Ha.12844	EGF-like domain, multiple 5	9.7
	434875	BE623003	Ha.23525	Homo sapiens clone TCCCTA00142 mRNA sequence	9.6
	432992	AW898292	Ha.137206	Homo sapiens mRNA; cDNA DKF7p564H1663 (from clone	9.6
10	412140	AA219681	Ha.73625	RAB6 interacting, kinesin-like (rabinosin)	9.6
	407721	T12735	Ha.33018	dual-specificity tyrosine-(Y)-phosphorylation regn	9.5
	432020	AL130659	Ha.61111	KIAA0307 gene product	9.5
	429782	NM_005754	Ha.220689	Ras-GTPase-activating protein SH3-domain-binding p	9.5
15	424945	A0221919	Ha.173438	hypothetical protein FLJ10582	9.5
	414972	BE625762	Ha.77695	KIAA0008 gene product	9.4
	432262	A443233	Ha.124399	ESTs	9.4
	403381	#(NCCAAT)		0	9.3
	424834	AX001432	Ha.153408	Homo sapiens cDNA FLJ10570 fls, clone NT2RP2003117	9.3
	435509	AA456679	Ha.181915	ESTs	9.2
20	445413	AA151340	Ha.128612	COS-147 protein	9.2
	414063	AL121282	Ha.257786	ESTs	9.2
	421373	AA080229	Ha.167771	ESTs	9.2
	430510	AW162916	Ha.241576	hypothetical protein PRC2577	9.1
25	446989	AA151520	Ha.279525	hypothetical protein PRC2605	9.1
	455987	AJ021956	Ha.49807	gluc2(Gcd4p1) Scores, pregnant, uterus, NHMPU Homo sa	9.1
	414569	AF109298	Ha.118258	Prostate cancer associated protein 1	9.1
	406687	M01126	Ha.272620	pregnancy specific beta-1-glycoprotein 9	9.0
	428470	Y00072	Ha.184672	cell division cycle 2, G1 to S and G2 to M	9.0
	408001	BE296227	Ha.48015	semaphorin/neuropilin kinase 15	9.0
30	431540	A0534271	Ha.57111	Homo sapiens cDNA FLJ13018 fls, clone NT2RP3000685	9.0
	433764	AW753676	Ha.39082	ESTs	9.0
	434636	AA083764	Ha.241334	ESTs	8.9
	451807	WS2654	Ha.27099	DKFZP684J0663 protein	8.8
35	437872	A0302015	Ha.49807	RNA-binding motif protein 7	8.8
	443054	A0745186	Ha.8909	yes-associated protein 65 kDa	8.8
	420092	AA814043	Ha.88045	ESTs	8.8
	420159	A0572400	Ha.593765	ESTs	8.8
	447164	AF026941	Ha.175218	Homo sapiens cigs mRNA, partial sequence	8.8
	451254	A0571016	Ha.172967	ESTs	8.8
40	432677	NM_004482	Ha.278611	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-a	8.7
	450424	AA169860	Ha.18645	ESTs, Weakly similar to perial CDS (C. elegans)	8.7
	400301	A033635	Ha.1657	Eatgrin receptor 1	8.7
	408029	NM_006042	Ha.45384	heparan sulfate (glucosaminase) 3-O-sulfotransferase	8.7
	434891	AA814309	Ha.123593	ESTs	8.7
45	436812	AW298067	Ha.184687	glu3LH-BW0-ajp-g-09-3-UL1 NQL_CGAP, Sub6 Homo s	8.7
	438885	A086558	Ha.184687	ESTs	8.7
	446765	N02290	Ha.220332	EST, Moderately similar to ALU8_HUMAN ALU SUBFAM	8.7
	447342	A119266	Ha.19322	ESTs; Weakly similar to III ALU SUBFAMILY J (WAFN)	8.6
	434424	A0811202	Ha.125365	Homo sapiens cDNA: FLJ23523 fls, clone L0NG05546	8.6
50	430876	A016577	Ha.131693	ESTs	8.6
	437212	A0765021	Ha.201775	ESTs	8.5
	417729	AW153437	Ha.247090	KIAA1573 protein	8.5
	438081	A09546	Ha.289954	ESTs	8.5
	411571	AA122393	Ha.70811	hypothetical protein FLJ20516	8.4
55	432963	A0323707	Ha.134273	ESTs	8.4
	424717	H02754	Ha.152213	winged-type MMTV integration site family, member	8.4
	425734	AF056209	Ha.153396	perylglycine alpha-amidating monooxygenase COOH	8.4
	450505	NM_004572	Ha.25051	pleiophitin 2	8.4
	436211	AK001581	Ha.80951	polymerase (DNA directed), gamma	8.3
60	436395	A083407	Ha.289132	Homo sapiens cDNA FLJ111441 fls, clone HEMBA1001323	8.3
	426695	NM_005401	Ha.159229	protein tyrosine phosphatase, non-receptor type 14	8.2
	438180	AA0806189	Ha.272151	ESTs	8.2
	447268	A0370413	Ha.36363	Homo sapiens cDNA: FLJ22418 fls, clone HRC08590	8.2
	431159	A0303898	Ha.150567	kinesin-like protein 1	8.1
65	400195			0	8.1
	424906	A0566096	Ha.153716	Homo sapiens mRNA for Hmoab33 protein, 3' untranslated	8.1
	438202	AW160287	Ha.22588	ESTs	8.1
	438915	AA280174	Ha.23282	ESTs	8.1
	446776	BE374664	Ha.30057	transporter similar to yeast MDS2	8.1
70	453884	AA355925	Ha.36232	KIAA0186 gene product	8.1
	420757	X78592	Ha.99015	androgen receptor (dihydrotestosterone receptor), t	8.0
	439759	AL350055	Ha.61709	Homo sapiens mRNA full length insert cDNA clone EU	8.0
	453102	NM_007917	Ha.31664	flucized (Drosophila) homolog 10	8.0
	424001	W67083	Ha.137476	KIAA1051 protein	8.0
75	434415	BE177494	Ha.82285	gluR5-HT0596-27/0300 011-C05 HT0596 Homo sapiens c	8.0
	417576	AA339449	Ha.82285	phosphoribosylglycineamide formyltransferase, phosph	7.9
	438966	AW979074	Ha.277252	glu-E5T391164 MAGE resequences, MAGP Homo sapiens c	7.9
	415245	N59560	Ha.277252	ESTs	7.9
	422352	AA766296	Ha.99200	ESTs	7.9
80	425482	AL021918	Ha.158174	zinc finger protein 184 (Kruppel-like)	7.8
	442655	AW027457	Ha.30323	ESTs	7.8
	445657	AW512741	Ha.275675	ESTs	7.8
	450221	AA378102	Ha.24564	cytoskeleton associated protein 2	7.8
	426320	W47595	Ha.163300	transforming growth factor, beta 2	7.8

WO 02/102235

PCT/US02/19297

5	414142	AW363997	Hs.153042	ESTs	7.7
	415170	D16532	Hs.73729	very low density lipoprotein receptor	7.5
	410011	AB030641	Hs.57156	PPTAIRE protein kinase 1	7.6
	436476	AA326108	Hs.53631	ESTs	7.6
	414132	AB01235	Hs.46480	ESTs	7.6
	437789	A951344	Hs.127812	ESTs. Weakly similar to AF141326 1 RNA helicase HD	7.6
	497192	AA351443	Hs.24656	RAD51-interacting protein	7.6
	446328	A962463	Hs.197547	ESTs	7.5
	440238	AW451970	Hs.155644	paired box gene 2	7.5
10	430357	RNOCAT	0		7.5
	403826	AF150777	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	7.5
	418735	HA5795	Hs.44609	ESTs	7.5
	413627	BE182082	Hs.246673	ESTs	7.4
15	446293	AA420213	Hs.146722	ESTs	7.4
	441627	AA547562	Hs.55066	ESTs	7.4
	425465	119564	Hs.1594	protein kinase C; α 1	7.3
	405242	AL091070	Hs.51662	DKFZP434C081 protein	7.3
	450262	AW409872	Hs.271166	ESTs. Moderately similar to ALU7_HUMAN ALU SUBFA	7.3
	440250	AA576176	Hs.134650	ESTs	7.3
20	451659	BE373561	Hs.14248	ESTs. Weakly similar to ALU8_HUMAN ALU SUBFAMIL	7.3
	458961	AJ530223	Hs.14248	gbr-ad0906.r1 Proliferating Erythroid Cells (LCB-2	7.3
	436032	AA150797	Hs.106276	leukemia protein	7.2
	407771	AL138272	Hs.62713	ESTs	7.2
25	435039	AW439321	Hs.133526	ESTs	7.2
	444342	NM_014588	Hs.10987	similar to lysosome-associated membrane glycoprotein	7.2
	407629	AA045064	Hs.29725	Homo sapiens cDNA FLJ13197 fa, clone NT2RP3004451	7.2
	405731	AA125685	Hs.56145	thymosin, beta, identified in neuroblastoma cells	7.2
	4404263	RNOCAT	0		7.1
30	424120	T35079	Hs.292070	ESTs	7.1
	429126	AW172356	Hs.59083	ESTs	7.1
	413573	A073869	Hs.149069	ESTs	7.1
	421464	AA251563	Hs.130096	ESTs	7.0
35	433386	AJ356623	Hs.240770	nuclear cap binding protein subunit 2, 20KD	7.0
	437939	A8560087	0	ESTs; Weakly similar to Gsp-Pol ⁺ polyprotein (M.mus	7.0
	420362	U97374	Hs.57206	huntingtin interacting protein 1	7.0
	444743	AA045646	Hs.11817	nudix (nucleoside diphosphate linked moiety X)-typ	7.0
	415138	C11535	Hs.79545	tissue factor pathway inhibitor 2 TFP2	6.9
	410569	AW162949	Hs.54542	pre-miRNA cleavage factor lam (55KD)	6.9
40	429419	AJ381028	Hs.95923	ESTs	6.9
	405178	BE393548	Hs.50515	kallikrein 5	6.9
	446606	N75217	Hs.287846	ESTs	6.9
	425695	AJ032569	Hs.161700	XAA-133 protein	6.9
	429532	AF157026	Hs.184786	TSP-interacting protein	6.9
	433426	H69126	Hs.133526	ESTs	6.9
45	431322	AW970622	0	gbEST382704 MAGE resequences, MAGK Homo sapiens	6.8
	437960	A866596	Hs.222194	ESTs	6.8
	423344	AL036375	Hs.205602	ESTs. Weakly similar to ubiquitous TPR motif, Y is	6.8
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40KD)	6.8
50	448674	W31178	Hs.154140	ESTs	6.8
	438122	AJ620270	Hs.129337	ESTs	6.7
	440046	AJ037461	Hs.158469	ESTs. Weakly similar to envelope protein (H.sapiens	6.7
	418479	U33845	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanoma, p1	6.7
	407162	N63555	Hs.142634	zinc finger protein	6.7
55	410804	U64620	Hs.66621	Mechado-Joseph disease (spinocerebellar ataxia 3,	6.7
	424639	AJ517494	Hs.131329	ESTs	6.7
	429415	T16971	Hs.269014	ESTs	6.7
	421470	R27456	Hs.1379	sinexin A3	6.7
	445459	AA78629	Hs.156465	ESTs	6.7
60	418203	X54942	Hs.83758	CDC28 protein kinase 2	6.6
	432806	AA655569	Hs.131703	ESTs	6.6
	406234	AA379419	Hs.27206	ESTs	6.6
	438394	BE376623	Hs.27693	OGT-124 protein	6.6
	452057	AB002364	Hs.27618	ADAM-TS3; a disintegrin-like and metalloprotease	6.6
	435745	AA652869	Hs.63308	Homo sapiens HSPC210 mRNA, partial cds	6.5
65	414138	AA52404	Hs.178227	ESTs	6.6
	423248	AA380177	Hs.125945	ribulose-5-phosphate-3-epimerase	6.5
	454018	AW016362	Hs.241652	ESTs	6.5
	452281	T93500	Hs.28792	ESTs	6.5
	424620	AA310143	Hs.151264	kallikrein 7 (chymotrypsin-like serine protease)	6.5
70	452594	AL076405	Hs.29561	solute carrier family 26 (sulfate transporter), me	6.5
	434149	243528	Hs.15574	ESTs. Weakly similar to katanin p60 subunit (H.sapi	6.5
	425776	U26128	Hs.159459	parathyroid hormone receptor 2	6.4
	419577	563308	Hs.93724	SRY (sex determining region Y)-box 5	6.4
	405917	X00760	Hs.54663	leptonin L confase	6.4
75	432666	AW204069	Hs.126250	ESTs. Weakly similar to unnamed protein product (H	6.4
	448706	AW261055	Hs.21814	class II cytokine receptor ZCYTOR7	6.4
	426163	AA847468	0	glucanase2041061 Scores_NFL_T_06C_S1 Homo sapiens cDN	6.4
	413362	AW259447	Hs.71321	Homo sapiens cDNA FLJ12971 fa, clone HEPG250	6.4
	419917	AA320068	Hs.53701	Homo sapiens mRNA, cDNA DKFZp434E232 (trans clone	6.4
80	424163	AA451737	Hs.141456	MAGE-like 2	6.4
	424265	AA049811	Hs.131554	Homo sapiens cDNA FLJ23086 fa, clone LN007061	6.4
	435332	AA654273	Hs.186104	Homo sapiens cDNA FLJ13803 fa, clone THYRO1000187	6.4
	441081	AJ584019	Hs.165006	ESTs. Moderately similar to plakophilin-2b (H.sapi	6.4
	443539	AJ076182	Hs.134074	ESTs	6.4

WO 02/102235

PCT/US02/19297

	443830	A142095	Hs.143273	ESTs	6.4
	452826	H45222	Hs.190112	Homo sapiens cDNA: FLJ23441 fs, clone HS00612	6.4
	416384	AW142095	Hs.251330	ESTs	6.3
	425371	D49441	Hs.155961	mesothelin	6.3
5	429441	AJ224172	Hs.204096	topophilin B (keratoglobulin family member), prostate	6.3
	449048	Z45051	Hs.22920	similar to 598401 (catfish) glucose induced gene	6.3
	437117	AL049256	Hs.122933	ESTs	6.3
	498579	AW027260	Hs.134014	prostate cancer associated protein 6	6.3
	453370	AW075023	Hs.182356	ESTs, Moderately similar to translation initiation	6.3
10	426514	BE16633	Hs.301122	bone morphogenetic protein 7 (osteogenic protein 1	6.3
	415076	NM_000657	Hs.77390	guanylate cyclase 1, soluble, beta 3	6.3
	408155	AB014528	Hs.43193	KIAA0625 gene product	6.2
	452904	AL157581	Hs.30957	Homo sapiens mRNA: cDNA DKFZp454D0626 (from clone	6.2
15	457030	A301740	Hs.173381	ethylogymnificans-like 2	6.2
	435641	AW111194	Hs.120051	ESTs	6.1
	407385	AA610150	Hs.272072	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFA	6.1
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferase	6.1
20	430437	A765801	Hs.163943	Homo sapiens cDNA FLJ13569 fs, clone PLACE1006369	6.1
	428143	AL060990	Hs.301549	Homo sapiens mRNA: cDNA DKFZp454H1172 (from clone	6.1
	415139	AW925842	Hs.46524	ESTs	6.1
	417404	NM_007350	Hs.82101	p/ectoderm homology-like domain, family A, member	6.1
	433527	AW235613	Hs.133020	ESTs	6.1
25	469448	D07730	Hs.57471	ESTs	6.1
	467733	AW674412	Hs.201971	ESTs	6.1
	457979	AA776855	Hs.270942	ESTs	6.1
	427867	L32137	Hs.1584	cartilage oligomeric matrix protein	6.0
	423554	M50516	Hs.1874	glutamine-fructose-6-phosphate transaminase 1	6.0
30	421502	AF111958	Hs.105029	z citric carrier family 34 (proton phosphate), member	6.0
	412733	AA984472	Hs.745654	KIAA0030 protein	6.0
	422095	AA868572	Hs.288966	ceruloplasmin (ferroxidase)	6.0
	443047	AW649748	Hs.295001	ESTs	6.0
	443670	AB67254	Hs.153539	Homo sapiens cDNA FLJ13793 fs, clone THY10100085	6.0
35	437478	AL330172	Hs.118811	ESTs	6.0
	411598	BE336454	Hs.70937	H3 histone family, member K	6.0
	418134	AA397769	Hs.66817	ESTs	6.0
	418845	AA652585	Hs.85237	chromobox homolog 5 (Drosophila HP1 alpha)	6.0
40	452039	A022568	Hs.172510	ESTs	5.9
	410555	U52649	Hs.645111	a disintegrin and metalloproteinase domain 17 (lum	5.9
	412719	AW016610	Hs.129911	ESTs	5.9
	413566	AA373210	Hs.432047	Homo sapiens cDNA FLJ13585 fs, clone PLACE1009150	5.9
	437099	N77793	Hs.484668	ESTs, Highly similar to LMAN1_HUMAN LAMNIN ALPH	5.9
	453431	AF924754	Hs.320923	glycine norep, beta	5.9
	408620	AL120071	Hs.48598	fibronectin leucine rich transmembrane protein 2	5.9
45	417666	AW067903	Hs.82772	"collagen, type XI, alpha 1"	5.9
	420440	NM_002407	Hs.97644	mammaglobin 2	5.9
	432291	AV660546	Hs.238126	CGI-49 protein	5.9
	455547	H(NOCAT)		0	5.9
50	427510	Z47542	Hs.179312	small nuclear RNA activating complex, polypeptide	5.9
	435793	AB037374	Hs.4903	ESTs	5.8
	427975	A353605	Hs.127460	ESTs	5.8
	426949	AA442153	Hs.104744	ESTs, Weakly similar to AF208855 1 BM-013 [H.sapi	5.8
	452693	T79153	Hs.48589	zinc finger protein 228	5.8
	440138	AB033023	Hs.6982	hypothetical protein FLJ10201	5.8
55	421246	AW682982	Hs.303081	ESTs, Highly similar to AF151805 1 CGI-47 protein	5.8
	445424	AB028046	Hs.12486	cortactin SHD domain-binding protein	5.8
	448186	AA282105	Hs.4094	Homo sapiens cDNA FLJ14205 fs, clone NT2P93003264	5.8
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	5.7
	419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fs, clone NT2P92004081	5.7
60	420837	AW987153	Hs.165445	ph-ESTS355C: NCAGE resequences, MAGE-H	5.7
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fs, clone A0CA01954	5.7
	446668	AV660737	Hs.135100	ESTs	5.7
	452971	A873878	Hs.91789	ESTs	5.7
65	426927	AA411637	Hs.30259	ESTs	5.7
	425312	AW16518	Hs.165445	huntingtin interacting protein 2	5.7
	419247	965791	Hs.85764	fragile X mental retardation 1	5.7
	445640	AW096026	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapiens]	5.7
	422938	NM_001810	Hs.1594	centromere protein A (TAD)	5.6
70	417078	AW685721	Hs.301570	ESTs	5.6
	421247	BE391727	Hs.102910	general transcription factor IIR, polypeptide 4 [5	5.6
	407896	D78435	Hs.41154	Zic family member 1 (odd-paired Drosophila homolog	5.6
	436558	A3364997	Hs.7572	ESTs	5.6
	417830	AW604786	Hs.132808	epithelial cell transforming sequence 2 oncogene	5.6
75	428056	NS026	Hs.40747	ESTs	5.6
	433030	A1060400	Hs.143789	ESTs	5.6
	443270	NM_004272	Hs.9192	Home, neuronal immediate early gene, 10	5.5
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	5.5
	411026	U8034	Hs.98583	mitochondrial intermediate peptidase	5.5
	419558	AW953679	Hs.278394	ESTs	5.5
80	427386	AW836261	Hs.177465	amyloid beta (A4) precursor protein (protease acti	5.5
	427961	AW293165	Hs.143194	ESTs	5.5
	404551	H(NOCAT)		0	5.5
	429852	NM_006306	Hs.211602	SMC1 [structural maintenance of chromosomes 1, yea	5.5
	407216	N91773	Hs.102267	lysyl oxidase	5.5

W00102236

PCT/US02/19297

	410658	AW105231	Hs.192035	ESTs	5.5
	412930	M66153	Hs.79618	RAB11A, member RAS oncogene family	5.5
	414315	Z24578		glnh585002: STRATAGENE Human skeletal muscle cD	5.5
5	42378	C0596	Hs.181022	CG4-07 protein	5.5
	431041	AA490967	Hs.105276	ESTs	5.5
	441645	A122279	Hs.201555	ESTs	5.5
	428071	A712948	Hs.102339	transcription factor ESE-38	5.4
	435406	AW050723	Hs.123546	ESTs	5.4
10	429181	AW979104	Hs.294039	ESTs	5.4
	410809	AW881861	Hs.53112	ESTs, Weakly similar to ALUR_HUMAN ALU SUBFAMIL	5.4
	424345	AK031380	Hs.145479	Homo sapiens cDNA FLJ10518 fs, clone NT2RF2000814	5.4
	451996	AW540201	Hs.246510	ESTs	5.4
	449318	AW265021	Hs.108798	ESTs, Weakly similar to zesto [D.melanogaster]	5.4
	441433	AA533609	Hs.42746	ESTs	5.4
15	445496	B652841	Hs.38489	ESTs	5.4
	410153	BE011286	Hs.15830	Homo sapiens cDNA FLJ12801 fs, clone NT2RF4002571	5.4
	420811	BE077156	Hs.177537	ESTs	5.4
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein 6	5.4
20	453161	AA629606	Hs.81656	ESTs	5.4
	419948	AB041035	Hs.93547	NADPH oxidase 4	5.3
	427710	A793600	Hs.25933	ESTs	5.3
	453667	AB29393	Hs.106196	HSPC037 protein	5.3
	422634	NM_016010	Hs.116821	CG4-62 protein	5.3
25	444478	NG7318	Hs.240	M-phase phosphoprotein 1	5.3
	426902	A447493	Hs.9450	glnzv5603.1 Soares, JHMHF4_S1 Homo sapiens cDNA c	5.3
	443406	NM_003428	Hs.9450	zinc finger protein 64 (HPF2)	5.3
	451177	A669716	Hs.13034	ESTs	5.3
	406289	A745325	Hs.271923	ESTs, Moderately similar to !!! ALU SUBFAMILY SB2	5.3
30	435957	AA564229	Hs.114062	ESTs	5.3
	423688	AA329796	Hs.1098	DNFZP43J1813 protein	5.3
	443543	AW507741	Hs.21330	Homo sapiens mRNA, cDNA, DKFZp596P1124 (from clone	5.3
	427660	A741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fs, clone CAE06954	5.3
	433045	AQ000352	Hs.238981	hypothetical protein FLJ28075	5.3
35	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALUR_HUMAN ALU SUBFA	5.3
	446532	W74653	Hs.271933	ESTs	5.3
	452922	X56599	Hs.298617	Homo sapiens cDNA: FLJ27621 fs, clone HSD50568	5.3
	437641	AA811462	Hs.291911	ESTs	5.2
	415379	AA216940	Hs.137616	Idyllic-like 1	5.2
40	416530	U8291	Hs.70381	kalirin-6 (neurosin, zyma)	5.2
	433589	AA866530	Hs.189912	ESTs	5.2
	406143	AW002080	Hs.138965	ESTs	5.2
	410303	AA324687	Hs.21861	Homo sapiens cDNA: FLJ12900 fs, clone NT2RF2004321	5.2
	413384	NM_000401	Hs.76334	ovastoxin (multiple)	5.2
45	424693	AA164366	Hs.151973	hypothetical protein FLJ10378	5.2
	431229	AA496479		glnzv3705.1 Soares ovary tumor NNH07 Homo sapien	5.2
	433377	A762713	Hs.43846	ESTs	5.2
	445336	AK001676	Hs.12457	hypothetical protein FLJ10814	5.2
	406387	#NOCAT		0	5.2
50	442500	AB19068	Hs.209122	ESTs	5.2
	490101	AB649899	Hs.24385	Human hbc547 mRNA sequence	5.2
	419140	A932847	Hs.215725	ESTs	5.2
	411078	A222002	Hs.182864	ESTs, Weakly similar to 25 kDa trypan inhibitor [5.2
	423020	AA330092	Hs.1806	replicase protein A3 (14kD)	5.2
55	427061	AB032971	Hs.173302	KAA1145 protein	5.2
	439042	AW979172		glnEST91232 MAGE resequences, MAGP Homo sapiens c	5.2
	452930	AW195235	Hs.194937	ESTs	5.1
	417781	AW865330	Hs.111471	ESTs	5.1
	433277	W27266	Hs.161010	ESTs	5.1
60	447935	AW591623	Hs.164129	ESTs	5.1
	434401	AB54131	Hs.71119	Potative prostate cancer tumor suppressor	5.1
	427496	A62278	Hs.170144	Homo sapiens mRNA, cDNA DKFZp567J125 (from clone D	5.1
	419849	AW474547	Hs.53565	ESTs, Weakly similar to B0481.1 [Calegari]	5.1
	428093	AW594506	Hs.104830	ESTs	5.1
65	403621	AB70672	Hs.46638	chromosome 11 open reading frame 8, fetal brain (5.1
	453306	AA294531	Hs.11325	ESTs	5.1
	419552	BE537037	Hs.273294	hypothetical protein FLJ20069	5.1
	436787	AA806654	Hs.192786	ESTs	5.1
	446577	AB040333	Hs.15420	KAA1500 protein	5.1
70	437287	AW511443	Hs.285110	ESTs	5.0
	419423	D26468	Hs.93315	KAA40037 protein	5.0
	404939			0	5.0
	439052	AF065917	Hs.37921	ESTs	5.0
	447020	T27308	Hs.16566	hypothetical protein FLJ11046	5.0
75	453878	AW694440	Hs.192026	ESTs	5.0
	410824	AW6954813	Hs.33264	ESTs	5.0
	427701	AA411101	Hs.221750	ESTs	5.0
	424602	AK002055	Hs.301129	Homo sapiens clone Z3850 mRNA sequence	5.0
	430044	AA464510	Hs.152812	EST cluster (not in UniGene)	5.0
	417423	AA191241	Hs.111184	ESTs	5.0
80	421477	AB04743	Hs.104650	hypothetical protein FLJ10292	5.0
	433364	AB021992	Hs.124244	ESTs	5.0
	434160	BE591196	Hs.114275	ESTs	5.0
	443565	N71710	Hs.21395	ESTs, Moderately similar to GNPL_HUMAN GLUCOSAM	5.0
	416198	BE7332	Hs.95996	ESTs	4.9

WO 02/102235

PCT/US02/19297

	435358	AB011540	Hs.4930	low density lipoprotein receptor-related protein 4	4.5
	457465	AW0301344	Hs.195969	ESTs	4.5
	418845	AUS2061	Hs.193465	ESTs	4.5
5	408321	AW005882	Hs.44305	coriastin	4.5
	447489	AW262630	Hs.147674	KIAA1621 protein	4.5
	424613	BE358564	Hs.146894	mitochondrial translocational initiation factor 2	4.5
	432731	R31178	Hs.257520	fibronectin 1	4.5
	444275	BE514434	Hs.20530	synaptic Ras GTPase activating protein 1 (homolog	4.5
10	430371	D87466	Hs.240112	KIAA0276 protein	4.5
	443683	AW004954	Hs.223230	Homo sapiens cDNA: FLJ23537 fls, clone UNG07690	4.5
	407259	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fls, clone MAMMA100042	4.4
	445141	AJVT1596	Hs.191931	ESTs	4.4
	434999	AA634367	Hs.149426	Homo sapiens cDNA FLJ11980 fls, clone HEMEB10101304	4.4
15	417718	T66540	Hs.193931	ESTs	4.4
	436454	AJ016176	Hs.259783	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.4
	427523	AJ027143	Hs.175665	mini-chromosome maintenance deficient (S. cerevisiae	4.4
	405902	AJ735283	Hs.172608	ESTs	4.4
	416241	NE2639	Hs.32693	ESTs	4.4
20	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA POLYMER	4.4
	444234	AW117264	Hs.126552	ESTs	4.4
	445743	AB032962	Hs.21056	KIAA1136 protein	4.4
	451339	N73222	Hs.21738	KIAA1008 protein	4.4
	453331	AJ240665	Hs.5095	ESTs	4.4
	454036	AA321476	Hs.53590	ESTs, Weakly similar to unnamed protein product [H	4.4
25	445133	AJ72157	Hs.23765	folate receptor 1 (adult	4.4
	429597	NM_003916	Hs.2442	a disintegrin and metalloproteinase domain 9 (melt	4.4
	435270	AW853540	Hs.50598	ESTs	4.4
	409459	D56407	Hs.54431	low density lipoprotein receptor-related protein 8	4.4
30	431705	A985139	Hs.103973	ESTs	4.4
	433905	AJF7816	Hs.43355	ESTs	4.4
	437953	BE139650	Hs.121663	ESTs	4.4
	441423	AJ763299	Hs.126377	ESTs	4.4
	428976	AG328577	Hs.225574	KIAA1054 protein	4.3
	446770	AW662039	Hs.154985	ESTs, Weakly similar to AF137395 1 plasminogen [H.	4.3
35	412078	X55695	Hs.73146	paired box gene 8	4.3
	422093	AF151582	Hs.111449	OGH-94 protein	4.3
	421233	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selenium	4.3
	446380	AL055414	Hs.21058	hypothetical protein	4.3
40	453820	AW043507	Hs.170137	ESTs	4.3
	449722	BE250074	Hs.23960	cydin B1	4.3
	436679	AJ127483	Hs.120451	ESTs, Weakly similar to unnamed protein product [H	4.3
	431592	R69516	Hs.239371	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.3
	427313	AJ020144	Hs.274449	Homo sapiens cDNA FLJ28137 fls, clone COL07137	4.3
45	415626	AW000692	Hs.93756	DKFZP560D223 protein	4.3
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.3
	401644	PIHOCAT	Hs.58160	highly expressed in cancer, rich in leucine heptad	4.3
	410944	BE56742	Hs.75823	nuclear GTPase	4.3
	413775	AW409834	Hs.168391	ESTs	4.3
50	424256	AJ631974	Hs.168391	ESTs	4.3
	431118	BE264801	Hs.265052	carbonic anhydrase VIII	4.3
	432201	AJ530613	Hs.136657	TKPRSS3a mRNA for serine protease (ECHOS1) (TAGD-1	4.3
	451073	AJ753505	Hs.200903	ESTs	4.3
	451592	AJ054416	Hs.213397	ESTs	4.3
	452453	AJ02519	Hs.213397	gbcw-8T009-101198-051 BT009 Homo sapiens cDNA, m	4.3
55	441020	W75283	Hs.35652	ESTs	4.2
	439024	R5666	Hs.35658	ESTs	4.2
	453619	H37643	Hs.33922	H.sapiens novel gene from PAC 117P20, chromosome 1	4.2
	453459	BE047032	Hs.257789	ESTs	4.2
	403427	AW194270	Hs.177236	gbcw66at12.21 NCL_CGAP_GCB1 Homo sapiens cDNA cto	4.2
60	419311	AA068591	Hs.153702	Homo sapiens cDNA FLJ11752 fls, clone HEMUA1005582	4.2
	425460	D79721	Hs.265165	ESTs	4.2
	444540	AB939227	Hs.31052	hypothetical protein FLJ10525	4.2
	452943	BE247449	Hs.235932	ESTs	4.2
65	417847	AJ521559	Hs.285312	Homo sapiens cDNA: FLJ22316 fls, clone HRC05262	4.2
	428556	AA436735	Hs.153171	Homo sapiens cDNA: FLJ22002 fls, clone HEP06638	4.2
	423679	AA431755	Hs.153171	gbcw80003.31 Soares_test5_NHT Homo sapiens cDNA	4.2
	441006	AW605267	Hs.7627	OGI-80 protein	4.2
	436209	AW650417	Hs.254020	ESTs, Moderately similar to unnamed protein produc	4.2
70	446936	H19207	Hs.47314	ESTs	4.2
	406076	AL390179	Hs.137071	Homo sapiens mRNA: cDNA DKFZp547P134 (from clone	4.2
	428319	AL135623	Hs.193914	KIAA0675 gene product	4.2
	406671	AA129547	Hs.235754	mid proto-oncogene (hepatocytoc growth factor recip	4.2
75	415432	MA1456	Hs.581152	insulin-like growth factor 1 (somatomedin C)	4.2
	417043	AJ039775	Hs.55455	geranylgeranyl diphosphate synthase 1	4.2
	431750	AA614086	Hs.253705	ESTs	4.2
	439314	AA382413	Hs.178144	ESTs	4.2
	446552	AJ533590	Hs.946112	ESTs	4.2
	444954	AJ652382	Hs.59592	ESTs	4.2
80	455700	BE059115	Hs.213397	gbcw1-8T0088-061239-060-g07 BT0388 Homo sapiens c	4.2
	409073	AA063459	Hs.27379	gbcw7a07.s1 Soares_pineal_gland_N3HPG Homo sapie	4.1
	433329	AJ375499	Hs.27379	ESTs	4.1
	415457	AW031710	Hs.72969	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMIL	4.1
	444381	BE387335	Hs.283713	ESTs	4.1

WO 02/102235

PCT/US02/19297

	451024	AA442176	gbcw3306.1	Source: Jctal, Jctus, Jct2H8, Jct Homo sa	4.1
	451539	AT73381	Ha.72472	BMFPL-1c: Bone morphogenetic protein receptor, ty	4.1
	421515	Y11339	Ha.105352	GalNAc alpha-2, 6-sialyltransferase 1, long form	4.1
5	420736	AW63022	Ha.82204	ESTs	4.1
	453293	AA382287	Ha.10653	ESTs	4.1
	403564	AA046857	Ha.54943	tachyline cactus 1 (traf) homolog	4.1
	418378	AW952081	Ha.154637	gb:EST374154 MAGE resequences, MAGG Homo sapiens	4.1
	429628	H09604	Ha.13268	ESTs	4.1
	439635	AA477288	Ha.94801	Homo sapiens cDNA: FLJ22729 8b, clone HSI15605	4.1
	440452	AA05135	Ha.55150	ESTs, Weakly similar to CAPP, HUMAN CALYPTROPHOSIN	4.1
	443655	AW024069	Ha.112759	ESTs, Weakly similar to AF126780 1 retinal short-e	4.1
	448816	AB033052	Ha.22151	KIAA1226 protein	4.1
	452795	AW935255	Ha.18878	hypothetical protein FLJ21620	4.1
	443171	BE281128	Ha.9030	TOR1D1	4.1
	423522	U53639	Ha.154637	protein kinase; DNA-activated; catalytic polypepti	4.1
	427177	H88362	Ha.180591	ESTs, Weakly similar to R06F6.5b [C.elegans]	4.1
	414747	U30872	Ha.77204	centromere protein F (350x400kD, mitosis)	4.1
	417300	AI765227	Ha.55610	solute carrier family 30 (zinc transporter), membe	4.1
	417329	BE269854	Ha.82345	Mitline (mouse growth-promoting factor 2)	4.1
	446105	AW931433	Ha.170675	ESTs, Weakly similar to TMS2_HUMAN TRANSMEMBR	4.1
	419131	AA406293	Ha.301622	ESTs	4.1
	406348	RI0NCAT	0	0	4.1
	419750	AL079741	Ha.183114	Homo sapiens cDNA FLJ14236 5b, clone NT29P4000515	4.1
	419790	U79259	Ha.83201	glyoxal 3-phosphate dehydrogenase 2 (mitochondria	4.1
25	420908	AL049974	Ha.100261	Homo sapiens mRNA: cDNA DKFZ5546222 (from clone	4.1
	421039	NM_003178	Ha.101299	cutlin 5	4.1
	426890	AA383167	Ha.41264	ESTs	4.1
	428571	HA_106533	Ha.22291	Probe nt7377 (polycystic kidney disease, autosomal	4.1
	452834	U536627	Ha.105685	ESTs	4.1
30	428771	AB026892	Ha.193143	KIAA1069 protein	4.1
	437949	U78519	Ha.41654	ESTs	4.1
	456558	AL050078	Ha.25159	Homo sapiens cDNA FLJ10784 5b, clone NT29P4000448	4.1
	424981	NM_005413	Ha.139100	ribonuclease P (30kD)	4.1
	418375	NM_003081	Ha.84399	synaptonemal-associated protein, 29kD	4.1
35	447204	AI366881	Ha.157897	ESTs, Moderately similar to ALUC_HUMAN !!! ALU CL	4.1
	407910	AA450274	Ha.41296	fibronectin leucine rich transmembrane protein 3	4.1
	412314	AA426247	Ha.296989	heat shock factor binding protein 1	4.1
	436291	BE568452	Ha.5101	ESTs; Highly similar to protein regulating cytokin	4.1
	450554	AL245587	Ha.25275	Kruppel-type zinc finger protein	4.1
40	426991	AK001536	Ha.285903	Homo sapiens cDNA FLJ12852 5b, clone NT29P2003445	4.1
	406935	AA702370	Ha.225440	Homo sapiens clone 24681 mRNA sequence	4.1
	410784	AW963201	Ha.154637	gbcLJ10007-070500-050-ES6 UMO1077 Homo sapiens c	4.1
	413374	NM_001034	Ha.75319	ribonucleotide reductase M2 polypeptide	4.1
	413425	F20956	gbcHSPD05390 FMS Homo sapiens cDNA clone 032-X4-1	4.1	
45	417655	AA780791	Ha.14014	ESTs, Weakly similar to KIAA0937 protein (Haplin	4.1
	424783	AA913909	Ha.153068	TATA box binding protein (TBP)-associated factor,	4.1
	425024	R39235	Ha.12407	ESTs	4.1
	445941	AD267371	Ha.172636	ESTs	4.1
50	448595	AB014544	Ha.21572	KIAA0644 gene product	4.1
	453448	AL036710	Ha.208527	ESTs	4.1
	458944	N53227	Ha.98403	ESTs	4.1
	400284			Estrogen receptor 1	4.1
	441134	V29092	Ha.7678	cellular retinoic acid-binding protein 1	4.1
55	408796	AA688292	Ha.118553	ESTs	4.1
	408296	AL117452	Ha.44155	DNF2P586G1517 protein	4.1
	438913	A380429	Ha.172445	ESTs	4.1
	402408		0	0	4.1
	411630	U42349	Ha.71119	Pulvative prostate cancer tumor suppressor	4.1
	420701	K93960	Ha.288467	Homo sapiens cDNA FLJ12280 5b, clone MAABAA100174	4.1
60	429780	AL102688		gb:homo sapiens mRNA full length insert cDNA clone	4.1
	418301	AW976201	Ha.187616	ESTs	4.1
	420077	AW512260	Ha.87767	ESTs	4.1
	420572	AB087783	Ha.170623	hypothetical protein FLJ11183	4.1
	403721		0	0	4.1
65	411945	AL033527	Ha.92137	v-myc avian myelocytomatous viral oncogene homolo	4.1
	408684	R61377	Ha.12727	hypothetical protein FLJ21610	4.1
	414369	AA157291	Ha.72163	ESTs	4.1
	427860	RS0393	Ha.278436	KIAA1474 protein	4.1
	451050	AW937420	Ha.59662	ESTs	4.1

TABLE 148:

Key: Unique Eas probe/identifer number

CAT number: Gene cluster number

Accession: Genbank accession numbers

75	Key	CAT Number	Accession
	469373	109851_1	AA053458 AA053018 AA44822
	410784	1221005_1	AW903201 BE079700 BE062540
	411560	124043_1	AW851186 AW996967 BE143456
80	413425	136885_1	F20956 AA129374 AA133740 AW819878
	414315	143512_1	Z24978 AA494036 FL3654 AA040404 AA143127
	418378	174656_1	AW903201 AA218826 AA384237
	418804	179138_1	AA080632 AB197245 AT071732 AA228406
	419311	183793_1	AA680591 AW974261 AA236240 AT077451 AA631399 AW974262

PCT/US02/19297

30 TABLE 14C
Play: Unique number corresponding to an Eos protein
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al" refers to the publication entitled "The DNA sequence of
human chromosome 22" Dunham, et al. (1999) Nature 402:489-495
35 Strand: Indicates DNA strand from which exons were predicted
Nt position: indicates nucleotide positions of predicted exons

55 Table 15A lists about 499 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 14A, except that the ratio was greater than or equal to 3.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g., Ig, Fn3, eaf, 7tm domains). Predicted protein domains are noted.

TABLE 15A: ABOUT 499 UP-REGULATED GENES ENCODING EXTRACELLULAR/CELL SURFACE PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

204

WO 02/02235

PCT/US02/19297

	413623	AA825721	Hs.246073	ESTs	TM	14.8
	447350	AI375872	Hs.172634	ESTs, HER4 (c-erb-B4)	SS,TM,Furin-the,kinase	14.2
	425227	AA321549	Hs.2249	INTS1/FRAN-GAMMA INDUCED PRO	IL8	11.5
	452461	N78223	Hs.108106	transcription factor	G8a,PHD	13.7
5	451106	BF382701	Hs.25890	N-myc	Myc_N_term	13.6
	416208	AW291168	Hs.41295	ESTs	TM	13.5
	452249	BF394412	Hs.61252	ESTs	TM	13.4
	415586	NM_003514	Hs.75378	cyclin A1	homobox	12.8
	416661	AA634543	Hs.75440	IGF-II mRNA-binding protein 3	cyclin	12.6
10	431725	X85724	Hs.2839	Novle disease (pseudotumoral)	SS,Cys_knot	12.3
	458027	L49054	Hs.85195	ESTs, Highly similar to K3.5(g25.1,p34) f	TM	12.2
	409460	AA064726	Hs.285374	ESTs	TM	12.2
	415263	AA940033	Hs.130853	ESTs	histone	11.9
	400298	AA032279	Hs.61635	STEAP1	TM	11.8
15	421451	AW291377	Hs.50831	ESTs	TM	11.8
	443715	AI653167	Hs.5700	cyclin E1	cyclin	11.5
	413472	BC242870	Hs.75379	solid tumor family 1 (gial high affinity gl	TM,SDF	11.5
	410102	AW246508	Hs.279727	ESTs	SS	11.4
	408562	AA436323	Hs.31141	Homo sapiens mRNA for KIAA1568 prote	TM	11.3
20	442353	BE379594	Hs.49136	ESTs	TM	11.2
	427344	NM_000869	Hs.2142	S-hydroxytryptamine (serotonin) receptor 3	TM,neur_chan	11.2
	453160	AI263307	Hs.146228	ESTs	histone	11.2
	412723	AA648459	Hs.179912	ESTs	TM	11.1
	402020			0	HEB_deacetyl-F105	11.1
25	431187	R28363	Hs.24286	ESTs	7m_1	11.1
	434539	AW1748078	Hs.214410	ESTs	TM	10.9
	450375	AA090547	Hs.8650	a disintegrin and metalloproteinase dom	TM	10.8
	400289	X07620	Hs.2258	Matrix Metalloproteinase 10 (Stromelysin 2	SS,hemopexin	10.0
	446142	AF54693	Hs.145968	ESTs	Carbonyl_C_term	10.7
30	421265	NM_000102	Hs.1393	cyclochrome P450, subfamily XVII (steroid	TM,p450	10.6
	433496	AF064264	Hs.49785	VERY-LOW-CHAIN ACYL-CoA SYNTH	SS,TM	10.6
	416506	AA084248	Hs.85339	G protein-coupled receptor 39	TM	10.5
	433447	U29185	Hs.3281	neuronal pentraxin 1	SS	10.4
	414245	BE148072	Hs.75550	WAS protein family, member 1	TM	10.3
35	426482	U59111	Hs.169993	dermatan sulphate proteoglycan 3	SS,LRNP	10.3
	418601	AA279430	Hs.86368	calmagin	SS	10.3
	415227	AW621113	Hs.72402	ESTs	TM	10.2
	409259	AA575963	Hs.23872	Homo sapiens cDNA FLJ13362 fs, clone O	TM	10.1
	425471	AC2440	Hs.170009	transforming growth factor, alpha	SS,EGF	9.8
40	407851	AW072003	Hs.40968	heparan sulfate (glucosamin) 3-O-sulfotran	SS	9.7
	445537	AJ245871	Hs.12844	EGF-the-domain; multiple 6	SS,EGF	9.7
	414972	BE263762	Hs.77695	KIAA0008 gene product	TM	9.4
	433509	AA586979	Hs.181915	ESTs	TM	9.3
45	445413	AA151342	Hs.12677	CSH-147 protein	UPF0089	9.2
	446999	AA151520	Hs.279525	hypothetical protein PRO2605	TM	9.1
	414569	AF109296	Hs.116258	Prostate cancer associated protein 1	TM	9.1
	409687	AB11126	Hs.272520	pregnancy specific beta-1-glycoprotein 9	TM	9.0
	409806	BE296227	Hs.46915	serumalbumin kinase 15	phos,TM	9.0
	451807	W52654	Hs.27099	DKFZP654J0863 protein	TM	8.8
50	420159	AI572490	Hs.99785	ESTs	TM	8.8
	432677	NM_004462	Hs.278611	UDP-N-acetyl-alpha-D-glucosamine poly	TM,Ricin_B_lectin	8.7
	406829	NM_005042	Hs.43384	heparan sulfate (glucosamine) 3-O-sulfotran	TM	8.7
	436865	AB65555	Hs.194987	ESTs	TM	8.7
	447342	AJ199265	Hs.19322	ESTs, Weakly similar to III ALU SUBFAM	TM	8.6
55	437212	AJ765021	Hs.210776	ESTs	UDP-GT	8.5
	424717	AB37554	Hs.152213	winged-type MMTV integration site fami	TM	8.4
	465055	NM_004572	Hs.25051	plakophilin 2	TM	8.4
	436396	AB63407	Hs.299112	Homo sapiens cDNA FLJ11441 fs, clone H	wnt	8.3
	425695	NM_005401	Hs.195238	H protein tyrosine phosphatase, non-receptor	Y_phosphatase	8.3
60	447286	AG704113	Hs.36563	Homo sapiens cDNA FLJ22418 fs, clone O	Ribosomal_S8	8.2
	400155			0	TM	8.1
	424908	AI566086	Hs.153716	Homo sapiens mRNA for Hmnb33 protein,	TM	8.1
	438202	AW169287	Hs.22588	ESTs	TM	8.1
	439763	AI350565	Hs.87709	Homo sapiens mRNA full length insert cDN	TM	8.0
65	453102	AA1007197	Hs.31654	frizzled (Drosophila) homolog 10	TM,Fz,Frizzled	8.0
	424001	W67893	Hs.137476	KIAA1051 protein	TM	8.0
	442656	AW027457	Hs.30323	ESTs	TM	7.8
	446657	AW612441	Hs.279675	ESTs	7m_1	7.8
	462620	W17635	Hs.169300	transforming growth factor, beta 2	SS,TGF-beta	7.6
70	412170	O16532	Hs.73729	very low density lipoprotein receptor	TM,LDL_recept_Lb,EGF	7.6
	436476	AA326108	Hs.53631	ESTs	TM	7.6
	414132	AB801235	Hs.48480	ESTs	TM	7.6
	437789	AB581344	Hs.127812	ESTs, Weakly similar to AF141326 1 RMA	TM	7.6
	450192	AA323143	Hs.24596	RAO51 interacting protein	TM	7.5
75	408826	BE216077	Hs.48376	Homo sapiens clone HE-2 mRNA sequence	TM	7.5
	413627	BE182082	Hs.246973	ESTs	TM	7.4
	446293	AA202113	Hs.145722	ESTs	LNUhomobox	7.4
	469242	AI180170	Hs.51692	DKFZP43C091 protein	TM,7m_1	7.3
	450262	AW426872	Hs.271166	ESTs, Moderately similar to ALU7_HUMA	TM	7.3
	451659	BE379701	Hs.14248	ESTs, Weakly similar to ALU8_HUMAN A	TM	7.3
	444342	NM_014398	Hs.10987	similar to lysosome-associated membrane g	TM	7.2
80	429126	AW172356	Hs.59063	ESTs	7m_1	7.1
	421464	AA221553	Hs.190088	ESTs	TM	7.0
	420362	U79734	Hs.57206	huntingtin interacting protein 1	TM	7.0

WO 02/102235

PCT/US02/19297

	44743	AA045648	Hs.11817	radix (nucleoside diphosphate linked moi	TM	7.0
	415138	C19366	Hs.18045	threonine factor pathway inhibitor 2 TFP2	Kunitz, BPTI,G-gamma	6.9
	424418	A5381028	Hs.30283	AAA	EST	6.9
5	409178	BE363948	Hs.50915	kallistatin 5	SS,hypox	6.9
	425905	AB032359	Hs.161700	KIAA1133 protein	TM	6.9
	428532	AF151326	Hs.184766	TBP-interacting protein	TM	6.9
	433426	H69126	Hs.133525	ESTs	TM	6.9
	448674	W31178	Hs.154140	ESTs	TM	6.5
	432415	T16971	Hs.289014	ESTs	TM	6.7
10	418203	X54942	Hs.83758	CDC28 protein kinase 2	TM	6.6
	435394	BE373623	Hs.27653	CGI-124 protein	pro_lactamase	6.6
	420297	AB000284	Hs.27516	ADAMTS-1, a disintegrin-like and metal	Reprolysin	6.6
	453745	AA552989	Hs.63506	Homo sapiens HSPC316 mRNA, partial of	TGFL_propeptide	6.6
	432448	AA380177	Hs.126545	ribulose-5-phosphate-3-epimerase	lhamerit	6.5
15	452281	T33500	Hs.26732	ESTs	TGF-beta	6.5
	424620	AA101043	Hs.115554	kallistatin 7 (thymolytic); stratum corneum	SS,hypox	6.5
	452594	AL076405	Hs.25981	solute carrier family 26 (sulfate transporter)	TM,Sulfate_transp	6.5
	431449	Z43629	Hs.119574	ESTs, Weakly similar to katanin p60 subun	kinase,fm3	6.5
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	TM,Tm_2	6.4
20	405517	X30160	Hs.54666	toprofin 1, centric	T_topophase	6.4
	432666	AW204069	Hs.128550	ESTs, Weakly similar to untransmem protein p	TM	6.4
	445706	AW261095	Hs.21814	class II cytokine receptor ZCYTOR7	SS	6.4
	413582	AW259647	Hs.71331	Homo sapiens cDNA: FLJ121971 its, clone	TM	6.4
	424133	AA451737	Hs.161498	MAZE-like 2	TM	6.4
25	411081	AA504019	Hs.169006	ESTs, Moderately similar to plakophilin 2b	PAX	6.4
	433539	AI078182	Hs.134074	ESTs	TM	6.4
	415384	AW145266	Hs.25130	ESTs	TM	6.3
	423371	D49441	Hs.155981	mesothelin	SS	6.3
	449048	Z45051	Hs.22620	similar to S69401 (cattle) glucose induced g	SS	6.3
30	437117	AL048256	Hs.122583	ESTs	ABC_3	6.3
	453370	AI470523	Hs.182396	ESTs, Moderately similar to translation init	ABC_tran	6.3
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic p	SS,TGF-beta	6.3
	428204	AL157501	Hs.30567	Homo sapiens mRNA: cDNA DKFZp434E	TM	6.2
	427030	A301740	Hs.173351	dihydropyrimidinase-like 2	TM	6.2
35	436281	AW411194	Hs.120051	ESTs	TM	6.1
	415139	AW575942	Hs.48524	ESTs	TM	6.1
	449448	D60730	Hs.67471	ESTs	TM	6.1
	457879	AA776655	Hs.270842	ESTs	TM	6.1
40	422667	L32157	Hs.1584	cartilage oligomeric matrix protein	SS,EGF,isp_3	6.0
	421502	AF111556	Hs.105039	solute carrier family 34 (podium phosphate)	TM	6.0
	412733	AA984472	Hs.74554	KIAA0390 protein	C2	6.0
	422085	AB958172	Hs.289996	ceratoplasmin (keratoderm)	SS	6.0
	418545	AA522265	Hs.86232	chromobox homolog 5 (Drosophila HP1 alp	Chromo_shadow	6.0
45	410555	U92649	Hs.84311	a disintegrin and metalloproteinase domain	TM,disintegrin,Reprolysin	5.9
	437099	N77793	Hs.46659	ESTs, Highly similar to LMA1_HUMAN L	laminin_EGF	5.9
	453431	AF094754	Hs.32973	glycine receptor, beta	TM,neur_chan	5.9
	417896	AF087903	Hs.52772	collagen, type XI, alpha 1*	TSPN,Collagen,COLFI	5.9
	430291	AF060346	Hs.238126	CGI-48 protein	TM	5.9
50	405547	#(NCCAT)	0		TM,ABC_membrane	5.9
	435793	AB037734	Hs.4993	ESTs	TM	5.8
	440135	AB035023	Hs.6962	hypothetical protein FLJ10201	TM	5.8
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	SS,Collagen,TSPN	5.7
	419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 its, clone N	TM	5.7
	452971	AI873878	Hs.91789	ESTs	TM	5.7
55	428527	AA441837	Hs.50250	ESTs	TM	5.7
	415247	985761	Hs.85764	fragile X mental retardation 1	TM	5.7
	445560	AB969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sap	TM	5.7
	447078	AW865727	Hs.301570	ESTs	kazal	5.6
60	421247	BE391727	Hs.102910	general transcription factor IIB, polypepid	TM	5.6
	420300	AB989400	Hs.143789	ESTs	SS	5.6
	443270	NM_004272	Hs.9192	Homes, neuronal immediate early gene, IB	TM	5.6
	411096	U08034	Hs.86953	mitochondrial intermembrane peptidase	Peptidase_M3	5.5
	419558	AW653679	Hs.278394	ESTs	SS	5.5
65	427386	AW586261	Hs.174746	amyloid beta1 (A4) precursor protein (protes	TM	5.5
	427591	AW231165	Hs.140134	ESTs	TM	5.5
	407216	N19173	Hs.102267	lysyl oxidase	TM	5.5
	413930	M66153	Hs.75619	RAB11A, member RAS oncogene family	ras,TM	5.5
	414315	Z24878	Hs.201655	gbr3565D052 STRATAGENE Human sk	TM	5.5
70	411645	A222279	Hs.105798	ESTs	TM	5.5
	448319	AW256021	Hs.42146	ESTs, Weakly similar to zosin [D.melanoga	TM	5.4
	441433	AA933809	Hs.38489	ESTs	TM	5.4
	445495	BE622641	Hs.38489	ESTs	L_LWEQUENTH	5.4
	410103	BE311926	Hs.15930	Homo sapiens cDNA FLJ12591 its, clone N	Glycos_transf_2	5.4
	442611	BE077155	Hs.171337	ESTs	TM	5.4
75	425401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	Xlnk,CUB	5.4
	419948	AB041035	Hs.33647	NADPH oxidase 4	TM	5.3
	427718	AW78650	Hs.25923	ESTs	histone	5.3
	453987	AS282633	Hs.109196	HSPC037 protein	SS	5.3
80	408206	AI745325	Hs.21923	ESTs, Moderately similar to R3 ALU SLUB	Glycos_transf_2_DSPr	5.3
	448543	AW897741	Hs.21360	Homo sapiens mRNA: cDNA DKFZp586P	TM	5.3
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALL8_HUMA	TM	5.3
	449532	W17463	Hs.271593	ESTs	TM	5.3
	453822	X58699	Hs.288517	Homo sapiens cDNA: FLJ25251 its, clone	TM,EGF_fn3	5.3
	418379	AA218940	Hs.137516	filaggrin-like 1	AAA	5.2

WO 02/102235

PCT/US02/19297

	415530	U52801	Hs.79361	halfrin 6 (neurosin, zyme)	TM,lypsin	5.2
	413364	NM_000491	Hs.75334	exotoxins (multiple) 2	TM	5.2
	445925	AK001575	Hs.12457	hypothetical protein FLJ10814	TM	5.2
	406367	#[NCAT]	0	0	TM	5.2
5	442600	A815968	Hs.209122	ESTs	proteasome,lypsin	5.2
	450101	AV649989	Hs.24385	Human hbc67 mRNA sequence	SS	5.2
	419140	AB92647	Hs.15725	ESTs	TM	5.2
	417751	AW695339	Hs.111471	ESTs	Alu_Xac_th_C	5.1
10	437456	AA452378	Hs.170144	Homo sapiens mRNA; cDNA DKFZ547J1	TSPN,Folate_carrier	5.1
	416849	AW474547	Hs.53365	ESTs. Weakly similar to B0461.1 [C.oleg	TM	5.1
	426053	AW654946	Hs.104630	ESTs	TM	5.1
	406931	AS70572	Hs.69536	chromosome 11 open reading frame 5; feta	TM	5.1
	416852	BE537037	Hs.273294	hypothetical protein FLJ20099	TM	5.1
	404529		0	0	TM	5.0
15	447020	T27308	Hs.15586	hypothetical protein FLJ11046	TM	5.0
	410264	AW849413	Hs.33264	ESTs	TM	5.0
	417923	AA157341	Hs.111164	ESTs	TM	5.0
	421477	AI504743	Hs.104650	hypothetical protein FLJ10292	TM	5.0
20	443666	N71710	Hs.21398	ESTs. Moderately similar to GNP1_HUMA	Glucosamine_iso	5.0
	494529	U02911	Hs.150402	activin A receptor, type I	SS,Activin_recep_kinase	4.9
	415665	AW002090	Hs.44070	ESTs	TM	4.9
	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic protein ly	SS	4.9
	408936	AA059013	Hs.22507	ESTs	TM	4.9
25	456794	AD61288	Hs.133437	ESTs. Moderately similar to gonadotropin I	TM	4.9
	425049	AA281132	Hs.146343	ESTs	TM	4.9
	458627	AV088642	Hs.97954	ESTs; Weakly similar to WASP-family pro	TM	4.8
	418882	NM_004696	Hs.89433	ATP-binding cassette, sub-family C (CFTR	TM,ABC_membrane	4.8
	422505	AL120682	Hs.124155	ESTs; (HSA)PAP protein (programmed co	TM	4.8
	423656	NM_002214	Hs.194938	integrin, beta 6	SS,integrin_B	4.8
	425209	NM_015369	Hs.30965	porence 1	TM	4.8
	449635	W15257	Hs.23672	low density lipoprotein receptor-related pro	SS,LDL_recep_La,EGF	4.8
	452232	AW028903	Hs.271898	ESTs	TM	4.8
	423161	AL049227	Hs.124775	Homo sapiens mRNA; cDNA DKFZ564N	Cadherin_C_term	4.7
	425405	Y02762	Hs.2255	cholinergic receptor, nicotinic, alpha polype	TM,new_chan	4.7
35	433330	AV207084	Hs.132816	ESTs	TM	4.7
	443633	AD91531	Hs.135501	Homo sapiens two pore potassium channel	TM	4.7
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	TM,EGF	4.7
	425300	U15979	Hs.165228	delta-like homolog (Drosophila)	TM	4.7
	453775	NM_020915	Hs.36120	aplication factor C (pedicular 1) 4 (7XK)	AAA,DEAD,helicase_C	4.7
40	420944	R13949	Hs.228440	Homo sapiens clone 24881 mRNA sequence	TM	4.7
	434938	AI418055	Hs.151150	ESTs	TM	4.6
	404640	#[NCAT]	0	0	lypsin,TM	4.6
	423301	AW526646	Hs.06840	ESTs	TM	4.6
45	446254	BE179829	Hs.179832	Homo sapiens cDNA FLJ12832 fls, clone N	TM	4.6
	469574	A7411122	Hs.101610	Homo sapiens cDNA FLJ14932 fls, clone N	TM	4.6
	409928	AL137163	Hs.67549	hypothetical protein dJ47364	TM	4.6
	432444	N77221	Hs.167624	ESTs	TM	4.6
	404699	#[NCAT]	0	0	TM	4.6
50	407935	AW103655	Hs.252905	ESTs	TM	4.6
	441675	AS14329	Hs.5461	ESTs	TM	4.6
	420276	AA250936	Hs.105051	ESTs. Highly similar to mosaic protein LR1	TM,lr3,ld_recep_La	4.6
	422529	AW015128	Hs.266703	ESTs	TM	4.5
	438018	AK001160	Hs.5699	hypothetical protein FLJ10298	TM	4.5
	457455	AW031344	Hs.159599	ESTs	Phibosyllan	4.5
55	418948	AB20961	Hs.130465	ESTs	TM,pkiso	4.5
	447499	AW252680	Hs.147574	KAA1521 protein	TM	4.5
	432731	R31178	Hs.267620	Ribonectin 1	SS	4.5
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11080 fls, clone H	Nucleoside_tra2	4.4
	427626	AW077143	Hs.179555	mitochondrion maintenance deficient (S.	TM	4.4
60	450502	AF752683	Hs.172508	ESTs	TM	4.4
	451369	N73222	Hs.21735	KIAA1008 protein	TM	4.4
	453331	A240655	Hs.8895	ESTs	TM	4.4
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	TM	4.4
65	425987	NM_003616	Hs.2442	a disintegrin and metalloproteinase domain	TM	4.4
	453779	AW859440	Hs.69868	ESTs	TM	4.4
	409469	DE5407	Hs.54481	low density lipoprotein receptor-related pro	TM,EGF,ld_recep_La	4.4
	431708	AW58135	Hs.108873	ESTs	TM	4.4
	433905	AI167816	Hs.43305	ESTs	TM	4.4
70	441423	AF753259	Hs.126577	ESTs	TM	4.4
	445770	AW60386	Hs.154066	ESTs. Weakly similar to AF137385 1 phas	TM	4.3
	412076	Y56959	Hs.73149	paired box gene 6	TM	4.3
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; H	AIRS	4.3
	446350	AL035414	Hs.21056	hypothetical protein	TM	4.3
	453626	AW243307	Hs.170167	ESTs	TM	4.3
75	430567	U71207	Hs.29275	eyus absent (Drosophila) homolog 2	TM	4.3
	413775	AA049934	Hs.75626	nuclear GTPase	MWR_HSR1	4.3
	451982	AB05415	Hs.213697	ESTs	TM	4.3
	419311	AW685981		gbr-mRNA12.51 NCL CGAP_CG81 Homo s	TM	4.2
80	426443	BE24749	Hs.31082	hypothetical protein FLJ10529	TM	4.2
	426575	AA431755		glcwr00c03.01 Soxas_Jeslin_NRT Homo s	TM	4.2
	435029	AW860417	Hs.254020	ESTs. Moderately similar to unnamed prote	TM	4.2
	405075	AL130179	Hs.137011	Homo sapiens mRNA; cDNA DKFZ564N	TM	4.2
	428619	AL136623	Hs.193514	KIAA0575 gene product	TM	4.2
	405571	AA129547	Hs.265754	mml proto-oncogene (hepatocellular growth fac	F-actin_cap_A	4.2

WO 02/102235

PCT/US02/19297

	431760	AA514986	Hs.283705	ESTs	TM
	445654	AA682382	Hs.55982	ESTs	TM
	450573	AA063498	glut1407.s1 Soares_pineal_gland_N3HP	ESTs	SEA
	433929	AG375499	Hs.27370	ESTs	TM
5	415457	AW081710	Hs.7368	ESTs, Weakly similar to ALU1_HUMAN A	TM
	444381	BE387335	Hs.283713	ESTs	TM
	415639	AT333981	Hs.72472	BMPTF-1, bone morphogenetic protein rec	TM
	421515	Y11336	Hs.105352	GaMuc2, alpha-2, 6-sialyltransferase I, lung	TM
10	453253	AA382267	Hs.106652	ESTs	TM
	409564	AA049557	Hs.54943	fracture callus 1 (rat) homolog	TM
	426528	H09604	Hs.12588	ESTs	TM
	404452	AE251136	Hs.55150	ESTs, Weakly similar to CAVP_HUMAN	TM
	443695	AW020409	Hs.112750	ESTs, Weakly similar to AF126790.1 retina	TM
	425322	U63630	Hs.159537	protein kinase; DNA-activated; catalytic po	TM
	417300	AT652277	Hs.55610	soluble carrier family 30 (zinc transporter), m	TM
	417389	BE260954	Hs.52045	MdKine (neutle growth-promoting factor 2	SS, TM
	425234	AE388271	Hs.109585	ESTs	TM
	428771	AB029992	Hs.153143	KIAA1069 protein	PI-PLC-X, PI-PLC-Y
	412314	AA252477	Hs.750999	heat shock factor binding protein 1	TM
20	452621	BE594542	Hs.5101	ESTs; Highly similar to protein regulating c	TM
	459454	AJ245583	Hs.25275	Kruppel-type zinc finger protein	TM
	409365	AA702376	Hs.229440	Homo sapiens clone 24881 cDNA sequenc	TM
	413374	NA_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	TM
	417655	AA793791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	TM
25	445841	AJ267271	Hs.128356	ESTs	TM
	441134	W25052	Hs.7578	cellular retinoic acid-binding protein 1	TM
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	TM
	413301	AW976201	Hs.187615	ESTs	TM
30	411945	UJ035257	Hs.82127	+myc avian myeloblastomatosis viral onco	TM
	428694	RS1327	Hs.12727	hypothetical protein FLJ21610	TM
	414869	AA157291	Hs.72163	ESTs	TM
	420281	AE823693	Hs.191533	ESTs	TM
	416658	UJ0372	Hs.79452	thrombin 2 (congenital) contractural arachnoid	TM
35	411274	NA_002776	Hs.89423	kalirin10 10	TM
	427222	AL117588	Hs.259593	ESTs	TM
	431958	X53629	Hs.28977	Cadherin 3, P-cadherin (placental)	TM
	430634	AB804651	Hs.25685	ESTs	TM
	415716	N92254	AA301141	Homo sapiens cDNA FLJ11669 fs, clone H	TM
40	420175	N74530	Hs.21165	ESTs	TM
	451250	AA491275	Hs.226540	Homo sapiens cDNA FLJ12542 fs, clone N	TM
	428496	AA453800	Hs.192793	ESTs	TM
	421764	AB81535	Hs.99342	ESTs, Weakly similar to KCC1_HUMAN C	TM
	447197	R50375	glucosylceramidase 1	TM	
	422939	AW934055	Hs.98427	ESTs	TM
45	414737	AI160386	Hs.125037	ESTs	TM
	411773	NA_005799	Hs.72026	protease, serine, 21 (testisin)	TM
	425247	NA_003940	Hs.155324	matrix metalloproteinase 11 (stromelysin 3)	TM
	424433	H04607	Hs.3219	ESTs	TM
	431646	BE019924	Hs.271590	Uroplakin 1B	TM
50	407792	AW077115	Hs.39334	putative secreted ligand homologous to Eyr1	TM
	417531	NA_003157	Hs.1057	serine/threonine kinase 2	TM
	424836	AA651629	Hs.118098	ESTs	TM
	429810	AL109710	Hs.85698	EST	TM
	418693	AT959575	Hs.87409	thrombospondin 1	TM
55	407964	AF369291	Hs.40339	chromosome 8 open reading frame 1	TM
	453534	AA338622	Hs.109867	ESTs	TM
	452259	AA317439	Hs.29707	signal sequence receptor, gamma (transloc	TM
	453468	W00712	Hs.32590	DKF2569F084 protein	TM
60	429543	AW061810	Hs.76736	ESTs, Weakly similar to KIAA1392 protein	TM
	411402	BE297555	Hs.69855	NF-kB-related gene	TM
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEFT_HUMA	TM
	400296	AA305627	Hs.138336	ATP-binding cassette, sub-family C (CFTR	TM
	407340	AA1010168	Hs.232119	ESTs	TM
	418524	AA303576	Hs.85769	acidic 52 kDa protein mRNA	TM
65	438279	AA305186	Hs.165165	ESTs, Moderately similar to ALU8_HUMA	TM
	429453	BE264974	Hs.6556	thyroid hormone receptor interactor 13	TM
	441111	AB06967	Hs.126594	ESTs	TM
	451906	NA_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	TM
70	409542	AW03020	Hs.36553	ESTs	TM
	425441	AA445644	Hs.153363	Homo sapiens cDNA FLJ14201 fs, clone N	TM
	428137	AA421752	Hs.170899	ESTs	TM
	423692	AB06890	Hs.208675	ESTs, Weakly similar to neuronal thread pr	TM
	436989	AW129261	Hs.750565	ESTs	TM
	443341	AW514810	Hs.8668	ESTs	TM
75	446261	AA313933	Hs.13359	hypothetical protein FLJ12615 similar to m	TM
	414343	AL036166	Hs.75514	coated vesicle membrane protein	TM
	414812	X27765	Hs.77367	macrolide induced by gamma interferon	TM
	410351	BE381804	Hs.67691	guanylate binding protein 1, interferon-indu	TM
	415706	AW115156	Hs.257524	ESTs	TM
80	427177	AW006537	Hs.173390	interleukin 1 receptor accessory protein	TM
	427687	AW003867	Hs.112403	ESTs	TM
	444619	BE380852	Hs.5172	ESTs	TM
	447236	AW129335	Hs.245437	ESTs	TM
	412519	AA156241	Hs.73580	tropocollin T1, skeletal, slow	TM

PCT/US02/19297

209

WO 02/102235

PCT/US02/19297

	410518	AW976443	Hs.286555	ESTs	RacGEF, PI3K, RhoGEF	3.1
	418396	AF765905	Hs.26691	ESTs	TM	3.1
	427855	R61253	Hs.56265	ESTs	TM	3.1
	428272	W025140	Hs.110567	ESTs	TM	3.1
5	450171	AL133661	Hs.24583	hypothetical protein DKFZp434C0326	TM	3.1
	414774	X02419	Hs.77274	plasminogen activator, urokinase	SS,irrigine, trypsin	3.1
	422363	T559179	Hs.115474	replication factor C (replicator 1) 3 (38kD)	TM	3.1
	420612	AW411086	Hs.94785	hypothetical protein LOC371453	TM	3.1
	428698	AA822773	Hs.297939	ESTs; Weakly similar to neogenin [Hs.sapi	TM	3.1
10	427051	BE178110	Hs.173374	ESTs	TM	3.1
	425242	H45709	Hs.2250	leukemia inhibitory factor (cholinergic diffe	SS	3.1
	425306	BE207039	Hs.15621	corin (or cyclotol) proteinase inhibitor, cla	TM	3.1
	425419	AB022325	Hs.202276	KIAA1009 protein	TM	3.1
	417517	AF001176	Hs.82238	POPI (processing of precursor, S. cerevisia	TM	3.1
15	406137	#(NCAT)	Hs.153203	MyoD family inhibitor	TM	3.1
	424800	AL035588	Hs.61418	microtubule-associated protein 1	TM	3.1
	410252	AW821152	Hs.97353	KIAA0328 protein	SS	3.1
	420392	AI242930	Hs.18612	Homo sapiens cDNA: FLJ121905 fs, clone	voltage_CLC,CBS	3.1
20	425334	DE3078	Hs.186180	Homo sapiens cDNA: FLJ23038 fs, clone	Glyco_hydro_2	3.1
	415902	AW901804	Hs.23564	hypothetical protein FLJ20147	TM	3.1
	405056	NM_004460	Hs.416	fibroblast activation protein; alpha	SS,Peptidase_S9	3.0
	433449	BE456884	Hs.230728	ESTs	TM	3.0
25	411984	NM_005419	Hs.72968	signal transducer and activator of transcript	SH2,STAT	3.0
	422530	AW672300	Hs.118110	bone morphogenetic cell antigen 2	TM	3.0
	422128	AW681145	Hs.123114	gls-DQO-Q70033-Q10400-152-a07 C10033	TM	3.0
	405757	NM_001898	Hs.54834	cystatin SN	SS,cystatin	3.0
	418727	AA227609	Hs.13593	ESTs	TM	3.0
30	422244	Y06890	Hs.113563	karyopherin (importin) beta 3	TM	3.0
	458444	AB54158	Hs.152961	CDP-diacylglycerol synthase (phosphatidyl	TM	3.0
	432358	AA053491	Hs.72830	ESTs	SS	3.0
	416895	A752862	Hs.5538	KIAA1572 protein	BTB	3.0
	447312	AA34345	Hs.38998	activating transcription factor 1	TM	3.0
	445021	AA002025	Hs.12251	Homo sapiens cDNA: FLJ11163 fs, clone P	TM	3.0
35	422611	AA155177	Hs.110722	luciferase-like 5 (alpha 1.2) luciferase	SS	3.0
	453597	BE281130	Hs.33713	myo-inositol 1-phosphate synthase A1	TM	3.0
	401197	#(NCAT)	Hs.151787	US snRNP-specific protein, 116 kD	artEb	3.0
40	403000	BE247275	Hs.151787	US snRNP-specific protein, 116 kD	TM	3.0
	410006	AA075552	Hs.151787	glna20b12.11 Stratiogene pancreas (g372)	TM,FG-GAP	3.0
	413268	AL038079	Hs.75256	regulator of G-protein signaling 1	RGS	3.0
	414080	AA138257	Hs.47783	ESTs; Weakly similar to T12540 hypothel	TM	3.0
	425682	AA393106	Hs.97365	ESTs	TM	3.0
45	427651	AFV45721	Hs.16468	Homo sapiens cDNA: FLJ12277 fs, clone M	TM	3.0
	430444	A027652	Hs.54578	ESTs	TM	3.0
	433001	AF217513	Hs.279905	clone HO0310 PR00310p1	TM	3.0
	444895	AA74363	Hs.301192	EST cluster (not in UniGene)	TM,ASC	3.0
	441962	AW972542	Hs.259308	Homo sapiens cDNA: FLJ21514 fs, clone	TM	3.0
	414725	AA765791	Hs.130355	Homo sapiens cDNA: FLJ13146 fs, clone N	TM,7tm_1	3.0
50	434241	AF119913	Hs.283007	hypothetical protein PRC3077	SS	3.0
	424962	NM_012298	Hs.153954	TRAM-like protein	TM	3.0
	411987	AA375975	Hs.103390	ESTs; Moderately similar to ALU7_HUMA	TM	3.0
	421977	W54157	Hs.110105	abscissa protein L25 homolog	TM	3.0
	436451	AA375657	Hs.5199	HSPC150 protein similar to ubiquitin-conju	TM	3.0
55	407672	AB035723	Hs.40735	frizzled (Drosophila) homolog 3	TM,7tm_2,Fz,Frizzled	3.0
	442577	AA292598	Hs.163900	ESTs	TM	3.0
	416120	H45739	Hs.204732	glycyl-tAC2.s1 Scores adult brain N25HB5	TM	3.0
	443775	AF281684	Hs.66295	metallo metalloproteinase 26	TM,Peptidase_M10,7tm_1	3.0
	414654	AA587775	Hs.66295	Homo sapiens HSPC311 mRNA, partial of	TM	3.0
	457590	AA12809	Hs.5378	spondin 1, (p-spondin) extracellular matrix	SS	3.0
60	418946	AF798641	Hs.132103	ESTs	TM	3.0
	457940	AL390159	Hs.30445	Homo sapiens mRNA full length insert cDN	TM,SPRY_7tm_1	3.0

TABLE 15B:

Key: Unique Eos probe/identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

65	Play	CAT Number	Accession
	407615	1005404_1	AW753085 AW753082 AW054744 AW753107 AW753067
70	459073	100951_1	AA263455 AA063016 AA448222
	409746	118237_1	AA07391 AA347616 AA361453 AA088754 AW207461 AA069012 AA321574 AA286483 AA150722 BE152363 AW188822 BE152400
	410008	116812_1	AA079552 BE162526 BE142507
	414147	142127_1	BE091634
75	414315	143512_1	ZZ4670 AA494398 F13654 AA494040 AA143127
	416120	1511256_1	H46730 H61613 H19179
	419311	183393_1	AA659591 AW914261 AA236240 AN077451 AA631399 AW914262
	419546	187666_1	AA244199 AA244272 H57440
	422128	211994_1	AW681145 AA490715 M65637 AA304575 T06067 AA331991
	427072	271684_1	H35045 H63545 AA387953 H58047
80	428679	294049_1	AA431765 AA432015
	438993	467651_1	AA828995 AA634679 AA925361
	447197	711623_1	R36075 AA366546 R36167

WO 02/102235

PCT/US02/19297

TABLE 15C:

Key: Unique number corresponding to an Eos probelet

Ref: Sequence source. The 7 digit number in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1990) *Nature* 402:460-465

Strand: Indicates DNA strand from which exons were predicted

NL_positon: Indicates nucleotide positions of predicted exons

Key	Ref	Strand	NL_positon
400881	2842777	Minus	91446-91603,92123-92295
401197	9719705	Plus	176341-176452
401435	6217934	Minus	54506-55233
404440	7528261	Plus	60430-841591
404929	6962937	Plus	175218-175476
404996	6007989	Plus	37999-38145,38652-38990,39727-39872,40557-40674,42351-42450
405547	1054740	Plus	124361-124520,124914-125050
406137	9166422	Minus	30487-31058
406367	6296126	Minus	58115-59469
406400	9256268	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 15A lists about 92 genes up-regulated in mucinous-type ovarian cancer compared to normal adult tissues. These were selected as for Table 14A, except that the "average" ovarian cancer level was set to the 75th percentile amongst various mucinous-type ovarian cancers, and the tumor/normal tissue ratio was greater than or equal to 2.5.

TABLE 15A: ABOUT 92 UP-REGULATED GENES, MUCINOUS OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Key: Primerkey

Ex_Acct: Exemplar Accession

UG ID: UniGene ID

Title: UniGene title

Prot. Dom.: Predicted protein domain structure

ratio: tumor vs. normal tissues

Key	Ex_Acct	UG ID	Title	Prot. Dom.	ratio
430691	C14187	Hs.103538	ESTs		34.9
432936	T27913	Hs.3132	chromidogenic acute regulatory protein	START	25.0
419307	M13829	Hs.83169	Matrix metalloproteinase 1 (interstitial collag	SS_Papildase_M10	22.3
451181	A796330	Hs.207461	ESTs		10.8
452836	U65011	Hs.30743	Preferentially expressed antigen in melanoma		10.0
407638	AJ404672	Hs.286693	EST		9.3
450169	A072416	Hs.200771	ESTs, Weakly similar to CAN2_HUMAN		9.2
426690	AA393167	Hs.41294	ESTs		9.1
421155	H87879	Hs.102267	lysozyme	SS_Lysozyme	8.9
437099	N77793	Hs.48669	ESTs, Highly similar to LMA1_HUMAN L	laminin_EGF	7.6
453966	AW291498	Hs.292567	ESTs		7.6
435466	AW94071	Hs.265298	ESTs, Weakly similar to transformation-rel		7.4
418738	AW388833	Hs.6682	solute carrier family 7, member 11		7.2
431966	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone P	RA	7.0
449679	AW207260	Hs.134014	prostate cancer associated protein 6		6.7
424886	NM_030401	Hs.150300	X-ray repair complementing defective repa		6.7
445891	AW291342	Hs.199460	ESTs		6.2
424717	H03754	Hs.152213	wingless-type MMTV integration site fami	wnt	6.1
452705	H49806	Hs.246006	ESTs		6.1
421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	TM_p450	5.5
408652	AK436323	Hs.31141	Homo sapiens mRNA for KIAA1568 prote		5.3
420159	A0572490	Hs.99785	ESTs		5.3
451105	A761324	Hs.146343	ghw160b11.x1 NCL-OGAP_Co16 Homo s		5.2
409049	AK23132	Hs.154140	ESTs		5.0
448974	N01178	Hs.154140	ESTs	TM	5.0
423811	AW299596	Hs.50995	homeo box C4		4.9
427469	AA403084	Hs.260347	ESTs		4.9
447033	A037412	Hs.157601	EST - not in UniGene	PH	4.9
424433	H04607	Hs.9219	ESTs	TM	4.9
449811	A1590371	Hs.174759	ESTs		4.8
444330	A1597655	Hs.49265	ESTs		4.8
409041	A0333025	Hs.50381	KIAA1199 protein		4.7
418735	H48769	Hs.44638	ESTs		4.5
415661	AK534543	Hs.794400	IGF-II mRNA-binding protein 3	KH-domain	4.5
430073	U86136	Hs.232700	Inolomerase-associated protein 1	WD40	4.4
407381	AW072003	Hs.403958	heparan sulfate (glucosamine) 3-O-sulfotran	SS	4.4
422260	AJ316993	Hs.105484	ESTs, Weakly similar to LITHOSTATHIN		4.4
421110	AJ250717	Hs.1355	cathepsin E	SS_zsp	4.3
443676	A1247463	Hs.163028	ESTs		4.2
430704	AW813091	Hs.163028	gbcRC3-ST0186-240400-111-c07 ST0186	Eplmerase	3.8
414569	AF109298	Hs.118258	Prostate cancer associated protein 1	TM	3.8
430876	A0163077	Hs.131693	ESTs		3.7
434032	AW008961	Hs.206892	ESTs		3.7
446557	AW612141	Hs.279575	ESTs	7tm_1	3.6
439759	AL339055	Hs.677309	Homo sapiens mRNA full length insert cDN		3.6
453566	BE065913	Hs.177164	gbcRC2-ST0318-110106-012-a08 BT0318		3.5
446844	A051519	Hs.177164	ESTs		3.5
449048	248501	Hs.22520	similar to S68401 (cat) glucose induced g	SS	3.5
438018	AK001160	Hs.5999	hypothetical protein FLJ10293	TM	3.4
468123	AW892676	Hs.272072	gbcCAG-AN0004-280300-131-c12 NN0004		3.4
407385	AH610150	Hs.272072	ESTs, Moderately similar to ALUT_HUMA		3.4
424694	H83920	Hs.153673	reproduction 8	SS_UBX	3.3

PCT/US02/19297

212

WO 02/102235

PCT/US02/19297

	412025	AI069319	Hs.179243	ESTs		15.7
	438617	AI023799	Hs.163242	ESTs		13.6
	447033	AI357412	Hs.157601	EST - not in UniGene	PH	13.5
	432222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMA		13.1
5	422966	BE545072	Hs.122579	ESTs		12.9
	450461	AIW591528	Hs.202072	ESTs		11.9
	452954	AI361466	Hs.12744	ESTs	homeobox	11.5
	424238	AI569996		ghr:cd26M3.1 NCL_CGAP_K05 Homo sa		11.4
10	431989	AW972870	Hs.291069	ESTs	SS	10.3
	413623	AA625721	Hs.246973	ESTs		9.7
	449091	AA909386	Hs.128612	ESTs		9.6
	416961	AA345454	Hs.79440	KCF-18 mRNA-binding protein 3	KH domain	9.6
	421478	AI683243	Hs.57258	ESTs		9.3
15	446706	AW291095	Hs.21814	class II cytokine receptor ZCYTOR7	SS,Tissue_fac	9.2
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13565 ts, clone P		8.7
	436953	AA526995		integrin beta 6	SS,inlinin_B	8.7
	427121	AJ273815	Hs.173656	KIAA0541 protein	C2,	8.4
	420510	AI663163	Hs.59346	distal less homeo box 5	homeobox	8.1
	427356	AW023482	Hs.57849	ESTs		8.0
20	446677	AB040533	Hs.15420	KIAA1500 protein		8.0
	431118	BE294001	Hs.259502	carbonic anhydrase VII	carb_anhydrase	7.6
	448112	AW245919	Hs.301018	ESTs, Weakly similar to ALU8_HUMAN		6.9
	451106	BE382701	Hs.25960	N-myc	HLH,Myc_N_term	6.6
25	449433	AI672096	Hs.5012	ESTs		6.3
	435922	AF633306	Hs.36708	binding uninhibited by benzimidazoles 1 (r		6.3
	434636	AA083764	Hs.241334	ESTs		6.1
	435988	AW361270	Hs.194110	Homo sapiens mRNA; cDNA DKFZp434C		5.9
	422805	AA436989	Hs.121017	H2A histone family, member A	histone	5.8
30	440292	AA250737	Hs.72472	BMP4R-1b, bone morphogenetic protein rec		5.7
	441779	AI264402	Hs.6933	Homo sapiens cDNA FLJ12664 ts, clone N		5.7
	416124	AA397769	Hs.66617	ESTs		5.5
	452249	BE394412	Hs.61252	ESTs	homeobox	5.5
	402056	AI576963	Hs.22372	Homo sapiens cDNA FLJ13352 ts, clone O	TM,UPF0016	5.5
35	413335	AI613316	Hs.46442	ESTs		5.4
	441081	AI584019	Hs.165006	ESTs, Moderately similar to plakophilin 2b	PAX	5.4
	428029	H05640	Hs.23071	ESTs		5.3
	419183	U06669	Hs.85663	cytochrome P450, subfamily X0V (vitami	p450	5.3
	409304	AW537237		glxn:cd201.1 NCL_CGAP_Pan 1 Homo sa		5.2
40	422936	IT7013	Hs.21332	steroidogenic acute regulatory protein	START	5.2
	410102	AW248506	Hs.279727	ESTs;	SS	5.1
	447635	AW591623	Hs.164129	ESTs		5.1
	432602	AW119567	Hs.22568	ESTs		5.0
	423992	AW596252	Hs.137206	Homo sapiens mRNA; cDNA DKFZp564H		5.0
45	425905	AE032559	Hs.161700	KIAA1133 protein	TM	5.0
	452461	N78223	Hs.108106	transcription factor	G9a,PHD	4.9
	430691	C14187	Hs.103538	ESTs		4.8
	441675	AI914223	Hs.5461	ESTs		4.7
	425696	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor	Eand_A1_Y_phosphatase	4.6
50	440340	AW895003	Hs.125276	ESTs		4.5
	428579	NM_005758	Hs.164942	G protein-coupled receptor 64	TM	4.5
	444783	AK001466	Hs.62180	ESTs	PH	4.4
	401489	AI797515	Hs.270560	ESTs, Moderately similar to ALU7_HUMA		4.4
	413396	AI286507	Hs.145969	ESTs		4.3
55	415263	AA946033	Hs.130653	ESTs	histone	4.3
	413988	MB1883	Hs.79968	glutamate decarboxylase 1 (brain, 67kD)	pyridoxal_deC	4.2
	452030	AL132578	Hs.27807	Homo sapiens mRNA; cDNA DKFZp564H		4.1
	416852	BE537037	Hs.272294	hypothetical protein FLJ20065		4.1
	446431	RI4952	Hs.153486	ESTs		4.1
60	434891	AA614309	Hs.123853	ESTs		4.0
	415139	AW975942	Hs.48524	ESTs	G-patch	4.0
	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN A		4.0
	447112	H17600	Hs.7154	ESTs		3.9
	420633	NM_014581	Hs.99525	odorant-binding protein 2B	TM,lipocalin	3.9
	456674	A741122	Hs.101810	Homo sapiens cDNA FLJ14232 ts, clone N		3.9
65	415138	C18366	Hs.78445	G protein-coupled receptor 39	Kunitz_EPTI,G-gamma	3.9
	414853	AL121282	Hs.257796	ESTs		3.7
	442006	AW975183	Hs.232663	ESTs		3.7
	409731	AA125985	Hs.58145	thymosin, beta, identified in neuroblastoma	Thymosin	3.7
70	424506	AI596086	Hs.153716	Homo sapiens mRNA for Hmnb33 protein,		3.7
	456662	NM_002448	Hs.1434	mtb (Drosophila) homeo box homolog 1 (fo	homeobox	3.7
	429125	AA446854	Hs.271004	ESTs		3.6
	435538	AB011540	Hs.4530	low density lipoprotein receptor-related pro		3.6
	456861	AI630223		ghr:cd050b.r1 Proliferating Erythroid Cells	PHD	3.5
75	416506	AA064246	Hs.65339	SELKOPHOSPHATE SYNTHETASE; H	AIRS,AIRS	3.4
	423123	NM_012247	Hs.124027	ESTs		3.4
	437960	AI669986	Hs.222194	ESTs		3.4
	402296	AA032279	Hs.61635	STEAP1	TM	3.4
	407162	BE36565	Hs.142634	zinc finger protein		3.4
80	406621	AI970672	Hs.46638	chromosome 11 open reading frame 8; beta		3.3
	445629	AA454267	Hs.145526	ESTs		3.3
	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMA		3.3
	457979	AA716655	Hs.270942	ESTs	TM	3.3
	402806	RI00CA11				3.2
	425471	M22440	Hs.170009	transforming growth factor, alpha	SS_EGF	3.2

WO 02/102235

PCT/US02/19297

430294	AJ538226	Hs.135184	ESTs	polyprolyl_synt	3.2
440827	AA488437	Hs.177224	ESTs		3.2
432519	AW251722	Hs.278628	related to the N terminus of the	TBC	3.2
413927	BE182062	Hs.246973	ESTs		3.2
441377	BE218239	Hs.202656	ESTs		3.2
441085	AW139581	Hs.181245	Human sapiens cDNA FLJ12532 fs, clone N		3.2
433527	AW235013	Hs.133320	hypothetical protein DKF7Z043C0328	TM	3.2
451771	AI.133681	Hs.24593	gcy7/9511.1 Soares placenta NB2HP Hom	homeobox	3.1
419807	R77402	Hs.80404	msh (Drosophila) homeo box homolog 2		3.1
418867	D31771	Hs.284137	Human sapiens cDNA FLJ12888 fs, clone N	z-C2H2	3.1
419335	AW500146	Hs.25040	zinc finger protein 239		3.1
405480	Y52115	Hs.68056	ESTs		3.1
420140	AA265320	Hs.34959	ESTs		3.1
413415	AA025082	Hs.105276	gk:EST351184 MAGE resequences, MAGE	Oxydant_BP	3.1
438956	AW570074	Hs.27252	ESTs		3.0
431041	AA403957	Hs.73525	RAB5 interacting, kinesin-like (rabkinesin5)	kinesin	3.0
415245	N59590	Hs.267905	hypothetical protein FLJ10422		3.0
412140	AA219691	Hs.22151	KRA1226 protein	homeobox	3.0
431707	R21326	Hs.21157	cytoskeleton associated protein 2		3.0
448616	AB033052	Hs.194762	Human metallothionein IV (MTIV) gene, c		3.0
447855	AW447554	Hs.133525	ESTs	TM	3.0
450221	AA326102	Hs.57844	myoglobin 2	Uteroglobin	3.0
408997	U07807	Hs.158951	ESTs		3.0
439426	H69126	Hs.158951	ESTs		3.0
420440	NM_002407	Hs.158951	ESTs		3.0
420181	AI380089	Hs.158951	ESTs		3.0
458927	AW086642	Hs.293772	ESTs; Weakly similar to WASP-family pro		2.9
450565	A1377431	Hs.293772	ESTs		2.9
422653	M68574	Hs.211507	Human phosphatidylcholine 2-acetylcholine	C2,PLA2_B	2.9
415125	AF051193	Hs.301541	Human sapiens mRNA for acetylcholine r	TM,SNF	2.9
412708	R26830	Hs.106137	ESTs	TM7tm_2,Rho_GOI	2.9
451380	N73222	Hs.21738	KAA1008 protein		2.9
423337	NM_004665	Hs.127337	avin 2 (conductin, avl)	DX,RGS	2.8
431185	AA054400	Hs.289109	dimethylarginine dimethylaminohydrolase		2.8
428054	AI649598	Hs.266610	ESTs		2.8
448243	AW365771	Hs.77499	ESTs		2.8
426723	NM_014420	Hs.153111	diokipol (Xenopus laevis) homolog 4	SS	2.8
432415	T16871	Hs.225014	ESTs		2.8
414747	U30872	Hs.77204	centromere protein F (35S/400kD, mitosis)		2.9
407195			0		2.9
448874	AA135098	Hs.10083	ESTs		2.8
452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	Hydrolyse	2.8
420393	AW544096	Hs.104830	ESTs		2.8
405640	U78722	Hs.55481	zinc finger protein 165	TM,z-C2H2,SCAN	2.8
424169	AA336399	Hs.153797	ESTs	mlo_carr	2.8
405638	AW465420	Hs.21336	ESTs		2.8
440346	AA057481	Hs.158469	ESTs; Weakly similar to envelope protein [2.8
428650	AA330167	Hs.41294	ESTs		2.8
452771	T05477	Hs.124166	gk:EST03366 Fetal brain, Stratagene (cat53		2.8
422505	AL120682	Hs.124166	ESTs; (HSA)PAP protein (programmed ce		2.8
416624	H93044	Hs.13406	gcy7/951.1 Soares fetal liver spleen TNF	z-C3HC4	2.8
445570	AW110053	Hs.260098	crystallin 15	TM	2.7
441952	AW372542	Hs.19322	Human sapiens cDNA: FLJ21814 fs, clone		2.7
447342	AI195266	Hs.102610	ESTs; Weakly similar to HIALU SUBFAM		2.7
421247	BE361727	Hs.102610	general transcription factor I(R), polypeptid		2.7
419752	A2416573	Hs.153815	ESTs		2.7
410558	AW105231	Hs.102035	ESTs		2.7
437698	R61837	Hs.7500	ESTs		2.7
458027	L45054	Hs.88195	ESTs, Highly similar to (35S)(q25.1;p30) f		2.7
438689	AW123251	Hs.253556	ESTs		2.7
439816	A1372579	Hs.100221	ESTs; Weakly similar to ALLU_HUMAN A	SCAN	2.7
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	kinase	2.7
436405	AW105723	Hs.125346	ESTs		2.7
437938	AI260387	Hs.33701	ESTs; Weakly similar to Gap-Pol polyprote		2.7
415517	AA320068	Hs.33701	Human sapiens mRNA: cDNA DKF7Zp43E		2.7
434836	AA61629	Hs.118088	ESTs		2.7
448404	BE086573	Hs.118088	gk:RC6-BT0709.310000-021-G07 BT0709		2.7
444076	BE246919	Hs.10250	U5 snRNP-specific 40 kDa protein (HNPg-	WD40	2.7
405757	NM_001958	Hs.123114	crystallin SN	SS,cystallin	2.6
443775	AF219584	Hs.204752	matric metalloproteinase 26	TM,Peptide,M10,7tm_1	2.6
427961	AW293105	Hs.143134	ESTs		2.6
426568	AW139334	Hs.97162	ESTs		2.6
424717	H03754	Hs.152113	whipple-type MMTV integration site form	wnt	2.6
434659	AF161534	Hs.59023	core histone mscnH2A.2	histone,Atpp,DUF27	2.6
417389	BE295064	Hs.82045	Midline (neurotrophin growth-promoting factor 2	SS,TM,TN1_MK	2.6
451009	AA013140	Hs.115707	ESTs		2.6
429774	AI522215	Hs.50883	ESTs	pinase	2.6
439551	AA047367	Hs.124636	ESTs	TM	2.6
417516	AA335449	Hs.82028	phosphothioester/glycinamide formyltransfera	NF5,formyl_transf	2.6
416805	NM_000286	Hs.79993	peroxisomal biogenesis factor 7	WD40	2.5
420900	AL045933	Hs.42269	ESTs	Akt_Xan_dh_C	2.5
457030	AS91740	Hs.173381	dihydroxyindolizone-like 2		2.5
459583	AS97693	Hs.173381	gk:U16152-003099-004 BT152 Homo sa	Dihydroxotase	2.5
440870	AB87264	Hs.150539	Human sapiens cDNA FLJ13793 fs, clone T	PAX,	2.5

WO 02/102235

PCT/US02/19297

469593	AW750373	Hs.42315	Homo sapiens cDNA FLJ13005 fs, clone N	TM	2.5
407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fs, clone M		2.5
408882			0		2.5
431322	AW570622		g:EBT382704 MAGE resequences, MAGK		2.5
424081	NM_006413	Hs.139120	ribonuclease P (30kD)		2.5
451956	AW514021	Hs.245510	ESTs		2.5
403381	[?NCCA?]		0		2.5
415488	AA315241	Hs.90591	nucleophosmin/nucleoplasmin 3	SS	2.5
418882	NM_004596	Hs.69433	ATP-binding cassette, sub-family C (CFTR)	TM,ABC_membrane	2.5

TABLE 17B:

Play: Unique Eco probe/seq identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

15	Play	CAT Number	Accession
	409094	1059611_1	AW337237 AWB61642 AWB61655 AWB68008 AWB57990 AWB58007
	416624	1604694_1	H69044 T47567 H75991 T50292
20		119807	R77402 AA262462 AA250688 R06794
	431322	331543_1	AW370622 AA503008 AA502956 AA502965 AA502965 T92188
	437538	44573_2	AB500871 H70206 T59040 N53600 AD309115 AW567577 H63320 A251473 H50357 AW371573 R07278 WD10505 AW367671 AA408958 AA251875
			AB20501 AJ820532 W87891 T85904 L71465 T82291 B320571 T75102 R34725 AA884522 BE328517 AJ219178 AA884444 N52578 F13493
25			AA322704 A5562051 AW874058 AL134043 AW235363 AA663345 AW008202 AA488964 AA283144 AJ890387 AJ950334 AJ741346 AJ689062
			AA622515 AW102858 AB72193 AD763273 AW173586 AW150332 A063032 AD762688 AA566777 AA448892 A3363394 AW103813 AJ539642
			AA642789 AA659575 AW555512 AB51530 AW629676 BE512861 AW727897 AW513001 AW512943 AA844425 AW186635 AA180005 AA537495
			AW691101 AA321669 AA551074 AB18225 AW205652 AW56338 AW270505 AW550305 AA572584 AA508741 AW072022 AW513695
			AA252373 AA695759 H57328 N22338 H64729 H00562 T92487 AD27056 AA730419 AA551005 WD0701 AW513456 A337032 A554269 F00531
			H34368 W37161 H78802 R50595 A002839 R57840 AA30202 AW65581 T63226 F04005
30		438966	407435_1 AW797074 AA634841 AA629550
		438966	447551_1 AA529595 AA634079 AB525361
		442438	642439_1 AA955938 AD165884 R61781 T77332 F07755 F08149 F07547
		448404	791515_1 BE089973 AJ436912 AW805032
		449034	794817_1 AB24049 AW117770 AB58360
35		452771	530683_1 T05477 T07855 AJ917711
		458951	790895_1 AB30223 AB30470

TABLE 17C:

Play: Unique number corresponding to an Eco probe/seq

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of

human chromosome 22" Dunham, et al. (1999) Nature 402:469-495

Strand: Indicates DNA strand from which exons were predicted

N_pos: Indicates nucleotide positions of predicted exons

45	Play	Ref	Strand	N_pos
	400882	2842777	Minus	110431-110708
	402505	9009429	Minus	81747-82094
	403381	9439267	Minus	26009-26178

Table 18 lists 178 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode proteins that are secreted into blood, lymph, or other body fluids. These genes, and/or their protein products, in combination or alone, are ideal candidates for the early diagnosis of ovarian cancer. These were selected from 5860 proteins on the Affymetrix HG133 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.4, and that are likely to encode secreted or extracellularly-released proteins. The "average" ovarian cancer level was set to the 50th percentile amongst various ovarian cancer samples. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various 145 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 18: ABOUT 178 UP-REGULATED GENES ENCODING SECRETED PROTEINS, OVARIAN CANCER VERSUS NORMAL ADULT TISSUES

Play: Primerkey

Ex. Acct: Exemplar accession

UG ID: UHGene ID

Title: UHGene title

ratio: ratio tumor vs. normal tissues

65	Play	Ex. Acct	UG ID	Title	ratio
	428379	NM_002595	Hs.184542	G protein-coupled receptor 64	30.5
	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular/mart	29.4
	427585	D31152	Hs.47529	collagen; type X; alpha 1 (Schmid metallo	27.0
70	423739	AA398155	Hs.37600	ESTs	22.7
	418007	H13629	Hs.83169	Matrix metalloproteinase 1 (matrilysin)	20.6
	438953	M73760	Hs.52520	integrin; beta 8	16.7
	428664	A0001666	Hs.185056	similar to SALL1 (sal) (Drosophila)-like	16.5
	439820	AL360204	Hs.263853	Homo sapiens mRNA full length insert cDN	16.5
	402089	H07620	Hs.2286	Matrix Metalloproteinase 10 (stromelysin	16.2
75	421155	H87873	Hs.102287	lysoz oxidase	16.1
	431989	AW572870	Hs.291069	ESTs	15.9
	428635	BE365109	Hs.123227	ESTs	15.9
	424381	M62063	Hs.150917	catenin (cashekin-associated protein), a	15.7
	428976	AL037624	Hs.194656	ras homology gene family, member 1	15.1
80	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	15.0
	439706	AW872527	Hs.59761	ESTs	14.7
	462055	A377431	Hs.293772	ESTs	13.2
	410102	AW248508	Hs.279727	ESTs;	12.5
	428352	H10233	Hs.2205	secretory granule, neuroendocrine protei	12.4

WO 02/102235

PCT/US02/19297

	430534	A1800551	Hs.26685	ESTs	3.8
	431346	B1019924	Hs.271530	Uroplakin 1b	3.7
	416559	U03272	Hs.79432	Rhrlin 2 (periplast contractural area	3.7
	407792	A0077715	Hs.39394	putative secreted ligand homologous to I	3.7
5	426585	AW505139	Hs.279844	hypothetical protein FLJ13033	3.7
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.6
	411773	NM_005799	Hs.72026	protease, serine, 21 (testis)	3.6
	427328	AF013765	Hs.105643	polydystole binding protein-interactin	3.5
	431958	X53629	Hs.2877	Cadherin 3, P-cadherin (placental)	3.5
10	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
	419193	AW332987	Hs.80474	prostaglandin-endoperoxide synthase 1 (p	3.5
	422778	AF072673	Hs.114218	ESTs	3.4
	431840	AW554908	Hs.2950	POU domain, class 5, transcription facto	3.4
	408730	AW660717	Hs.47144	DKFZP566N0819 protein	3.4
	419452	U33635	Hs.90572	PTK protein tyrosine kinase 7	3.3
15	421841	AA308197	Hs.108550	KIAA0336 protein	3.3
	430964	AF220075	Hs.291997	ESTs	3.3
	456546	AW60321	Hs.203845	ESTs, Weakly similar to TWK-related aci	3.2
20	410687	U24389	Hs.65436	lysyl oxidase-like 1	3.2
	414774	X02419	Hs.17724	plasminogen activator, urokinase	3.2
	422552	AA004042	Hs.58066	hypothetical protein	3.1
	421991	NM_014918	Hs.110488	KIAA0590 protein	3.1
	418140	BE613836	Hs.83651	microfilament-associated protein 2	3.1
25	458924	BE242158	Hs.24427	DKFZP66O1646 protein	3.1
	411789	AF265355	Hs.72157	Homo sapiens miRNA, cDNA, DKFZP564419	3.1
	434241	AF111913	Hs.263607	hypothetical protein PR03077	3.1
	422611	AA158177	Hs.118722	fucosyltransferase 8 (alpha 1,6) fucosy	3.1
	408633	AW965843	Hs.21291	mitogen-activated protein kinase kinase	3.1
	415331	AB789227	Hs.79584	mesoderm specific transcript (mouse) hom	3.1
30	412604	AW976324	Hs.47144	DKFZP566N0819 protein	3.1
	425851	NM_001490	Hs.156542	glucosaminyl (N-acetyl) transferase 1, c	3.0
	431259	NM_006680	Hs.261391	claudin 16	3.0
	418557	BE140692	Hs.246645	ESTs	3.0
	428242	HS6769	Hs.2220	hemkima inhibitory factor (cholestergic	3.0
35	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	3.0
	457590	AW12809	Hs.5378	spondin 1, (f-spondin) extracellular mat	2.9
	419741	NM_007019	Hs.93002	ubiquitin chain protein E2-C	2.9
	428530	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.9
	417315	AB090442	Hs.180480	rhodonal protein S24	2.9
40	438777	AA825457	Hs.142179	ESTs, Weakly similar to ORF2 [M.musculus	2.9
	442255	AB27248	Hs.224398	ESTs	2.9
	428248	AI126772	Hs.40479	ESTs	2.9
	403019	AA834026	Hs.60718	RA0584 (S.cerevisiae)-like	2.8
45	435262	AA335151	Hs.120669	Homo sapiens cDNA FLJ11562 lis	2.8
	419488	AA316241	Hs.90691	nucleophorin/nucleoporin 3	2.8
	434288	AW180075	Hs.116265	ESTs	2.8
	407872	AE039723	Hs.40735	hizzled (Drosophila) homolog 3	2.7
	431611	U08795	Hs.261428	tissue specific transmembrane antigen	2.7
50	433981	R04812	Hs.237146	Homo sapiens cDNA FLJ14234 lis, clone NT	2.7
	453779	N36187	Hs.43388	ESTs	2.7
	433068	NM_006456	Hs.288215	staiyltransferase	2.7
	426841	A052355	Hs.193728	ESTs	2.7
	426778	AA006530	Hs.193326	fibroblast growth factor receptor-like 1	2.7
55	461346	NM_006338	Hs.26312	glioma amplified on chromosome 1 protein	2.6
	434853	AA114212	Hs.9930	serine (or cysteine) proteinase inhibitor	2.6
	420162	BS378432	Hs.95877	cyclin-dependent kinase 4	2.6
	447149	BE258867	Hs.338	TAR (piv) RNA-binding protein 2	2.6
	433656	AW974541	Hs.292335	ESTs	2.6
	408210	N81189	Hs.43104	ESTs	2.6
60	430651	AA961694	Hs.106187	kinasin protein 9 gene	2.5
	422699	BE037202	Hs.13638	non-metastatic cells 1, protein (HM23A)	2.5
	421802	BE261458	Hs.108408	CGI-7 protein	2.5
	446211	A027193	Hs.14331	S100 calcium-binding protein A13	2.5
	404029	W72891	Hs.26470	protocadherin beta 2	2.5
65	453012	T95034	Hs.31324	putative mitochondrial outer membrane pr	2.5
	415931	AA857631	Hs.120773	ESTs	2.5
	448153	Y10805	Hs.20621	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
	419220	AA811938	Hs.291759	ESTs	2.5
	432180	Y18418	Hs.272822	Row6 (E coli homolog)-like 1	2.4
70	406550	AB24380	Hs.172623	collagen, type I, alpha 1	2.4
	406993	AW247080	Hs.57101	minichromosome maintenance deficient (S,	2.4
	421654	AW153267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	2.4
	409956	AW103364	Hs.727	H.sapiens activin beta-A subunit (exon 2	2.4
	407594	W22945	Hs.18745	ESTs	2.4
75	448796	AA147829	Hs.33193	ESTs, Highly similar to AC007229 3 BC372	2.4

Table 19 lists about 17 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode proteins that are secreted into blood, lymph, or other body fluids. These genes, and their products, in combination or alone, are listed candidates for the early diagnosis of ovarian cancer. These genes were selected from 59950 probesets on the Affymetrix/Hu03 GeneChip array such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 2.4, and that are likely to encode secreted or extracellularly-shed proteins. The "average" ovarian cancer level was set to the 90th percentile amongst various ovarian cancer samples. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 19th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

WO 02/102235

PCT/US02/19297

TABLE 19: ABOUT 17 GENES, AND COMBINATIONS THEREOF, USEFUL FOR DIAGNOSIS OF OVARIAN CANCER

US ID: UniGene ID			
Title: UniGene Title			
% tumors: percent of tumors detected expressing gene			
Single genes:			
US ID	Title	% tumors	
10	Hs.5378	spodin 1, (l-spodin) extracellular matrix protein	77
	Hs.12644	EGF-like-domain 6	66
	Hs.151254	kallikrein 7 (phymatryptic; altatum conueum)	66
	Hs.97444	mammaglobin 2	73
	Hs.155961	mesothelin (cytokine)	57
15	Hs.2258	Matrix Metalloproteinase 10 (Stromelysin 2)	21
	Hs.50915	kallikrein 5	27
	Hs.301122	bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)	54
	Hs.79361	kallikrein 6 (neuridin, zymase)	38
	Hs.83169	MMP 1 (interstitial collagenase)	23
20	Hs.72026	protease, serine, 21 (testisin)	16
	Hs.39384	putative secreted ligand homologous to ltr1	46
	Hs.2719	epididymis-specific, whey-acidic protein type, four-disulfide core	91
	Hs.155324	matrix metalloproteinase 11 (stromelysin 3)	11
	Hs.1554	cartilage oligomeric matrix protein	25
25	Hs.169300	TGF beta 2	21
	Hs.2250	leukemia inhibitory factor (cholesterol differentiation factor)	23
Exemplary Combinations:			
	EGF-like-domain 6 + mammaglobin 2	93	
	kallikrein 7 + mesothelin	71	
30	mammaglobin 2 + bone morphogenic protein 7	88	
	EGF-like-domain 6 + bone morphogenic protein 7	91	
	kallikrein 7 + bone morphogenic protein 7 + testisin	75	
	kallikrein 7 + mammaglobin 2 + mesothelin	84	
	mammaglobin 2 + bone morphogenic protein 7 + TGF beta 2	91	
35	EGF-like-domain 6 + bone morphogenic protein 7 + MMP 1	95	

Table 22A lists about 1625 genes up-regulated in ovarian cancer compared to normal adult tissues. Genes associated with ovarian cancer were selected from the 53462 probesets such that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 5.0. The "average" ovarian cancer level was set to the 93rd percentile value amongst various ovarian cancer specimens; the "average" normal adult tissue level was set to the 96th percentile value amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Tables 20B-24B list accession numbers for Pkey's lacking UniGeneID's for tables 20A-24A. For each probeset is listed a gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using ClustalW and Alignment Tools (Double Twist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Tables 20C-24C list genomic positioning for Pkey's lacking UniGene IDs and accession numbers in tables 20A-24A. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

TABLE 20A:

Pkey: Unique Eos probeset identifier number
 ExAccess: Exemplar Accession number, Genbank accession number
 UniGeneID: UniGene number
 UniGene Title: UniGene title
 Pred. Protein Dom.: Predicted protein domain
 RT: Ratio of tumor to normal body tissue

Pkey	ExAccess	UniGene ID	UniGene Title	Pred. Protein Dom.	RT
421296	U02666	Hs.103233	perlepin	perlepin, SS	32.5
453028	AB005532	Hs.31442	RecQ protein-like 4	DEAD, helicase_C, Fork_head	27.5
422310	AA316622	Hs.96370	cytochrome P450, subfamily IIS	SS, TM, kinase, JN, Jg	26.5
437897	AA770961	Hs.145170	hypothetical protein FLJ22969	SS, TM, z-DHHC	26.3
445374	AA326256	Hs.24755	ESTs, Moderately similar to al		22.5
441021	AW327516	Hs.7544	H1 Helicase family, member 2		22.3
409518	BE384836	Hs.3454	KIAA1821 protein	SS	21.3
413436	AF238083	Hs.68051	sphingosine kinase 1	DAGKc	21.2
424420	BE51743	Hs.149588	prostaglandin E synthase	MAPEG, SS, TM, MAPEG	20.7
422645	L40027	Hs.116890	glycogen synthase kinase-3 alp	kinase, SS, Fts	20.7
422098	H03117	Hs.111497	similar to mouse neuronal prot	TM	20.2
429556	AW139399	Hs.98968	ESTs	SS, kinase, FMP/22, Claudin	20.1
436485	X59135	Hs.156110	Immunoglobulin kappa constant	SS, Ig, SS	19.9
423652	AF051222	Hs.130112	Homo sapiens clone Z3529 mRNA	ADIC, SS, P, PD, PD	19.8
431773	BE409442	Hs.255557	pleckstrin homology-like domain	PH, SS, LIM, Troponin	19.4
422179	AF091619	Hs.112657	dynein, axonemal, intermediate	WD40, SS	19.3
420839	A1782952	Hs.252950	hypothetical protein MGC10870	SS, DS, UPF0139, Glyco_hydro	18.5
441356	BE384361	Hs.182885	ESTs, Weakly similar to JC2024	SS, TM, ank	18.5
421659	AW091238	Hs.331501	Homo sapiens, Similar to cyste	SS, Fork_head	18.4
439924	A1565967	Hs.125293	ESTs	SS	18.1
458814	AA048957	Hs.170861	ESTs, Weakly similar to Z195_H	SS, TM, JH, recept_a, M, re	17.5
451643	M61437	Hs.234799	breakpoint cluster region	RhoGEF, RhoGAP, PH, C2	17.2
439108	AW153034	Hs.5467	synaptophysin 3	Synaptophysin, SS, TM, PD, WD	16.9
422945	AL043863		hypothetical protein FLJ110803	SS	16.8

WO 02/102235

PCT/US02/19297

410418	D31382	Hs.63325	transmembrane protease, serine	SS,TM,ld_recept_Lutypsi	16.8
438424	A812468	Hs.25895	hypothetical protein FLJ14956	SS,TM	16.7
420435	A810721	Hs.35424	ESTs	SS	16.4
418969	W33191	Hs.28907	hypothetical protein FLJ20258	SH3,SH3	16.2
421612	A8161254	Hs.106196	8D6 antigen	ld_recept_a,SS,TM	16.0
456177	NM_012391	Hs.79414	prostate epithelium-specific E	Ets,SAM_PNT	15.7
414037	L24296	Hs.77448	aldolase dehydrogenase 4 family	aldol	15.6
423831	H03379	Hs.165383	hypothetical protein DNF2p3349	TM,DnaJ,UBA,Air/Gap,homoc	15.4
454017	AW023617	Hs.347130	hypothetical protein FLJ22709	SS,TM,myosin_head,RA,DAG_	15.5
401278			Target Exon	Band_41	16.5
444634	A1084452	Hs.22158	hypothetical protein FLJ21988	SS	15.4
410259	A020337	Hs.61495	myosin, heavy polypeptide 9, n	CPD_IDH_MocA,GF-0_IDH_MocA	15.1
406520	M00100	Hs.140550	myosin, heavy polypeptide 9, n	myosin_head,Myosin_tail	16.4
423081	A262992	Hs.123159	sperm associated antigen 4	TM	14.9
421436	A1583067	Hs.149152	ESTs, Weakly similar to RHOP M		14.7
416683	AA453558	Hs.62406	hypothetical protein FLJ22573	SS,mm,SS	14.7
413344	A1569551	Hs.155265	knagel-related rice finger pr	SS,TM,BTB,Pop_M128_propop	14.6
406901	M14624	Hs.78950	glucuronid 4 beta galactosyltran		14.6
436186	BE-30717	Hs.5074	branched chain keto acid dehyd	E1_dehydrog	14.5
455537	A19295439		similar to S. pombe dmi1	Dmi1,SS	14.5
434518	H56995	Hs.37372	knagel-related rice finger pr	Metaphase	14.4
421489	A822821	Hs.32433	Homo sapiens DNA binding pepi	SS	14.2
444441	AW613841	Hs.301394	ESTs	SS,PI-PLC-X,PI-PLC-Y,C2	14.1
435017	A336522	Hs.12654	hypothetical protein MCC3101		14.0
446572	A1089191	Hs.262661	angiotensin II, type I recepto	ESTs	13.9
434068	A4977935	Hs.127274	ESTs	SS	13.7
432481	AA451645	Hs.161504	Homo sapiens cDNA FLJ11973 Its	SS,Collagen,COLFI,TSPN	13.7
447334	Z28883	Hs.18079	phosphatidylinositol glycan, c	SS,Poplilase_C2	13.6
421182	A4204855	Hs.104480	ESTs	SS,TsTopoisomerase_1,Topois	13.3
407767	W15398	Hs.38628	hypothetical protein	SS,z-CCCH	13.3
456642	AA451623	Hs.109752	putative c-Myc-responsive		13.3
437457	A4757900	Hs.270623	ESTs, Weakly similar to S65657	SGS_PSY	13.2
430176	AA449612	Hs.152475	ESTs	SS	13.1
403369	A1512684	Hs.195671	ESTs	Sec7,PH	12.9
436725	BE045223	Hs.136912	hypothetical protein MGC10796		12.9
410219	T98226	Hs.171952	occludin	SS,TM,Occludin,BIR	12.7
442620	C00138	Hs.8535	Homo sapiens mRNA for KGA1969	SS,RNA_pol,X	12.7
439233	A4311833	Hs.225767	hypothetical protein FLJ23109	z-C2H2,LM,SS,Sso_endo_p	12.7
425018	CE245277	Hs.154196	E4F transcription factor 1	RhoGAP,SH3,PH	12.6
423801	NM_015071	Hs.132942	GTPase regulator associated wi	SS,cadherin,Cadherin_C_1e	12.6
417826	BE1506	Hs.15471	ESTs		12.6
402681	CE115042	Hs.152110	hypothetical protein MGC11308	catheirin,SS,TM,cadherin	12.6
420668	F09547	Hs.247735	proteolysin alpha 1		12.6
411570	BE144684	Hs.143431	ESTs		12.5
430387	AE124533	Hs.105607	bicarbonate transporter relate	HO33_coltransp,SS,TM	12.5
423767	H16283	Hs.132753	F-box only protein 2	F-box,SS,F-box,HORMA	12.4
411895	A4265136	Hs.301914	neuronal specific transcripto	LM,SS,LM	12.3
402365			Target Exon	SS,SS,TM,lg	12.2
414371	A905665		Thymosin, beta 4, X chromosome	Thymosin	12.2
444780	R31107	Hs.153400	glycylglycyl-L1 Sources placenta		12.1
428782	X12330	Hs.153400	interleukin 8 receptor	SS,TM,jn3,lg,SS,TM	12.1
427695	R84983	Hs.172862	intron of ElcAcd1 D homolog 1		12.1
409460			C11002257:sp[12909]pp[P23267	SS,TM,SCAN,z-C2H2,KRAB	12.0
407341	A4918886	Hs.204918	ESTs, Weakly similar to ALUR_H	SS,TM	12.0
424046	AB114524	Hs.136380	KIA0024 protein	SS	11.9
422872	BE267866	Hs.187846	ESTs	TM	11.9
450800	BE395161	Hs.1350	proteasome (prosome, macropain	SS	11.8
428648	A4062728	Hs.188021	potassium voltage-gated channe	cNMP_binding	11.7
423229	NM_002962	Hs.2360	S100 calcium-binding protein A	S_100,ehfand,SS,ehfand,S_	11.7
417361	A817594	Hs.188091	Homo sapiens cDNA FLJ12033 Its	CITF,IFI	11.6
451195	H10492	Hs.438	mesenchymal homeo box 1	homeobox,SS	11.5
417595	AA424317	Hs.62299	KIA11606 protein	SS,TM,Glyco_hydro_31,Glyc	11.5
428500	NM_014638	Hs.170156	KIA0450 gene product	SS	11.4
433124	U51712	Hs.13776	hypothetical protein SHAP31		11.4
444001	A095087	Hs.152229	ESTs, Moderately similar to S6	CPase_1_chain,PYC_OADA_H	11.4
419298	AA863479	Hs.85890	pyruvate carboxylase	SS	11.4
428553	AW207410	Hs.185973	degenerative spermatocyte (hom	SS	11.3
411408	U78666	Hs.65949	calcium channel, voltage-depen	ion_trans,SS,TM	11.3
424338			Target Exon		11.2
427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (ecze	WH1,PEQ,WH2,SS	11.2
406230			Target Exon		11.2
432125	AW972657	Hs.183006	Homo sapiens cDNA FLJ12300 Its	Band_41,ERM	11.2
408632	AW069590	Hs.63428	ESTs, Weakly similar to Z19C_H		11.1
402096			Est Control	SS,SS,Glyco_transf_43,COLF	11.1
450503	R35917	Hs.301338	hypothetical protein FLJ12587	SS	11.0
407805	W03512	Hs.6479	hypothetical protein SHAP31272	SS,Sema,kinase,TIC,P5Le	11.0
432143	AL140183	Hs.123484	Homo sapiens, clone IMAGE:4178	SS,TM,cys_401_FGFR	10.9
446839	BE191928	Hs.16234	mitotic spindle coiled-coil re	Topoisin,SS,glycyl_en	10.9
443559	A076765	Hs.285899	ESTs, Moderately similar to AL	SS,TM,BIR,UQ_2	10.8
411298	AW835658		ph-PMD-T0017-031259-001-hd/L		10.8
409557	BE182896	Hs.211193	ESTs		10.8
451158	AW063117	Hs.61508	Dx7 associated protein 1	mmSS,mm	10.8
444410	BE387390	Hs.33719	ESTs, Moderately similar to S6	SS	10.8

WO 02/102235

PCT/US02/19297

428948	BE514362	FK506-binding protein 3 (25AD)	FKBP,PIPK	10.6
424707	BE061914	Human sapiens cDNA FLJ14476 fls	SS,SS,TM,Sema	10.6
448619	U77735	plm-2 oncogene	phnase,SS,TM,OTU,K,Jetra	10.5
443841	N71463	ESTs, Weakly similar to ALU1_H	SS,TM,UPF0016	10.5
444369	A0697160	ESTs, Weakly similar to H546_H		10.5
404333		C7001735>g(763633)gbgAA95	vwd	10.5
401210		C1200519>g(770349)gbgAA95		10.5
457941		ESTs, Weakly similar to AF1516	SS,TM,SS,TM	10.4
401594	A0004525	NM_024817: Homo sapiens hypothe		10.3
441790	AW294909	ESTs	SS,SS,SA/C3_GANP	10.3
444006	BE544055	ESTs, Weakly similar to SFRA_H		10.3
433185	U719188	ESTs	SS	10.2
430361	AF091196	huesless protein (putative sin	jmc	10.2
410471	T88872	ghyd3.1a2s1 Soares fetal liv	SS,TM,7m_2_EGF_catharin,	10.1
433573	AF234087	cadherin, EGF LAG seven-pain G		10.1
417371	N74613	ESTs		10.0
428187	AA770021	ESTs	SS,jg,ln3	10.0
419563	AA526235	Homo sapiens cDNA FLJ11963 lles	ethand,SS,CAP_GLY	10.0
412674	X04106	catpain 4, small subunit (30K)		9.9
425883	U43604	Human unidentified mRNA, part		9.9
442739	NM_207274	cytosolic acyl coenzyme A:cho	Acyl-CoA_hydro,SS,TM	9.9
429469	MG6590	glycine dihydrogenase (decarbo	GDC-P,GDC-P	9.9
420029	BE250876	polyamine-modulated factor 1	almo,lna_red,SS,TM,glg	9.8
445625	BE246743	hypothetical protein FLJ22035	SS,TM	9.8
435339	AA356001	ESTs	SS,ras	9.8
407235	D00569	SAC2 (suppressor of acin muta	SS,TM,Ribosomal_S13,Galac	9.8
428758	AA433988	CA125 antigen; mucin 16	SS	9.8
401349		inositol polyphosphate-1-phosp		9.7
437915	A037393	Homo sapiens clone N111 Ntera20		9.7
424511	BE300512	ESTs, Moderately similar to AL	Acyl-CoA_dh,Acyl-CoA_dh_M	9.7
423398	Z80345	acyl-Coenzyme A dehydrogenase,	ank,SS,TM,CPGF_A	9.6
405143		NM_013432: Homo sapiens nuclea		9.6
427487	AW139478	ESTs	SS	9.6
424943	AA827716	ESTs	ldh,bch_CSS,ldh	9.6
431512	BE270734	lactate dehydrogenase A	zf-CHC4,zf8_box	9.6
450052	AA81238	ESTs	homeobox	9.5
412738	N04731	slah binding protein 1; FBP in	SS,TM,Na_H_Exchange,ABC2	9.5
444202	AL031686	HLA12785 KIA00939 protein		9.5
451185	A1A40575	WRP-1 protein		9.5
411450	HA5619	ESTs	SS,kinase	9.5
405371		NM_005699: Homo sapiens LIM do	phnase,LIM,PDZ	9.5
435782	NA5433	Homo sapiens cDNA: FLJ20955 l	SS,GP'D,Glucosaminase Iso,G	9.5
418895	AA237359	seimide/mouse protein phosph	Metalloprotease,Metallopro	9.4
454714		NM_001053: Homo sapiens acetyl	CPase_1_chain,biofin_lip	9.4
412837	A022293	hypothetical protein MGC4090		9.3
448133	AA723157	folate receptor 1 (adult)	Folate_rec,SS	9.3
431081	AA481584	polycystic kidney disease 1 (a	SS,TM	9.3
427840	AF055253	D-aspartate isomerase	MF,late_protein_L2,SS,CS	9.2
427435	AW638739	hypothetical protein FLJ13881	SS	9.2
407688	W25317	Human D9 splice variant B mRNA		9.2
407507	U73799	gh:Human dyadacin mRNA, parlia	SS,TM,HOO3_cotransp,CAP_G	9.2
401033		C1100059>g(374644)gbgAAC639	SS,TM,7m_1	9.2
422084	AW452689	ESTs	TM	9.2
452434	D30934	C-type lectin-like receptor-1	lectin_c,SS,TM	9.2
451752	AB032957	KIAA1171 protein	TBC,SS,TM,kinase,Jaminiis	9.2
423231	AF174487	Bcl-2-related ovarian killer p		9.1
407853	BE408309	hypothetical protein, Similar to lipo	SS,SS,ar,ras,ln3,ras	9.1
427397	A029865	catmodulin 1 (phosphorylate ki	ethand,Rma/D,SS,ethand	9.1
405159		ENSP0000024337>cDNA FLJ13584		9.1
422283	AW11307	CDC45 (cell division cycle 45,	CDC45	9.1
407058	X91463	gh:tc:sapiens dhicadp gene exp		9.0
448045	A1297438	prostate stem cell antigen	SS,TM,UPAR_LV5,lovin,SS,T	9.0
400772		NM_010310: Homo sapiens sortil	ln3_recop_a,ln3_ML_recop	9.0
427315	AA179949	Homo sapiens mRNA: cDNA DKF2p5	specfin,SH3,PH,CH	9.0
414381	BE408672	gbc601296556F1 NIH_MGC_21 Homo		9.0
447867	A0525269	ESTs	TM	9.0
422639	A0293777	creatine kinase, brain	ATP-gua,Phans,ATP-gua_P1	9.0
454319	AW247738	ESTs, Weakly similar to T32527	SS	8.9
426781	AF164799	putative 28 kDa protein		8.9
426845	AW215738	hypothetical protein MGC4365	SS,TM	8.9
429527	AA454184	ESTs		8.9
406651	A0592224	gh:tc32022.x1 NCL_CGAP_Uni Hom		8.9
430893	BE502068	ESTs		8.8
414413	BE294677	gh:601174162F1 NIH_MGC_17 Homo	SS	8.8
413726	A0278465	annexin A11	annexin,SS,annexin	8.8
432211	BE274530	hypothetical protein FLJ10086		8.8
421694	BE387430	lysln-like		8.8
453663	AL079864	Homo sapiens mRNA for KIAA1878		8.8
456741	W57606	ESTs	SS,kinase	8.8
442995	AA535511	Homo sapiens cDNA: FLJ23270 l		8.7
415898	Z43379	gh:HSC1AE111 normalized infant		8.7
456977	AK000252	hypothetical protein FLJ20245		8.7
439632	AW101074	hypothetical protein MGC4248	SS,TM,transmembrane4	8.7
431482	AW653572	grain-like neuroendocrine pop	SS	8.7

WO 02/12235

PCT/US02/19297

40128			Eos Control	
438882	A1521310	Hs.283365	ESTs, Weakly similar to AUUS_H	
450988	AL137689	Hs.348012	Homo sapiens mRNA; cDNA DKFZp4	
410855	X37975	Hs.66718	RAD54 (S.cerevisiae)-like	
415126	D60945		gb:HUM141D04B Clontech human f	
418736	I18979	Hs.87908	Snf2-related CBP activator pro	
411157	A823369	Hs.132678	ESTs	
418443	AJ251016	Hs.86220	potassium intermediate channel c	
419167	A1859326	Hs.94875	ESTs, Weakly similar to A36363	
432343	NM_022960	Hs.2961	S100 calcium-binding protein A	
458440	A056468	Hs.135254	Homo sapiens clone 1 thrombox	
407065	Y10141		gb:h.sapiens DAT1 gene, paraf	
452851	AW173191	Hs.213117	ESTs	
422418	AK001383	Hs.116385	hypothetical protein FLJ10521	
420836	AW956453	Hs.204959	hypothetical protein FLJ14886	
455588	U125933	Hs.74669	vesicle-associated membrane pr	
431974	AW97269	Hs.200934	ESTs	
410720	AF035154	Hs.65756	regulator of G protein signal	
449751	AW207115	Hs.25555	ESTs	
434030	AW162336	Hs.3709	low molecular mass ubiquinone-	
403557			Target Exon	
443780	NM_012068	Hs.9754	activating transcription facto	
428660	U38291	Hs.194301	microtubule-associated protein	
421901	AB014554	Hs.109239	protein tyrosine phosphatase,	
411845			Target Exon -	
443382	A1550407	Hs.107875	ESTs	
432662	AW004956	Hs.236720	amionless protein	
441363	AW450211	Hs.126825	ESTs, Weakly similar to A46302	
407363	AF035332	Hs.181125	gb:homo sapiens clone MCAN1L	
425380	AA363389	Hs.321148	AD-015 protein	
424993	AW295112	Hs.153648	Homo sapiens cDNA FLJ13303 tis	
424080	AW189883	Hs.139119	Homo sapiens cDNA FLJ10397 tis	
439772	AL355406	Hs.10268	Homo sapiens mRNA full length	
431765	AF124249	Hs.288541	novel SH2-containing protein 1	
404365			Target Exon	
424310	AA338648	Hs.50334	testes development-related NYD	
401935			Target Exon	
434796	AA812046		ESTs	
423308	AA321080	Hs.204682	ESTs	
434552	AA639810	Hs.325116	Homo sapiens, clone MCC.2962,	
467082	AA470687	Hs.104772	ESTs	
432603	AA654500	Hs.105794	UDP-glucose:glycoprotein gluco	
422445			Target Exon	
422078	AW872378	Hs.120170	hypothetical protein FLJ21415	
418361	AW605368	Hs.12460	gb:U1-HF-BN0-ahb-03-04U1r1	
431354	BE046956	Hs.251673	DNA (cytosine-5)-methyltransf	
403885			Target Exon	
450329	AW073380	Hs.267963	hypothetical protein FLJ10535	
425212	AW363406	Hs.337635	ESTs	
420138	BE288854	Hs.177729	ESTs	
439788	N71241	Hs.119275	ESTs	
422622	AK021035	Hs.133081	B-cell CLL/lymphoma 11A (zinc	
449556	AA002208	Hs.188633	ESTs	
462295	BE379936	Hs.28866	programmed cell death 10	
448650	AW769385	Hs.204891	ESTs	
449035	NM_005558	Hs.13565	Sam58-like phosphotyrosine pro	
444406	AL147257		immunoglobulin heavy constant	
437215	AL117488		Human clone 23564 mRNA sequenc	
408891	NM_006577	Hs.284284	ESTs, Highly similar to beta-1	
404049	AF135341		Homo sapiens winged helix/fork	
443801	AW268942	Hs.263594	Interon of histone/histone-pla	
432581	AA444380	Hs.155482	hydroxycygl glutathione hydrol	
458216	AW024282	Hs.104938	hypothetical protein MCC15006	
401907			C15000610.g111131272bpP793	
401180			eukaryotic translation elongat	
454291	AW368447	Hs.213534	ESTs, Weakly similar to MUC2_H	
444014	A1095718	Hs.135015	ESTs	
412128	AW894709		gb:CM.NM0032.020500-212.d05 N	
408363	NM_005389	Hs.44398	coronin, actin-binding protein	
425904	U51533	Hs.193237	hesionease 3 (white cell)	
425263	NM_001197	Hs.155419	BCL2-interacting killer (apopt	
447045	AW302384		sorting nexin 17	
467613	AA589869	Hs.173770	ESTs	
410328	W03445	Hs.38295	gb:c25g11.r1 Scores melanocyt	
402945			Target Exon	
454246	AW245185	Hs.6996	ESTs	
410079	US4362	Hs.58589	glycoprotein 2	
443878	AW009606	Hs.231923	ESTs	
404076			Target Exon	
406649	A1569392	Hs.284186	gb:h186a02.x1 NC1 CGIAP_U12 Hom	
402030	AL034344		forkhead box C1	
413524	BE146561		gb:QW4-H10222.011199-019-b12 H	
446828	U10120	Hs.242	glucose-6-phosphatase, catalyt	
410539	NM_006848	Hs.56581	protein disulfide isomerase	

TME1-E2_ATPase,HMA/hydro	8.7
SS	8.7
SNF2_NHasease_C,SS	8.7
SS,TM	8.7
SS,helicase_CAT_hook,SS,	8.6
SS,MAPEQ,SS,MAPEQ	8.6
TM,calMED,SP_channel,TM	8.6
SS	8.6
S_100,SS,ethand,S_100,eth	8.6
GNF,SS,TM	8.6
SS,Sema	8.6
RhoGEF	8.6
SS,ras	8.6
synaptobrevin,SS,TM	8.5
bZIP	8.5
RGS,G-gamma,DEP,SS,RGS,DI	8.5
SS	8.5
Cdc3AM_PNT	8.5
bZIP,NTP_inactf_2,SS,TBC	8.5
M	8.5
SAM,SS,TM,mm,P2	8.4
kinase,SS,TM	8.4
SS,mm,atRanBP	8.4
SS,MAT,at-TRAF_2,C3HC4	8.4
SS,TM,HSP20,7m_1	8.4
SS,gb,SS,gb,gb,Transpact	8.4
SS,TM,IRP,Peptidase,SS	8.4
SS,SAM,SS,TM,7m_1	8.4
	8.3
SH2,SS,TM	8.3
SS	8.3
SS,TM	8.3
PH	8.3
SS,myb_DNA-binding,myb_DN	8.3
SS	8.3
SS	8.2
SS	8.2
SS,TM	8.2
at-35,TM,BNR	8.2
SS	8.2
SS,PWWP,PHD	8.2
TM,Sulfate_inactf,STAS,HM	8.2
SS_Pyridox_oxidase,at-C2H	8.2
SS	8.2
SS	8.2
UQ_oon	8.2
SS	8.2
PIPSK	8.1
SS,aprin	8.1
SS,IL8	8.1
NH-domain	8.1
SS	8.1
SS	8.1
SS,TM,DOX,POZ,DEP,Dehehe	8.1
SS,TM	8.0
GATA	8.0
lactamase_B,SS	8.0
	8.0
	8.0
SS,TM,mm,trans,JQ	8.0
SS,XRCC1_N,UBR1,Ubiquitinase	8.0
	8.0
	8.0
SCAN,atf_C2H,KRAB	7.9
WD40	7.9
transducin,transducinase2,he	7.9
SS,TM,asp_MER	7.9
SS,JF-2B,PP2C	7.9
	7.9
	7.9
phnase	7.9
	7.9
Glyco_inactf_8	7.9
SS	7.9
	7.9
	7.9
Fork_head,SS,Fork_head	7.9
SS,TM	7.8
PAF2,SS,TM	7.8
thione,gb_GDI,gnR,SS,T	7.8

WO 02/102235

PCT/US02/19297

444046	A1369834	Hs.130594	ESTs
439591	AF085321	Hs.287452	Homo sapiens cDNA FLJ11760 fls
415411	U13977	Hs.9634	ESTs
450451	BEA09581	Hs.46735	hypothetical protein FLJ23476
448993	A471530		KAA0144 gene product
400623	A161994		Target Exon
446546	A477380	Hs.03570	gb267793.x1 NC1_OGAP_U02 Hom
419757		Hs.26915	specfin, beta, non-enzoyl
451721	NM_006945	Hs.19646	ESTs
458834	A1569883	Hs.118904	endase 3, (beta, muscle)
422633	X8532	Hs.286933	hypothetical protein FLJ20050
439452	A1226911	Hs.104433	Homo sapiens, clone IMAGE-4054
421445	AAS13059	Hs.104433	ribosomal protein S18
437473	A1363410	Hs.25237	mesenchymal stem cell protein
450635	AW403954	Hs.285193	ESTs
442394	R62926	Hs.292154	stromal cell protein
434333	A1187133	Hs.174007	von Hippel-Lindau syndrome
472721	L15409	Hs.196177	phosphorylase Kinase, gamma 2
429099	BE439952	Hs.332538	hypothetical protein MGCS370
444670	H58373	Hs.332538	gb26211.x1 NC1_OGAP_G06 Hom
454945	A1026833		ESTs
444607	AW056335	Hs.253657	ESTs
449125	AB71439	Hs.199029	Homo sapiens mRNA for KIAA1657
447151	A022813	Hs.92679	Homo sapiens clone CDABP0014 m
448626	U757678	Hs.53913	hypothetical protein FLJ22631
430432	AB537758	Hs.241449	KAA1537 protein
401822			C17011422.g12695895emb1CAA75
428609	A1190714	Hs.98945	ESTs
414334	BE257253	Hs.75366	BCL-2 antagonist of cell death
421620	A4446183	Hs.91586	ESTs, Weakly similar to 195214
411650	A126190	Hs.132545	ESTs
42232	A1337813	Hs.337460	ESTs, Weakly similar to A47582
438539	BE348395	Hs.121589	ESTs
450286			C10001922.g17499103pilT209
426333	BE559681	Hs.30736	KAA0124 protein
417390	A4195552	Hs.85852	hypothetical protein MGCS3169
427721	A1582843	Hs.180455	RAD23 (S. cerevisiae) homolog
450716	T57758	Hs.10265	gb-Homo sapiens LENC8 mRNA, pa
407435	AZ711576	Hs.183133	ESTs, Weakly similar to ALU7_J1
413956	AB21351	Hs.332553	serum amyloid A1
427899	AA822986	Hs.332553	Target Exon
454545			nuclear cap binding protein su
430387	AK372884	Hs.240770	protein A
408601	U47528	Hs.96122	ESTs, Weakly similar to G01763
424364	AW383226	Hs.153834	gb:EST1753556 IMAGE resequences,
408932	AW963293	Hs.201881	ESTs
448043	A455653	Hs.102178	synthase 16
421148	AF098936	Hs.1342	cytochrome c oxidase subunit V
428970	AA305078	Hs.140227	ESTs
419295	BE387712	Hs.91753	ESTs
448330	A0238449	Hs.257594	KAA1364 protein
419639	AX001592	Hs.212957	suppressor of Ty (S.cerevisiae)
431488	AB037795	Hs.177972	ESTs
456487	AF064804	Hs.11197	chromosome 4 open reading fram
448615	A910958	Hs.58006	Homo sapiens, clone IMAGE:3343
427433	D62670	Hs.271430	ESTs, Weakly similar to ALUS_H
441076	N48895	Hs.271430	ESTs, Weakly similar to 130222
452554	AW452434	Hs.179219	ESTs
411448	AA178955	Hs.95819	ESTs
442318	A179219	Hs.95819	tubulin-specific chaperone c
425545	AW618158	Hs.76604	Target Exon
412935	BE267045	Hs.197505	ESTs
43748		Hs.253438	ESTs, Highly similar to AF1584
447282	A1869963	Hs.346316	ESTs, Moderately similar to AL
422305	A023842	Hs.107376	hypothetical protein UNFZP434N
415472	AA1180758	Hs.35154	hypothetical protein FLJ12457
427273	AW136032	Hs.19351	peroxisomal biogenesis factor
412265	A1011325	Hs.277807	calcium channel, voltage-gates
447859	AK082194	Hs.2185	eukaryotic transition elongal
422471	NM_014404	ENSP00000211797	SS, RAS GAP, PH, SS, PHD
407672	A1219282	Hs.2185	SS, G-gamma
404199			SS, Ras GAP, PH, SS, PHD
445434	BE391590	Hs.9255	SS, PWWP, Enkephalinase, Apoc
426550	AW297789	Hs.93861	ESTs
454718	AW815144	gb-QV4-ST0212-120100-Q75-410 S	SS, TM, Tm, 11
407686	AW901258	Hs.125043	chromosome 21 open reading fra
418304	AA215702	gb:z97g10.r1 NC1_OGAP_G081 Ho	SS, TM, JSK_Channel
424263	W17640	Hs.1757	seigin
407591	FA04492	Hs.17589	h5, h3, IRK, SS, TM, h3, h3, R
430746	AW977370	Hs.222012	P3C8C
402651			ESTs
407233	AA181183	Hs.143554	NM_000721
407619	AL153241	Hs.37855	Stratagene endot
434035	A1752074	Hs.320139	collagen, type IX, alpha 2

WO 02/102235

PCT/US02/19297

	400419	AF084545	Target	ECGF,glucan_c,ush1,XII	7.2	
	424241	AW095948	Ho.182239	Homo sapiens pyruvate dehydrog	7.2	
	446837	AF261700	ESTs	SAM1_PNT	7.2	
5	427726	U66839	Ho.180353	mitogen-activated protein kinase	7.1	
	421879	AW059607	glb1EST1371677 MAGE, resequenc	SS	7.1	
	412885	H06816	Ho.293756	ESTs	SS,ENP24_CP25L	7.1
	442893	H78133	gcyu18611.1s1 Soares fetal liv	ESTs	7.1	
	437829	A1358522	Ho.103834	ESTs	SS,r_C2H2zm	7.1
	450873	BE464016	Ho.238956	ESTs	SS, TM	7.1
	433396	A742071	Ho.133206	ESTs	SS, TM	7.1
	419596	RS4144	Ho.278707	chromosome 21 open reading fra	SS	7.1
	436629	AA861011	Ho.249795	ESTs	TM	7.1
	414593	BE366764	gb150127349F1 NH1_MGC_20 Homo	BITK,SS, TM	7.1	
	422765	AW049701	Ho.1578	hazardous Vp repeat-contain	SS, TM	7.1
	419823	AW271708	Ho.1185918	ESTs, Weakly similar to M2CM-H	SS	7.1
	405247		Target Exon	SS	7.1	
	455778	BE0508746	gbcCM2-8T0/93-210300-123-009 B	WD40	7.1	
	431036	AA043644	Ho.127269	ESTs, Weakly similar to T02345	Glyco_transf_8	7.1
	435717	AF227396	Ho.105794	VGFp-glucosylglycoprotein gluc	SS	7.1
	406113		Target Exon	SS	7.1	
20	428070	T63918	Ho.182233	retinol-binding protein 2, cel	lipocalin, lipocalin, WD40	7.1
	429029	AA443443	Ho.85524	for muscle specific ring finger	SS	7.1
	430354	AA954810	Ho.239764	human homolog of Drosophila Sc	SS, TM, ly	7.0
	412970	AB026436	Ho.177534	dual specificity phosphatase 1	Rhodanese, DSPc, SS, DSPc	7.0
25	438701	AA937112	Ho.207788	ESTs	TM, sushi	7.0
	454766	AW819273	gbcCM2-ST0284-06 1299-046-a12 S	SS, laminin_Norm, laminin_N	7.0	
	407264		C1800009-0p6786667p67NP_0	ESTs, Weakly similar to T00273	SS	7.0
	420940	AW149754	Ho.248652	a disintegrin and metalloprote	disintegrin, Reprolysin, Pe	7.0
	418641	BE243136	Ho.85947	ESTs	7.0	
	431402	AA743634	Ho.250861	ESTs	7.0	
	423790	BE152383	gbcCM2-H0323-171199-033-a08 H	SS	7.0	
	454588	AW272352	Ho.50450	Target Exon	TM	7.0
	406958		cell division cycle 27	SS, cytofla, Reprolysin_oxid	7.0	
	454438	AA224063	Ho.164421	ESTs	SS, TM, SPFY, 7im_3, ANF, roo	7.0
35	407281	AB07226	Ho.164421	ESTs	SS	6.9
	423386	AW130868	Ho.314081	ESTs	SS, WD40_EPO_TPO	6.9
	459860	BE384326	Ho.24734	gbc01277913F1 NH1_MGC_20 Homo	ank, TM	6.9
	429187	AK001714	Ho.105744	hypothetical protein similar 1	ank, TM	6.9
	431549	AA507036	Ho.197073	ESTs	SS	6.9
40	423384	AL133032	Ho.127808	Homo sapiens mRNA; cDNA DKFZp4	SS, lipocalin	6.9
	454577	AW059272	gbcHNF4-ST0118-040100-034-a08_1	SS	6.9	
	438118	AW175311	Ho.175311	gbczp13g01s1 Stratagene fetal	SS	6.9
	416233	AA176633	Ho.194214	ESTs	SS, perlipin	6.9
45	417012	N38970	Ho.29344	hypothetical protein, clone 24	PNF-AH, ly, lipase, GDSL, SS,	6.9
	452399	BE143533	Ho.105309	platelet-activating factor ace	ET-E2_ATPase, HMA, Hydrolase,	6.9
	418416	U11700	Ho.84399	ATPase, Cu transporting, beta	PK, P4_Kinase, PKC_C2, PI	6.9
	404956		C1003210p678912552p67NP_03	AIE-75 binding protein protein	SS	6.9
	451696	AA018791	Ho.7945	ESTs	SS	6.9
50	438525	AW055528	Ho.100655	C1800032cgl12229289cpl09PTW	SS	6.9
	409096		ESTs, Weakly similar to KIAA13	SS	6.8	
	411411	AA345241	Ho.55950	gbcba4909.x1 NCL CGAP_L25 Ho	SS, CCenasease, SS, CCenase	6.8
	409834	AK11890	Ho.7668	carboxyltransferase 1 (monocytic)	SS, TM, Nc_C, Ex_Cat, beta,	6.8
55	414629	AA345824	Ho.143826	KIAA1087 protein	SS, PABP_rmp, kinase, 14-3-	6.8
	421198	AB029010	Ho.281946	poly(A)-binding protein, cytop	SS, TM	6.8
	445873	AA250970	Ho.22380	ESTs	SS, TM, kinase	6.8
	439605	AF084431	Ho.106822	ESTs	SS, TM, kinase	6.8
	432284	AA532807	Ho.105309	hypothetical protein FLJ20035	Exostosis, SS, TM	6.8
60	421904	BE143533	Ho.105309	exostosis (multiple)-like 3	SH2, SH3, kinase	6.8
	443136	NM_001440	Ho.9018	Gardner-Rasheed feline sarcoma	PHD, Virus_HIS, SS, Cln_chan	6.8
	421768	BE397336	Ho.1422	HEV pX associated protein-8	SS	6.8
	448148	NM_016579	Ho.20509	NM_002697-homo sapiens RAD21	SS	6.8
	420266		ESTs	SS	6.8	
	434316	AW196608	Ho.141015	Homo sapiens cDNA FLJ14015 fa	SS	6.8
	418184	AA367375	Ho.272018	hypothetical protein FLJ20013	TM, Refectol	6.7
	431898	AK000020	Ho.123473	ESTs	Y_phosphatase, DSPc, TM	6.7
	430649	AA115916	Ho.55506	hypothetical protein FLJ20442	oxidized, g6, SS, TM, rm	6.7
	429712	AW245825	Ho.211914	ENSP00000233627-WADH-ubiquin	6.7	
	456886	AW080903	Ho.144996	ESTs, Weakly similar to 138022	SS, TM, ACAT1, LRR	6.7
	427461	AA631527	Ho.332040	hypothetical protein MGC13010	ESTs	6.7
	434200	BE026946	Ho.112664	ESTs	SS, proteasome	6.7
	426330	AF131786	Ho.276303	Homo sapiens clone 25220 mRNA	SS, TM	6.7
	436141	AA970021	Ho.150319	Homo sapiens, clone IMAGE:3610	ESTs	6.7
	441794	AW197794	Ho.255909	ESTs	SS	6.7
	450287	AW291483	Ho.141015	ESTs, Weakly similar to ALUF_H	SS, TM, TNFR, c6	6.7
	411523	AW514263	Ho.257170	ESTs	SS, integrin_B, fn3, Cdc-4e	6.7
	452798	AF116771	Ho.257170	transcriptional regulator prot	6.7	
	451937	AF119664	Ho.27299	ESTs	6.7	
80	421417	AA291004	Ho.326038	ESTs	6.7	
	440317	BE051888	gbc01540093F1 NH1_MGC_8 Homo	aminotran_1_2, SS, TM, LRR	6.7	
	421321	NM_000330	Ho.103502	glutamate-pyruvate transaminase	6.7	
	444904	AW452064	Ho.161139	ESTs	6.7	
	449730	R72290	Ho.117557	ESTs, Weakly similar to 138022	RasGAP, thyroglobulin_1, R	6.7

WO 02/102235

PCT/US02/19297

403672			C4001244g[539533]p[6]A61275	tubulin,TM	6.3
448269	BE622236	Hs.61260	hypothetical protein FLJ13164		6.3
430217	N47863	Hs.100450	ribosomal protein S24	Ribosomal_S24o	6.3
426675	AW064791	Hs.133122	hypothetical protein FLJ14524	SS,TM,amrintran_1,2	6.3
423510	AB000824	Hs.129712	trehalase [brush-border membra	Trehalase	6.3
428573	AA430651	Hs.209249	ESTs		6.3
427052	BE167242	Hs.47099	hypothetical protein FLJ21212	SS	6.3
445999	BE153341		gbc-CVS-H10459-230200-059-b01 H	SS,TM,segar_fr	6.3
450334	AF035959	Hs.24879	phosphatidic acid phosphatase	PAP2,SS	6.3
416000	R82342	Hs.79556	ESTs, Weakly similar to S6557		6.3
427850	AA436011	Hs.98167	ESTs		6.3
425722	U53263	Hs.171932	occludin	Occludin,SS,TM,BIR	6.3
425202	BE258557	Hs.27744	RAB3A, member RAS oncogene fam	ras,ar,SS,PDEase	6.2
431161	AA493591		gblm01a12.51 NCL_CGAP_Thy1 Ho	SS	6.2
413055	AV655701	Hs.75183	cytochrome P450, subfamily 1E	p450	6.2
431250	BE264649	Hs.251377	tissue resistance associated g		6.2
406373			Target Exon	SS,TM,wa,FG-CGAP,integrin	6.2
403003			NM_024944: Homo sapiens hypoth	TM	6.2
437834	AA769294		gblm235g03.s1 NCL_CGAP_GCB1 Ho	SS	6.2
406299			Target Exon		6.2
433827	AF086141	Hs.50760	ESTs, Highly similar to f1mL_1	SS	6.2
414246	BE391090	Hs.280278	EST		6.2
427812	AA770424	Hs.98162	ESTs	SS	6.2
423926	AA530402	Hs.221216	ESTs	UCL_on	6.2
443766	N91071	Hs.109650	ESTs		6.2
431082	AA491600		gblm01a12.51 NCL_CGAP_Ew1 Hom		6.2
429530	AI219431		coagulation factor VIII-associ		6.2
407360	X13075		gblHerman 2a12 mRNA for kappa-I		6.2
446806	AW576033	Hs.22826	trypsin, alpha 3 (sublingual)		6.2
429946	AW162263	Hs.312468	ESTs, Weakly similar to ALUC_H	Ras,GAP,C2,PH,BTK	6.2
413272	AA127923		ESTs		6.2
445050	AW205483	Hs.147760	ESTs	SS,tyrosin,kringle,II,EG	6.2
453130	AA1115911	Hs.8539	ras homolog gene family, membe	ras,ar	6.2
409940	AW221126	Hs.107520	Homo sapiens, clone IMAGE:3934	SS,cf-C2H2	6.2
440390	AW207385	Hs.35475	KIAA0493 protein		6.2
423106	N52572	Hs.13702	ESTs, Moderately similar to AL		6.2
402591			sperm specific antigen 2	Ig,MHC,I,SS	6.1
431470	AA332417	Hs.139550	ESTs	SS,g,phnase,LRRL,PRCT	6.1
416597	H66891		gblT103.r1 Scanes fetal liv		6.1
412122	AW562707		G-rich RNA sequence binding fa	SS,W040	6.1
415056	AB004082	Hs.77367	adenosine A1 receptor	7m_1,SS,TM	6.1
403358	AF181296		Homo sapiens mutant dystrophin		6.1
405473			NM_001097: Homo sapiens acetyl	CP,ase_1,chain,biotin,lip	6.1
422625	AW504656	Hs.155976	cuffin 4B	SS,SS,Cuflin,Cuflin	6.1
422262	AL023315	Hs.113987	lectin, galactoside-binding, s	Gal-bind,lectin	6.1
401121	AJ020052	Hs.155071	C12001539* gij729196(gbjAAAF-7		6.1
425138	AA452354	Hs.155071	hypothetical protein FLJ11190	TM	6.1
457216	BE246228	Hs.233657	ESTs, Weakly similar to AA4798	b7p_Mat,SS,PSOR,EF1B	6.1
456021	BE246228	Hs.260725	gblTCBAP1D5030 Pediatric pre-B	SS,TM,SS	6.1
420319	AW406239	Hs.95593	hypothetical protein	res,ar	6.1
410082	AA061594	Hs.155311	Musashi (Drosophila) homolog 1	SS,HECT,phallo	6.1
450553	AF120385	Hs.25197	STP11 homology and U-box conta	TPP,SS,TM,Phomab(Lactam	6.1
437050	AA766420		ESTs	SS	6.1
456835	A1866753	Hs.76372	ESTs	SS	6.1
412777	A335773		ESTs		6.1
454364	BE235928	Hs.323006	gbl061191272F1 NH_MGC_7 Homo	SS,TM	6.1
446877	A553698	Hs.253313	ESTs		6.1
413045	X92121	Hs.75180	protein phosphatase 5, cataly	Metallophos,TPR	6.1
408064	AW616490	Hs.8102	ESTs		6.1
417852	AJ250662	Hs.82749	transmembrane 4 superfamily me	transmembrane4,SS,TM	6.1
410445	AA199330		gblm23010.Lr1 Stratogene LINT n		6.1
415670	H15578	Hs.211017	ESTs		6.1
436723	M34429		gbl-Human PVT-IGLC fusion prote		6.1
441307	AW071085	Hs.209065	hypothetical protein FLJ14225	SS,TM	6.0
405375			Target Exon		6.0
401488			Target Exon	Glyco_hydro_1	6.0
437650	AA614336	Hs.292297	ESTs		6.0
439827	AA645638	Hs.167369	ESTs	pkinese,DA_PGE-bind,PH	6.0
465373	BE247706	Hs.89751	membrane-spanning 4-domain, s	SS,TM	6.0
454513	BE158271	Hs.109751	gbl-MR0-H10407-180100-004-105 H		6.0
414944	C15044		gbl-C15044 Clontech human aorta	SS,TM	6.0
451277	AP001123	Hs.26176	hypothetical protein FLJ10261	TM,SS,TM,death,DED	6.0
421190	U93031	Hs.102482	mucin 5, subtype B, tracheobron	Oys,trans,vwc	6.0
401215			C1200045* gij751217(gbj)130	hypox,SS,TM	6.0
406117	AL138255	Hs.12396	ESTs, Weakly similar to C30022	SS,cf-C3HCA,BIR	6.0
426357	AW73757	Hs.12396	gbl-RC3-C0283-271099-021-a08 C		6.0
419530	AJ351311	Hs.251946	poly(A)-binding protein, cytop	SS,phnase	6.0
403369	AL135641		oligosaccharide receptor, family 2	7m_1,SS,TM,CSD	6.0
447128	AJ271588		cyclin K		6.0
431297	AA651771	Hs.3076	ESTs		6.0
431857	W19144	Hs.271742	ADP-ribosyltransferase (NAD, p	PARP,PARP_reg,SS,TM,Popl	6.0
430023	AA159243	Hs.271729	FK506-binding protein 2 (13kd)	SS,PRF,SS,PDGF,C2,PL-CLC	6.0
453101	AW062776	Hs.34943	ESTs	TM	6.0
407383	AA532576		ESTs, Moderately similar to AL	SS,Potatin,ank	6.0

WO 02/102235

PCT/US02/19297

430132	AA234686	Hs.234149	hypothetical protein FLJ20547	SS,SS,TMlg	6.0
459111	AU077013	Hs.28757	transmembrane 9 superfamily me	EMRP70	6.0
459770			NM_002352:Homo sapiens melanoma	MAGE	6.0
419611	T26376		gbrA8123C1R1 rat brain, LLN	SS,TM,mu,sushi	6.0
453413	AJ003294		gbrA003294 Selected chromosome	SS,Folate_cantier	6.0
424415	NM_001597	Hs.146580	enkestatin 2, (gamma, neuronal)	enkestatin,SS,Atrophin-1,At	6.0
426048	AU76853	Hs.134478	ESTs	TM	5.9
435750	AB029012	Hs.4990	KIAA1089 protein	SS,TM	5.9
439469	W69636		gbrz48a02zr1 Scanes_fetal_hes	SS,kinase,C2,kinase_C,D	5.9
445654	AB068638	Hs.237691	ESTs, Weakly similar to KIA0416	ESTs	5.9
416830	BE513731	Hs.88659	hypothetical protein MGC45816	TM,CDP-CHL_P_transf	5.9
452113	AB59393		gbrwm1Ta02x1 NCL_CGAP_Um Hom	actin	5.9
449101	AA025847	Hs.23016	G protein-coupled receptor	7/m_LSS,TM	5.9
437640	AA764893	Hs.271255	ESTs, Weakly similar to B8022	SS,Peptidase_M10,hemopexin	5.9
400748			NM_002122:Homo sapiens matrix	ESTs	5.9
442370	AI143593	Hs.129419	ESTs	SS	5.9
442419	AI749853	Hs.270532	ESTs, Weakly similar to B8022	Adaplin_N_Alpha_adaplinC2	5.9
439986	AW750272	Hs.128608	ESTs	SS,TM,SK_Channel	5.9
407553	Z11168		gbrHs,spiens SHT1A receptor re	SS	5.9
431424	AU222959		ESTs	PDEase	5.9
442297	NM_006202	Hs.89901	phosphodiesterase 4A, cAMP-spo	SS,TM,WD40	5.9
457845	H93040	Hs.297729	ESTs	SS	5.9
446912	A347650	Hs.128521	ESTs, Moderately similar to AL	SS	5.9
451381	EE241631	Hs.172330	hypothetical protein MGC22705	SS,Ribosomal_L28e	5.9
416024	AW396484	Hs.343522	ATPase, Ca transporting, plasma	E1-E2_ATPase,Hydrochloric,Ca	5.9
446329	NM_013272	Hs.14805	solute carrier family 21 (orga	katal,OA1P_N,OA1P_C	5.9
431321	AI9136372	Hs.1852	acid phosphatase, prostatic	SS,TM,acid_phosphat	5.9
420339	NM_004605	Hs.94581	phosphodiesterase family, cyclic	SoluteTransfer,SS,DAGKc	5.9
426223	AA024313	Hs.98402	ESTs	HECT	5.9
433333	AI016521	Hs.71810	v-akt murine thymoma viral onc	homeobox,kinase,Ph,kinase	5.9
460251	BE080483		gbrQV1-ET0630-260200 086-a05 B	SS	5.9
406811	AW265404	Hs.27265	ESTs	SS	5.9
414346	AF041430	Hs.75922	brain protein l3	SS,SH3	5.9
456950	AF111170	Hs.306165	Homo sapiens 14q32 Jagged2 gen	SS,TM,DSL	5.9
412173	T17071		gbrx50605r1 S1ralagene liver	CPase_L_chain	5.8
445263	H57546	Hs.42586	Target Exon		5.8
415653	AT791499	Hs.206742	KIAA1550 protein	SS	5.8
430168	AW563343		ESTs, Weakly similar to ALUA_H	SS,TM,ethand,ethand	5.8
454682	AW616029		DKFZP434I735 protein	filament	5.8
453628	AL136200		gbrMP3-S10220-151299 627-b10 S	SS,TM,ATP-synt_C,Galactos	5.8
437372	AA323968	Hs.283631	gbrDKFZ547N032_r1 547 Bynony	SS	5.8
421726	AQ001237	Hs.319088	hypothetical protein DKF26470	TM	5.8
451045	AA216572		gbrz96a05r1 NCL_CGAP_GCB1 Ho	SS,Peptidase_C1,z-C2H2	5.8
439616	BE018635	Hs.58582	Homo sapiens cDNA FLJ12789 ls	SS,TM	5.8
456979	BE056520		gbrFC3-870333-300309 017-r12 B	UEX	5.8
451725	AW444451	Hs.134812	ESTs	SS	5.8
430600	AW565097	Hs.274348	HLA-B associated transcript-3	ubiquitin,SS,TM,G-patch,a	5.8
421707	NM_014921	Hs.107054	Ischemin-2	Lairophilin,OLF_7m_2,Gal	5.8
435127	AW5424	Hs.11565	RNEN cDNA, 201010002 gene	Corona_T,SS,TM	5.8
414347	BE275835		gbr001221639F1 NH_MGC_20 Homo	SS	5.8
439910	H66766	Hs.339397	ESTs	SS	5.8
410382	AW564971	Hs.253546	ESTs	LM	5.8
423391	AW161050	Hs.169611	second mitochondria-derived ac	SS	5.8
423358	AU51474	Hs.343695	gbrvAT10,r1 Schneider fetal	SS	5.8
440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22330 fl	Peptidase_M1	5.8
402189			ENSP00000247 423*D diglac proc		5.8
439849	AW979197	Hs.252073	ESTs, Weakly similar to ALUT_H		5.8
457978	AT776538		gbrv78p04r1 Strategies soliz	SS,PLQ,RozGEF,RozGEF,R	5.8
436655	W28651	Hs.5288	Homo sapiens mRNA: cDNA DKFZ4	SS,TM,kinase,Activin_rec	5.8
411602	L01406	Hs.767	growth hormone releasing hormo	7m_2,HFM	5.8
433357	T05639		gbr:EST03528 Fetal brain, Sital	SS	5.8
404311			Target Exon	TM	5.8
428902	AW879141		ESTs	SS,TM	5.8
452620	AA436504	Hs.119286	ESTs	SS	5.8
401938			Target Exon	SS,PHD,proteasome	5.7
407202	N58172	Hs.109370	ESTs	SS,FS_F3_type,Cp,kinase,E	5.7
456882	RS4393	Hs.226566	ESTs, Moderately similar to l5	SS,CYAL,ThioPjv	5.7
452357	AU381876	Hs.283655	ESTs	SS,TM,SS,TM	5.7
452625	AA724771	Hs.61425	ESTs		5.7
430281	AU878642	Hs.237924	C9A9 protein	mlo_carr,SS,TM	5.7
430480	AWX02651	Hs.301123	Homo sapiens cDNA FLJ12914 ls	TM	5.7
450122	BE313765	Hs.343643	ESTs, Weakly similar to B8022	SS,TM,Y_phosphatase,LDNA	5.7
456801	AI739013	Hs.203348	ESTs	SS,TM,Het,HH_signal	5.7
413413	D82520	Hs.132390	zinc finger protein 36 (KIX) ls	SS,m,DUF185	5.7
445631	AQ001822		Homo sapiens cDNA FLJ10960 ls		5.7
419390	A701162	Hs.90207	hypothetical protein MGC11138	SS,TM,PM22_Claudin,PM22	5.7
423138	AW002725	Hs.286580	hypothetical protein FLJ21106		5.7
426221	AB07881		KIAA0421 protein	PI3_P4_kinase,FATC,SS,TM	5.7
443785	AW449952	Hs.190725	basic-helix-loop-helix-PAS pro	W40,SS,TM,l3,EGF,n3,l3g	5.7
417900	BE250127	Hs.82605	CCD20 (cell division cycle 20)		5.7
446596	AW204515	Hs.155113	ESTs, Weakly similar to G01025	SCAN	5.7
423253	NM_016558	Hs.274411	SCAN domain-containing 1		5.7
427625	AF008216	Hs.285013	putative human HLA class II as		5.7

227

WO 02/102235

PCT/US02/19297

	422837	U25441	Hs.121478	deponase receptor D3	7m_1,SS,Tm,Tm_1	5.1
	407143	C14076	Hs.332328	EST	SS,TM	5.1
	422295	NM_007275	Hs.8165	lung cancer candidate	SS,TM,Glyco_hydro_S6,Glyc	5.1
	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin	p46,SS	5.1
5	427336	NM_005658	Hs.2134	TNF receptor-associated factor	MATHL5S,MATHL2M_NA2MNT	5.1
	447990	NM054377	Hs.26412	mg finger protein 26	SS,TM,CM_N,CM_N2,CM_N3	5.1
	402663			C116226(gH)160557(gH)AAG39	SS	5.1
	409034	A084149	Hs.172035	hypothetical protein similar t	SS	5.1
10	421696	AF035306	Hs.106890	Homo sapiens clone 23771 mRNA	AF03	5.1
	427687	BE349244	Hs.284239	ESTs, Weakly similar to I7885	SS,UOPGT	5.1
	407204	R14533	Hs.145237	ESTs, Weakly similar to ALU1_H	SS,halone,halone	5.1
	454219	W76042	Hs.44313	e-el avian reticulohyaloblast	R60,TIG	5.1
	430513	AJ012008	Hs.241595	G6C protein	SS,TMGST_C,abhydrolase	5.1
15	438902	AA701867	Hs.257726	ESTs	ESTs	5.1
	442743	A801351	Hs.302710	ESTs, Weakly similar to MUC2_H	SS,halogenin_C,Rhodase	5.1
	454523	A0897236		glt-C4V-WN057-15040-335-c06 N	SS,Callosem	5.1
	440518	AA880496	Hs.233335	ESTs	SS,TM	5.1
	448237	AA471790	Hs.309396	ESTs	TM,Ribosomal_S7	5.1
20	428924	AJ016405	Hs.59859	ESTs, Weakly similar to JC5314	SS,TM,leu_n_c	5.1
	112081	Z14355	Hs.253818	glt-AS937F122-STRATAGENE Human	SS,TM,SOB_PSY,GATA	5.1
	437141	BE330417	Hs.31097	hypothetical protein FLJ21478	SS,TM,Glyco_transf_4	5.1
	421658	X94048	Hs.301760	Ileucin (Drosophila) homolog	efhand	5.1
	423467	AK002214	Hs.129014	hypothetical protein FLJ20207	SS,TM,GOPD,SS,TM,SH3,POZ,	5.1
25	417151	AA194056	Hs.253658	ESTs	PH	5.0
	405307	A1761796	Hs.204674	ESTs	Amesillo_seg	5.0
	404752			NM_024773:Homo sapiens hypothe		5.0
	453126	AA032155	Hs.61622	ESTs	ESTs	5.0
	413983	BE348394	Hs.279194	ESTs	SS	5.0
30	405386			NM_003871:Homo sapiens vzw 2	SS	5.0
	412425	AW949156	Hs.133022	glt-C4V-FT0055-110500-205-a06 F	SS,TM,Glyco_transf_2	5.0
	437036	A1571514	Hs.133022	ESTs	SS,TM	5.0
	448455	A252825	Hs.268960	ESTs, Moderately similar to S6	SS,TM	5.0
	411413	BE379436	Hs.211573	heparan sulfate proteoglycan 2	lg,aminin_B,aminin_ECF,	5.0
35	425279	AF043244	Hs.276439	nuclear protein 3 (gapostase	CARD,SS,HF_DNA-bind_E2F,	5.0
	424874	AA347851		Homo sapiens cDNA FLJ20812 fls	SS	5.0
	408023	BE018269	Hs.277688	ESTs	ESTs	5.0
	411758	AW806067		glt-C4V-CT0383-210400-204-403 C	homeobox,homeobox	5.0
	419659	A081118	Hs.65328	Fanconi anemia, complementatio	ESTs	5.0
40	427411	A4402242		ESTs	SS	5.0
	437018	AA889076		ESTs	SS,TM,ERG4_ERG24	5.0
	427029	AA397896		ESTs	SS,ras	5.0
	452047	N35953	Hs.43510	ESTs, Weakly similar to BCX B	SS	5.0
	452005	H23593		glt-C4V-CT003-110500-205-a06 F	SS	5.0
45	453099	H62087	Hs.31659	thyroid hormone receptor-associ	SS	5.0
	441456	A1453911	Hs.127785	ESTs	ESTs	5.0
	414356	AW805085	Hs.335147	glt-C4V-HF-BN0-ale-a-10-4-Uk.r1	SS,TM	5.0
	434967	H18913	Hs.124023	Homo sapiens cDNA FLJ14218 fls	SS	5.0
	436393	AW022213		ESTs	Galactosyl_T_2	5.0
50	406227	AA806165	Hs.130323	Homo sapiens, clone IMAGE3960	WD40,SS,TM,KOW,HJH	5.0
	448680	AW245890	Hs.21753	JMS protein	SS,PIOPZ	5.0
	433343	AF066161	Hs.114611	hypothetical protein FLJ11808	SS,TM,tyrosin	5.0
	429079	AA421000	Hs.200819	ESTs	SS	5.0
	421951	BE327432	Hs.109904	H1 histone family, member X	SS	5.0
55	427204	AA405404	Hs.215725	ESTs	SS,SS	5.0
	409690	W45335	Hs.55398	activating transcription facto	ESTs	5.0
	436574	AW235827	Hs.125465	ESTs	SS,LIM,SS	5.0
	457761	AW401809	Hs.4779	KAA1180 protein	HM,box	5.0
60	435294	T84084	Hs.190900	Homo sapiens cDNA FLJ11723 fls	SS,PIOPZ	5.0
	445372	N36417	Hs.144298	ESTs	SS,TM,AGE,Ribosomal_S17,	5.0
	440511	AF152959	Hs.7236	eNOS interacting protein	CUT,homeobox,helix-helix	5.0
	424437	BE244790	Hs.147049	cut (Drosophila) fls 1 (CCAAT	SS,box,cf-C4H4SS	5.0
	401539			NM_002675:Homo sapiens promyel	TNFR_c4,SS	5.0
65	417903	NM_002342	Hs.1116	lymphotxin beta receptor (TNF	SS	5.0
	442451	AA490000	Hs.129916	ESTs	SS	5.0
	453536	A082925		glt-T1A02.x1 NCLCGAP_G06 Hom	SS,G-alpha,arf	5.0
	425169	AW225200	Hs.128514	ESTs	SS	5.0
	435262	AA677088		ESTs	SS	5.0
70	444855	BE402961	Hs.12084	Tu translation elongation fact	GTP_EFTU,GTP_EFTU_D3,GTP_	5.0
	433507	A1817336	Hs.131791	ESTs	phnase	5.0
	432396	AW259596	Hs.11180	hypothetical protein FLJ14972	SS	5.0
	438395	AA217514	Hs.6211	methyl-CpG binding domain prot	MEB,zf-COXC,SS,zf-COXC	5.0
	446603	NM_014836	Hs.15519	oxysterol-binding protein-rela	Oxysterol_BP,SS	5.0
	407052			Target Exon		5.0
75	440133	A105655	Hs.133349	ESTs	ESTs	5.0
	445903	A1347487	Hs.132781	class I tyrosine receptor	SS,TM,EF1B0	5.0
	412940	BE259701	Hs.819	homeo box B7	homeobox,SS,homeobox,home	5.0
	419269	AA239338		glt-zf1b0A.51 Scans_NhMpu_51	TM	5.0

TABLE 20B:

Play: Unique Eos probaset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

WO 02/102235

PCT/US02/19297

	434316	383402_1	AW196608 AA864617 AA756108 AI126321 AA628921 AW196549 AI200031
	434743	3925_1	AI383410 AI390019 HD0141 I178746 AI048085 AI079511 AI750972 Z42802 AW462523 AI223626 AA215407 AI633079 AA392122 HA2783
			AW55959 AI670806 HD0401 HD5271 AA131836 AW660723 AA527132 I132315 AA0421961 I134951 AW366580 MT887 AI31947 AA521151
5	434796	393400_1	AA812046 AW974514 AA764599 AA649302
	435186	402143_1	AL119470 AA069462 AI026351 AI263835 AL119498
	435262	403805_1	AA677098 AI022245 AA671797
	435339	404485_1	AI058020 AI762981 AA671803 AA988621
	436094	414444_1	AI796701 AW008826 AA704731
10	436369	41894_1	AI811706 AW397940 AI272857 AA875850 AA228003 AI610234 AI915816 AI768606 AI37039 AI8041104 BE1172693 D55503 Z28585 I26651
			AA322398 AA293502 KB2751
	436393	41903_1	AW002215 AI274552 AI227856 AI160412 AI084451
	437018	413133_1	AA893078 AA907263 AA742199
	437050	432210_1	AA766420 AA743319 AW076442
15	437215	404731_1	AI117488 AI044479
	437662	440374_1	AA765367 AA632241 AI222134 AI216405 AI935043
	437834	443674_1	AA765294 AW745299 AW749302 AW745295 AW749304 AW749293 AW749298 AW749294 AW749298 AW749291 AW749297 AW749292
			AW749296 AW749299 AW745287 BE353508
	438118	450293_1	AW753311 AW663061 AA778411
20	438723	46392_1	IS34425 I034531 I034332 M25802 AW938720
	439034	46902_1	AF075083 H52291 H52590
	439150	46919_1	AF068006 H64722 H65212 H65282
	439469	47274_1	W69636 AF086287 W69657
	440317	49187_1	BE561686 BE600618 BE502102
25	440546	490762_1	AA919394 AW138009 AA903618 AA700895
	441358	515468_1	AW173212 AA983848 AI080705 AA931334
	441523	519040_1	AW514263 AI567906 AI259828 AI299043 NS1706 AA936483
	441794	526289_1	AW197794 AW195867 AW197767 AA969466
	442146	533972_1	R52569 T62501 F11984 F13156 AW971679 I77028 H12167
30	442318	536584_1	AI792199 AI733401 AA919378
	442472	543371_1	AW006658 AW006852 AF049582
	442780	551405_1	AI017821 AI017613 AI05811133
	442893	553987_1	H76153 H50849 AI023482
	443952	586524_1	AI149106 AW003316 AI534156 AI030329 AI765679 AI769652 AI167308 AI128885
35	444406	590504_1	AI147237 AI080517
	445099	629785_1	BE163341 AW027755 BE171477
	445625	64558_1	BE246743 AA438642 AW024744 AW242177 AA973476 AW385185 R07536 R73462 AW654529 TS7442 AI309986 R50073 R48743 AI769689
			H563500 AA117806 AA678000 AW109863 AI986207 AW471273 R73463 AI335104 AI909161 AA552927 AA564604 H21954 I25141 AA596793
			R50074 AI708255 AI2
40	445631	6457_1	AW001827 AW660325 AA332296 AW666531 AW130957 AW193961 AI347975 AW081323 AW662527 AI343924 AI380749 AA338153 T66966
			AI655000 AA118837 AI63485 AA410698 AI020726 BE001355 AI873925 AW779200 AI054755 AW593996 AI336327 AI336928 AI370306 R60692
			H19058 H11224 T1
			AI261700 AI733196 AA095160 AI793007
45	445637	652098_1	R71107 AI241136 AI653196 H04563
	446780	652897_1	AW542105 AI341280 AB717445
	446790	693032_1	AW392394 AW579531 AW382131 AA010316 BE146145 AW573962 AW579577 BE146152 BE146540 BE145972 BE146099 AW003280 AA868470
	447045	70510_1	BE146336 T63800 AW687294 BE146289 BE145319 BE146307 W44912 AI978134 AW026917 BE382873 AA093733 AI656533 AI652123 AA847654
			AW173352 AW57240
50	447128	70934_1	AI217696 BE46902 AA025000 AI244810 X84721 AIB80001 AI653937 AA149683 H00719 AI765229 AW373696 F25787 F35149 AI658815
			AW015380 AA554539 C00021 AA961610 AW059537 R77127
	447394	719113_1	AW063035 AW207644 AI765705
	448330	758900_1	AI038440 AW015705 AI4384282
	448993	79225_1	AI471630 BE540637 BE255481 AW407710 BE513382 BE546730 AA053897 BE145093 BE218514 AW1566702 AI656234 AI636283 AI667265
55			AA340658 BE027794 AA053085 R65173 AA292343 AA454908 AA253504 AI659571 AI824778 AA394602 AI760441 AA364616 BE024745
			AA730180 AA354063 AA4454
	449324	804605_1	AI638706 BE550292 AI14026
	449495	808345_1	AI652833 AI676304 AW588195
	450251	829897_1	BE080483 BE080416 AA892026
	450636	837846_1	AI699629 BE161654 BE077251
60	450807	847559_1	AI739262 F26816
	451145	86673_1	AI215672 AI656628 AW013335 H86334 AA017006
	451752	88218_1	AD032997 N74055 BE467119 AW237035 AI141676 AA934474 AW978722 AI761408 H05497 AI844521 AA715567 H62600 AI749668 Z40632
			AA832081 Z44658 H05496 BE396335 AW296901 BE450977 AI621269 BE465893 M79056 H52533 AA325444
65			AI859393 BE177742
	452113	898664_1	AI003234 AA003165 AI003293
	452413	962190_1	AL138200 T71830 T71828
	453829	967373_1	AW003021 AW027475 AW025951
	453904	968581_1	AA224024 AA114150 AA214275 AA224027 I58431 AA211906 AA699567 AA199744 AA630511 AA1164864 T58463 AA214394 AI161378
	454438	120132_1	AA161381 AA170821 AA167624 AA064940 AI223625 AA191159 AA304946 AW551804
70	454463	1206827_1	AW072781 BE143740 AW757527 AW752559 AW752576 AW752584 RA5742
	454577	1225671_1	AW085277 AA809169 AW609139 AW809192 AW809166 AW809172 AW809191 AW809165 AW809197 AW809181 AW809237 AW809226
			AW809259 AW809199 AW809259 AW809239 AW809273 AW809270 AW809147 AW809186 AW809245
			AW810029 AW813292 AW816155 AW813333 AW816159 AW813302 AW813344 AW813172
			AW815144 AW815150 AW810007
75			AW815273 AW815283 AW815281 AW819274 AW815282 AW815277 AW819286
			AW857236 AW845406
	454982	1249762_1	AW851734 AW851676 AW851693 AW851713 AW851722 AW851615 AW851731 AW851616 AW851648 AW852215
	454983	1272212_1	BE151622 BE151636 AW885648
	455246	1273576_1	BE144384 AW887474 AW881403 BE144336
	455557	1325974_1	AW956339 AW956907
80	455604	1371197_1	BE011183 BE011170 BE011333 BE011188 BE011161 BE011324 BE011161 BE011169
	455679	1349914_1	BE068629 BE068274 BE066396 BE066356 BE086419 BE086345 BE066298 BE066292 BE059389
	455716	1354398_1	BE087465 BE088807 BE088175 BE088876 BE088945 BE089081 BE089862
	455985	1380385_1	BE153524 BE153576 BE153583

WO 02/102235

PCT/US02/19297

456467 1027_1 AF064804 AA320309 N89343 AAG64988 AF089734 AA348248 AW964366 T98641 AW511100 T58642 AW070452 AG031372 AT67005 T32140
W05727 T30869 T30910 N74883 AA903211 AB392796 AA348222 AA829283
457892 432926_1 T224289 AA742470 AA742824 AA744299 AA745380 AA744537 AA869305 AA847698
457978 449500_1 AA776638 BE439540
458198 504384_1 AD286100 A0652934 AA1816305
458644 670856_1 AW270149 AW664628 AD285912

TABLE 20C:

Phy: Unique number corresponding to an Eos probotest

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham 1 et al." refers to the publication entitled "The DNA sequence of

human chromosome 22" (Dunham, et al. (1999) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Phy	Ref	Strand	NL_position
400460	8389428	Plus	35559-36295
400500	9796136	Minus	120238-120496
400528	6081824	Plus	472381-472526,474170-474277,475328-475542,475878-476000
400668	8118719	Plus	121756-122043
400740	8115633	Plus	64231-64336
400762	8131616	Plus	7235-7605
400772	8131629	Minus	34896-35021,41078-41197
400833	8705148	Minus	187650-188138
400863	9798616	Plus	21575-22330
400906	9966290	Plus	112963-112968,120162-120286
400923	7637636	Minus	94518-94669
401121	8507296	Plus	57211-57526
401180	9438648	Minus	150581-152128
401203	9743387	Minus	172591-173035,173868-173928
401210	7712287	Plus	166963-167133,169780-169877,171563-171733
401216	9858408	Plus	103739-105919
401264	5797154	Plus	130810-130927,133367-133604
401278	9795336	Plus	96428-96573
401340	9330791	Plus	72440-73030
401402	7710564	Plus	75730-76077
401488	7341775	Plus	54523-54686,55384-55451,55737-55646,58047-58175,58251-58356
401507	7634110	Plus	71055-71259
401530	8072433	Minus	62808-62906
401563	8095284	Minus	63590-84161
401594	7230963	Plus	7597-8170
401674	7695503	Plus	136766-138927,139157-139296,139440-139593,139660-140159
401677	5956537	Minus	62686-63096,63093-63894
401722	7656694	Plus	143651-144054
401724	7656664	Plus	150063-150241
401822	6730824	Plus	68400-69099
401886	8140731	Plus	148234-149321,150365-150669
401935	3800251	Plus	46329-46473
401938	6102666	Plus	151891-152032
401984	4454511	Plus	103825-104024
402189	8576043	Minus	126318-129601
402197	8676113	Plus	104466-105385
402286	2638070	Minus	92389-92634
402366	9454515	Minus	70928-71185
402445	9798614	Plus	90325-91064,91172-91331
402501	9797862	Plus	8601-8878
402545	9380114	Minus	46547-46678,50604-50737,51384-51467
402651	7595391	Plus	174215-174380
402616	7406502	Minus	35147-54148
403003	5441423	Minus	794037-79560,79712-80021
403128	72191428	Plus	123804-123918,123194-123283,123372-123695,123779-123940,124059-124256
403672	7283286	Minus	96600-96801,96951-97280,97353-97594
403748	7658423	Minus	129503-130344
403865	7710403	Plus	53289-53524
403938	7711795	Plus	48638-48822
404001	8658948	Minus	137956-138217
404066	3367505	Minus	71040-71268
404140	7534008	Plus	121831-121951,124044-124150
404190	6010716	Minus	1669-2740
404311	6570412	Plus	149105-149303
404333	9802821	Minus	137948-138024,138111-138300
404366	9564977	Plus	60151-60319,60859-61038
404430	7407579	Plus	42921-43109
404438	6584205	Plus	63413-63553
404571	7249165	Minus	112460-112548
404596	9958262	Minus	104807-105043
404676	9797204	Plus	56167-56347,58066-58189,58891-59046,60452-60628
404710	5901097	Minus	45190-45336,47509-47622,48137-48264,48805-48946,50073-50345,51467-51658
404782	7105522	Plus	120168-120236
404807	4165210	Minus	124246-124422
404956	7387343	Plus	58683-58203
405085	8072509	Minus	44045-44230
405113	8056527	Plus	170073-170294
405143	9438278	Plus	5984-59883,7355-7427
405159	9966252	Plus	79659-79904

Table 21A lists among 533 genes up-regulated in ovarian cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" ovarian cancer level was set to the 90th percentile value amongst various ovarian cancer specimens, the "average" normal adult tissue level was set to the 75th percentile value amongst various non-malignant tissues, the "average" ovarian cancer value was greater than or equal to 400 units (this selects for the most abundant of the up-regulated genes), and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g., jn, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

TABLE 2 (A):

Key: Unique Eos probe set identifier number
ExAcct: Exemplar Accession number, Genbank accession number
UG ID: Unigene number
Title: UniGene gene title
Pred. Protein Dom.: Predicted protein domain
Rt: Ratio of tumor to normal body tissue

234

WO 02/102235

PCT/US02/19297

456572	AK002016	Ha. 114727	Homo sapiens, clone MGC 16327,	SS.PKPK_Cmyosin_head,Rh	8.2
421592	AF039801	Ha. 103941	bagpoin homeobox (Drosophila)	homeobox,SS	8.2
425829	AK35552	Ha. 557720	lymphocyte-specific protein 1	Calcitriol,SS,Ribosomal_S2	8.1
443431	AI142027	Ha. 145590	ESTs	SS.TM.Reprolysin_Pap_M120	8.0
413762	AW411479	Ha. 848	FK506-binding protein 4 (58kD)	FKBP_TPR,SS	8.0
435685	W26561	Ha. 5288	Homo sapiens mRNA; cDNA DKFZp4	SS.TM.glicase,Activin_roc	8.0
429332	AK374695	Ha. 116807	ESTs, Weakly similar to T16597	SS,i23P_Mel	8.0
413483	AT91453	Ha. 129173	ESTs, novel cytochrome P450	SS,p450_Mel	7.9
447598	AT95956	Ha. 199630	ESTs	SS.TM	7.9
415758	BE270465	Ha. 78793	protein kinase C, zeta	pkinae,DAG_Pe,bind,pkina	7.8
457022	AK377258	Ha. 165902	hMGCo2-CT222-261089-003-e10 C	SS,Ribosomal_L7Ae	7.8
425440	BE327266	Ha. 165902	soluble carrier family 2, field	surp,2,SS,TM,carp,fr	7.8
432747	NM_014404	Ha. 278907	calcium channel, voltage-depot	PKMP22_Claudin,SS,TM,PMP22	7.8
441064	W24563	Ha. 9911	hypothetical protein FLJ11773	SS,TM,homone_jac,c2-C4	7.8
424443	AT51281	Ha. 284161	hypothetical protein from EUKO	SS,TM,SS,TM	7.7
424198	AK026010	Ha. 143026	KIAA1087 protein	SS,TM,Nu_Ca_Ext,Calc-hela	7.6
430513	AJ012008	Ha. 241596	GFC protein	SS,TM,GST_Cathylase	7.6
417900	BE250127	Ha. 82905	CDC20 (cell division cycle 20,	WD40,SS,TM,h3,EGF,h3,Jg	7.6
432891	AF181483	Ha. 279761	HSPC134 protein	SS,TM,tubiquitin,Transglut	7.5
432234	AA531128	Ha. 115803	ESTs	SS	7.5
453485	BE520912	Ha. 33026	hypothetical protein PP2447	SS,TM	7.5
441327	AK001706	Ha. 7773	hypothetical protein FLJ10751	SS,TM,7m_1	7.5
436540	BE397032	Ha. 14468	hypothetical protein MGC14226	SS,TM	7.5
418256	AW846318	Ha. 12271	I-box and leucine-rich repeat	SS,SS,TM,HSP_DNA-bind	7.5
457274	AW874153	Ha. 227152	protein-binding leucine core p	SS,TM,SS,TM,Cathrin_h3_S	7.5
437141	BE304617	Ha. 31097	hypothetical protein FLJ21478	SS,TM,Glycop,transf_4	7.5
425428	AL110261	Ha. 157211	DKFZP596B021 protein	Ctq,Collagen,SS	7.4
431934	AB031481	Ha. 272214	STG protein	SS	7.4
418340	NM_001393	Ha. 24163	diphtheria toxin resistance pro	Opilhamide_zym,SS	7.4
430600	AW959267	Ha. 274548	HLA-E associated transcript-3	ubiquitin,SS,TM,SS-patch,a	7.3
421758	BE397336	Ha. 1422	Gardner-Rasheed pilose sarcoma	SH2,h3,h3,phosphatase	7.3
412841	AT511157	Ha. 101395	hypothetical protein MGC11352	SS,TM	7.3
418313	BE244231	Ha. 84203	CG-06 protein	SS,wip	7.3
423637	AK079657	Ha. 275311	plexin b1	Sema,PB,TM,SS,TM,TIG,Se	7.3
418837	HA4825	Ha. 69040	preproenkephalin	Opoid_neuropep,SS	7.2
423015	U18648	Ha. 123034	G protein-coupled receptor 12	TM	7.2
440188	AK001812	Ha. 7036	N-Acetylglucosamine kinase	ROK,SS,TM	7.2
421975	AW81017	Ha. 6459	hypothetical protein FLJ11656	SS,TM,ACAT	7.2
423568	AL137326	Ha. 133463	Homo sapiens mRNA; cDNA DKFZp4	SS,TM	7.2
446143	BE245342	Ha. 356079	sec11 homolog	secY,SS,TM	7.2
417704	NM_001747	Ha. 82422	capping protein (actin filament	Gelsolin,SS,Gelsolin	7.2
443659	NM_014297	Ha. 7436	protein expressed in hybrid	lactamase,B,SS,KRC1_NBR	7.1
431599	AC234770	Ha. 4755	flap structure-specific endonu	XPC_H,XPB,I,SS,S_enucleas	7.1
438556	NA40027	Ha. 7473	ESTs	SS,TM,common	7.1
428268	AF083420	Ha. 168913	serine/threonine kinase 24 (St	pkinae,SS,kinase	7.1
418373	AW750770	Ha. 84344	OGI-135 protein	SS,TM,PAF22_Olaudin,2OGF	7.1
445057	AW934949	Ha. 12303	suppressor of Ty (Scen)visc	ST,SH2,Ribosomal_L23,phk	7.1
421746	NM_014718	Ha. 107399	KIM-4726 gene product	cathelin,TM,TPR	7.1
413337	AW163525	Ha. 107399	lin-csp (telomelin)	SS,Methyltransf_3	7.0
426591	NM_005201	Ha. 171834	PCTAIRE protein kinase 1	pkinae,SS,UCH-2,UCH1_r	7.0
409125	R17268	Ha. 343567	axonal transport of synaptic v	SS,Kinesin,PH,FHA,Presin	7.0
424261	AW77466	Ha. 143068	cofactor-arginine-associated	SS,SPF2_Nucleate_C,Chro	7.0
431630	NM_002204	Ha. 285829	Integrin, alpha 3 (panlysin CD4	Integrin_AFG-GAP,PTAbd_g	7.0
428195	BE269388	Ha. 182598	mitochondrial ribosomal prot	SS	7.0
429255	AJ432444	Ha. 235500	ESTs	SS	7.0
441323	AA328413	Ha. 190809	ESTs, Weakly similar to ALU7_H	SS,SPidase_C1,af-C2H2	6.9
456928	BE173013	Ha. 205736	gbcDNA-170558-040500-193-602 H	SS	6.9
429556	BE513294	Ha. 205736	HLA class II region expressed	kazal,SS,TM,g,phosphatase	6.9
421543	AK003519	Ha. 105906	hypothetical protein FLJ20512	TM	6.9
442296	NM_007275	Ha. 8186	lung cancer candidate	SS,TM,Glyco_hydrol_56,Glyc	6.9
445937	BE429044	Ha. 321221	UDP-Galactose-4-epimerase beta 1,4-g	Galactosyl_T_2,SS,TM,wip	6.8
435732	AW529604	Ha. 167541	hypothetical protein from EUKO	SS,TM,SS,TM(A2M,A2M_N,NTR	6.8
425542	AF038660	Ha. 206713	UDP-Galactose-4-epimerase beta 1,4-g	Galactosyl_T_2,SS,TM,A	6.8
420190	AL162609	Ha. 95867	hypothetical protein EST00098	SS,dynamitin_Z,dynamitin,PGA	6.8
406215	BE814299	Ha. 105906	synaptic	SS,TM,NAH,UTR,transf-COOH	6.7
410277	R88621	Ha. 26249	ESTs, Weakly similar to T2D3_H	SS,TM,SS	6.7
419567	AK077005	Ha. 92208	a disintegrin and metalloprote	disintegrin,Reprolysin,Pe	6.7
448577	AS60769	Ha. 92208	ESTs	SS,TM	6.7
425226	NM_005253	Ha. 301612	FGS-like antigen 2	i23P,SS	6.6
425336	BE398332	Ha. 278907	anti-epitope antigen	SS,TM,AAA_Ribosomal_L2	6.6
421864	BE387198	Ha. 108973	dolichyl-phosphate mannosyltra	SS,TM,SS,TM	6.6
429962	M69113	Ha. 226755	glutathione S-transferase pi	GST_C,GST_N,SS,ethand	6.6
409867	AA157857	Ha. 182265	keratin 19	Keratin,i23P,SS,Manne	6.6
425068	AF029778	Ha. 195154	jagged 2	DSLR,EGF_wic,granulin,SS,T	6.5
419344	UJ4005	Ha. 277445	disacylglycerol kinase, zeta (1)	onk,DAGKs,DAGKs,DAG_Pe,ti	6.5
424681	AA054400	Ha. 151706	KIAA0134 gene product	helicase_C,PRK,SS,TM,Tm	6.5
417903	NM_002342	Ha. 11116	lympholysin beta receptor (TNF	TNFR_c,SS	6.5
423676	BE502835	Ha. 13463	Homo sapiens, clone IMAGE-2959	SS,shand	6.4
433439	AA431176	Ha. 133293	ribosomal protein S15	SS,SS,TM,TPR,SS	6.4
441379	AW175787	Ha. 336451	selenium binding protein 1	SS,SPF_DNA_binding	6.4
432968	BE614102	Ha. 279869	melanoma-associated antigen re	SS,TM,SGS,DIK	6.4
456963	T18637	Ha. 4241	ESTs	fusulin,tyr,homeobox,TM	6.4
422269	NM_002447	Ha. 29424	mesangial stimulating 1 recep	pkinae,Sema,PB,TM,CA,E	6.4
425676	AW410656	Ha. 159161	Rho GDP dissociation inhibito	Rho_GDI,homeobox,SS,Cyfid	6.4

WO 02/102235

PCT/US01/19297

434240	F08846	Hs.191208	ESTs	SS	6.4
438322	A1350392	Hs.120243	protein, gamma	CH,SS,TM,CTCF,NFI	6.4
440268	B135268/77	Hs.153532	hypothetical protein FLJ22638	SS,zf-C3HC4,SPRY,zf-box	6.4
447666	B6044245	Hs.30011	hypothetical protein MGC2963	SS,TM	6.3
431785	AJ292865	Hs.286763	Breakpoint cluster region prot	BAF,kazal,TM	6.3
440136	A0101636	Hs.119367	KIAA0792 gene product	DUF221,SS,TM,TGfr,prospept	6.3
434916	AF161183	Hs.24007	Homo sapiens, Similar to RIKEN	TM	6.3
444561	B615636	Hs.76354	enoyl-Coenzyme A hydratase, sh	ECH,Phosphatase_UT,SS,TM	6.3
413264	U40272	Hs.75263	isochlorogenic acid dehydrogenase 3 (NA	isoch,SS	6.3
458367	AJ080470	Hs.81315	Homo sapiens, Similar to RIKEN	SS,IRF4-synt_2d	6.3
415010	NM_004203	Hs.77763	membrane-associated tyrosine-	phkase,SS,MMP22_C,acidfin	6.2
410070	T5367	Hs.7091	ESTs	SS	6.2
412940	BE295701	Hs.819	homoio box B7	homoio,SS,SS,homoio,home	6.2
440042	AJ073387	Hs.133686	ESTs	SS	6.2
414023	BE243626	Hs.76267	gT-CBPAP101053 Pedialin pro-B	SS	6.2
414613	U028400	Hs.15827	G protein-coupled receptor kin	phkase,RGS,phkase,C,SS,	6.2
446662	NM_013323	Hs.15827	sorting nexin 11	PX,SS	6.2
408882	AJ243191	Hs.58674	heat shock 27kD protein family	HSP20,SS,TM,zf-C2H2,8T3,E	6.2
414576	AJ004005	Hs.78490	ubiquitin-like 4	ubiquitin,SS,TM,GFPD,GFPD	6.2
447907	H159896	Hs.15747	PCP7 (processing of precursor,	SS,TM,W340,wvd,MAME,PEO_TP	6.2
453447	AW771316	Hs.326566	hypothetical protein MGC11134	SS,TPR	6.1
439988	AW161461	Hs.111677	integral membrane protein 3	TM	6.1
424441	X14850	Hs.147097	H2A histone family, member X	histone,CBFD_NFYB_HMF,SS,	6.1
434668	AW264102	Hs.39108	ESTs	SS,TM,LRCT,LR	6.1
424202	BE35411	Hs.3784	guanylate kinase 1	Guanylate_kin,Coase,Viral_	6.1
432163	AW151952	Hs.46679	hypothetical protein FLJ20739	SS	6.0
444416	AW289085	Hs.11166	hypothetical protein	zf-C3HC4,SpoA,PHD,TM,myos	6.0
447266	BE817015	Hs.11006	ESTs, Moderately similar to T1	SS,TM,LRCT,Sema	6.0
447704	BE311672	Hs.76766	marginal cell expression-enha	TM,MOCAT,SS,TM	6.0
453180	AJ022354	Hs.32112	KIAA0355 gene product	PI,PHD,RTN,SS	6.0
439975	AW323061	Hs.6817	inositol triphosphatase (nucleo	HamP_lik,SS	6.0
449514	AW07440	Hs.23642	protein predicted by clone Z36	SS,PX,zf,lipocalin,PHD,z	6.0
432635	X34633	Hs.3107	CD67 antigen	SS,TM,7m_2,GPS,EGF,SS,TM	6.0
414362	A347834	Hs.76932	H-ethylmalonate-sensitive fac	HSP,SS,TM	6.0
417483	BE546343	Hs.82206	acyl-Coenzyme A dehydrogenase,	Acyl-CoA_th,Acyl-CoA_th_1m	6.0
427988	AA785333	Hs.181349	hypothetical protein 628	SS,SS	6.0
423473	H49104	Hs.128868	hypothetical protein FLJ14768	zf-C2H2,ss,mm,ENTH	6.0
446773	AJ4512424	Hs.76367	heat shock 27kD protein 1	SS	5.9
449936	AW974648	Hs.153937	gbc:EST38672 MAGE recognizes	AD,Adg_comp_sub,GYF	5.9
442969	NM_005761	Hs.153937	activated p71cdc121b kinase	phkase,SF3	5.9
453082	H18835	Hs.31608	hypothetical protein FLJ20041	SS,TM,lon,trans	5.9
452094	AF340106	Hs.27910	centromere protein 2	zNP,zf_3,anucleotide,ss,ss	5.9
451524	AJ021466	Hs.28616	hypothetical protein FLJ10604	SS,SS,phkase,ss,phkase	5.9
427436	AW323516	Hs.178011	hypothetical protein FLJ20257	SS,SS	5.9
439665	AW565781	Hs.293937	ESTs, Weakly similar to FXD2_H	SS,MMPW,T8C22	5.9
440811	AF132489	Hs.7236	eMOS interacting protein	SS,TM,MAGE,Ribosome,S17,	5.9
417334	AJ333792	Hs.157400	hypothetical protein MGC4737	SS,TM,lon,trans	5.9
429976	C75394	Hs.334514	N522 protein	SS,TM,phkase,SH2,SH3,BNR	5.8
433173	Z35093	Hs.3196	surfeit 1	SURF1,SS,TM,SURF1,SURF4	5.8
437891	AW009689	Hs.6311	hypothetical protein FLJ20859	TM,SGT	5.8
410239	AW66380	Hs.61273	hypothetical protein MGC2450	SS,ART,TM	5.8
456840	R95950	Hs.293429	hypothetical protein MGC3121	SS	5.8
409591	AA532663	Hs.9100	Homo sapiens cDNA FLJ13100 fs	SS,TM,LM,homocorb	5.8
409866	AJ000002	Hs.55679	Homo sapiens mRNA: DNA DKF2p4	SS,ABC,tran,SS,TM	5.8
450776	U81378	Hs.25450	soluble cellular factor 29 (mud	Nucleoside,tran,SS,TM,HSP	5.8
429612	NM_020267	Hs.1085	quercetin nucleotide binding pro	G-alpha,af,SS,G-alpha	5.8
422701	NM_014699	Hs.119273	KIAA2295 gene product	zf-C2H2,SGT_C,PHD,SS,TM,H	5.8
412958	BE381670	Hs.75087	Fat-activated 6-oxohexanoine	SS,phkase	5.8
436957	AA902468	Hs.122952	ESTs	SS,DAGKc,DAGKa,RA,DAG_PE-	5.8
423158	H97391	Hs.193313	Target CAT	MeqA_WIB_Pqq,SS,TM	5.8
414786	H73242	Hs.77313	cyclic-dependent kinase (CDC2-	SS	5.8
429504	AJ339664	Hs.100221	nuclear receptor subfamily 1,	hormone_rec,zf-C4,SS,DNA_	5.7
410431	BE281320	Hs.158196	transcriptional activator 3 (ADA	phkase	5.7
420508	AJ270993	Hs.98426	homoio box B6	homoio,SS,homoio,home	5.7
435553	R68672	Hs.49044	DKF279B11624 protein	Hesper_HEPA,SS	5.7
433064	D79691	Hs.30002	SH3-containing protein SH3GLB2	TM	5.7
461920	AJ224463	Hs.27239	DKF279B11624 protein	SS,TM,SS,TM	5.7
453024	H67808	Hs.31647	Target CAT	SS	5.7
415117	AF132489	Hs.78016	polynucleotide kinase 3' phosph	Viral_helicase,SS,Amino	5.7
413163	Y00615	Hs.75216	protein tyrosine phosphatase	fuJag_Y_phosphatase,SS,T	5.7
425246	AJ065561	Hs.155321	serum response factor (c-fos s	SRF-TF,Avodand,SS,TM,p	5.7
433271	BE821687	Hs.14317	nucleolar protein family A, me	SS,TM	5.7
448484	BE613340	Hs.334725	Homo sapiens, Similar to RIKEN	SS,TM,SS,TM,SPIT	5.7
460139	BE393116	Hs.29111	phosphatidylserine-ATP synthase-	new,SS,zf-C2H2,DNAse_II	5.7
469181	X98753	Hs.23179	phosphatidylserine	C2,SS,TM,Y_phosphatase,T	5.6
414457	AW514320	Hs.76195	ATPase, H transperring, lysoso	ATP-synt,C,SS,TM,phkase	5.6
424064	AW161271	Hs.153661	ARF1 (actin-related protein 1,	actin,SS	5.6
415193	AJ349881	Hs.12165	hypothetical protein MGC14333	SS,TM,kinintran_1,2,LR	5.6
407764	AA523346	Hs.88569	Homo sapiens cDNA FLJ14105 fs	SS,TM,SS,TM,TPSP,Up_3,SE	5.6
413049	NM_002151	Hs.823	hepsin (transmembrane protease	hepsin,SS,TM,ATP1G1_PLM_	5.6
454252	H60256	Hs.63236	ribosomal protein S15a	SS	5.6
431787	AW072224	Hs.343661	rat finger protein	SS,WD40,phkase	5.6
421607	AR133097	Hs.183689	KIAA1271 protein	SS,TM	5.6
406782	AA430373		gbc:z0M11.1:1 Sources ovary tun	SS	5.6

WO 02/102235

PCT/US02/19297

	444364	AL137294	Ha. 10964	hypothetical protein FLJ22351	SS, TM, pkinase	5.6
	427834	AA506101	Ha. 26813	hypothetical protein FLJ11807	SS, TM	5.5
	443759	BE300302	Ha. 134729	FXO domain-containing protein	SS, TM, ATP1G1, PLM, MATB, ATP	5.6
	416322	BE019494	Ha. 79217	pyroline-5-carboxylate reduct	PCRD, Octopine, DHD, N, SS, th	5.5
5	406673	M34996	Ha. 195253	major histocompatibility comp	SS, TM, MHC, II, alpha, g, SS,	5.5
	143531	U44755	Ha. 79403	small nuclear RNA activating c	SS, TM, pkinase	5.5
	411030	BE338193	Ha. 57895	740 protein	SS, Collagen, Collagen	5.5
	410653	BE333758	Ha. 63239	95 kDa reticuloblastin	ct-CHC4, SS, SNF2, Nhelica	5.6
	433012	NM_004045	Ha. 279910	ATX1 (antioxidant protein 1, y	HMA, SS, TM	5.5
10	437741	BE561610	Ha. 5809	putative transmembrane protein	SS, TM, SS, TM, RA, VP69, SH2	5.5
	421853	X55079	Ha. 14317	glucosylase, alpha, acid (Pomp	infat1, Gyo, ydr1, SS, SH2	5.4
	427361	AW724240	Ha. 7673	cellular retinoic acid-binding	SS, TM, laminin, 1, 2, LIFR	5.4
	415754	BE242642	Ha. 6830	protein tyrosine kinase 9-like	collin, ADF, SS, TM	5.4
15	457313	AF047002	Ha. 241520	transcriptional coactivator	SS, mm, SS, Cytidylyltransf	5.4
	426345	U242431	Ha. 118282	PAP-1 binding protein	SS, TM, Cytidylyltransf	5.4
	434845	BE267057	Ha. 52537	hypothetical protein R32184_1	SS, TM, C1, Cat, pten, ARID	5.4
	427162	AB011133	Ha. 173864	KIA0561 protein	SS, pkinase, PDZ, SS, SH2, Rho	5.4
	447402	HS4520	Ha. 18490	hypothetical protein FLJ20452	SS, TM	5.4
20	433676	AW371389	Ha. 250173	hypothetical protein FLJ13158	SS	5.4
	424375	A.153758	Ha. 146219	copine VII	CS, SS	5.4
	423402	BE107615	Ha. 141558	Homo sapiens cDNA FLJ12976.6	SS	5.4
	409983	050922	Ha. 57729	Kelch-like ECH-associated prot	ETB, Kelch, SS, TM	5.4
	450184	W31095	Ha. 237617	Homo sapiens, clone IMAGE3447	SS	5.3
25	431629	AU700725	Ha. 265827	"inhibitor, alpha-inducible pr	kinase, SH2, SH3	5.3
	430413	AW842182	Ha. 241392	small inducible cytokine A6 (R)	IL5SS	5.3
	403323	A1378424	Ha. 288761	hypothetical protein FLJ21749	SS, TM, UP, Jtrama, pkinase, pk	5.3
	424927	AW973665	Ha. 153585	hypothetical protein C321024	SS, TM	5.3
	412276	BE242621	Ha. 73799	macrophage migration inhibito	MF, SS, TM, MF, eugar, i	5.3
	416181	AA174126	Ha. 332163	ESTs	SS, TM, GAP, UDP, transfr, Gd	5.3
30	424009	A207585	Ha. 7301	G protein pathway suppressor 2	SS, Acyl-CoA, dh, Acyl-CoA, L	5.3
	435327	BE301671	Ha. 4687	mannose (alpha-1,3)-glycop	SS, HLUH, Myc, N, term, Myc, L2	5.2
	421139	AW953833	Ha. 301372	KIAA1552 protein	SS, TM	5.2
	453449	W16752	Ha. 32281	sema domain, immunoglobulin do	SS, Sema, Ig, PSI, SS, TM, g-f	5.2
	414411	X54079	Ha. 73087	heat shock 27kD protein 1	HSPO2, SS	5.2
35	440906	AW161556	Ha. 240710	hypothetical protein MGC2731	SS, TM, Fceta, hsc, pkinase,	5.2
	421899	AJ011895	Ha. 109281	Nef-associated factor 1	Virus, HS, ZIP, G-gamma, Myo	5.2
	439473	A215529	Ha. 144787	ESTs	SS	5.2
	451585	AK021171	Ha. 256422	hypothetical protein MGC4546	SS, SM, Adipoph	5.2
40	427191	AA608751	Ha. 179516	glucosylase/OT-1 Stralagene lung	SS, Peptidase, C1	5.2
	427515	T79526	Ha. 179516	integral type I protein	EMP2, N, GP2S, SS	5.2
	405325			C1400789-g102351-g104b1AA9	SS	5.2
	438441	AF193844	Ha. 3758	COP9 complex subunit 7a	SS	5.1
	413502	BE246871	Ha. 246871	gl-600A-06B72 HLJ, MJC, 15 Homo	SS, TM, SS, TM	5.1
45	445109	AF039916	Ha. 12330	adenonucleotide triphosphate d	SS, TM, GDA1, CD39, SS, TM, rho	5.1
	408323	H28855	Ha. 53447	amino acids system mRNA; cDNA DKF2p	TPR, SS, TM, pkinase, Ig	5.1
	437027	U8239	Ha. 324051	amino acid systems N transpore	SS, TM, ACAT, MEGAT, SS, TM, TB	5.1
	424598	AF070037	Ha. 236360	RetA-associated inhibitor	SR3, ant, SS, TM, HH, Ig	5.1
50	425372	AW990049	Ha. 236360	Homo sapiens, clone IMAGE3535	SS	5.1
	436576	AA58213	Ha. 77542	ESTs	SS, TM, 7m, 1, DnaJ	5.1
	439012	BE383814	Ha. 6455	RuvB (E coli homolog)-like 2	AAA, DnaJ, UPF00709, SS, Cys, k	5.1
	418910	X25521	Ha. 69466	Homo sapiens, Similar to dodec	SS, TM, 7m, 1, BAJ, ct COX, D	5.1
	414849	AW572721	Ha. 291623	ESTs, Weakly similar to usmane	Adipocyte, SS	5.1
	425743	BE396495	Ha. 159428	BCL2-associated X protein	Bcl-2, SS, lentin, Bcl-2, e	5.1
55	418231	AA326695	Ha. 83548	inosophosphate isomerase 1	TM, SS, TM, ct-UEP, UCH-2, UE	5.0
	419238	AW993538	Ha. 321214	hypothetical protein DKF2554D	SS, TM, WH2	5.0
	449179	A386925	Ha. 24851	ESTs, Highly similar to unknown	SS, TM, C1, C, amonion, transp	5.0
	437617	BE246701	Ha. 5716	KIAA0331 gene product	SS, ct-CHC4, Peptidase, M16	5.0
	412867	AF076861	Ha. 74637	testis enhanced gene transcrip	UPF0005, SS, TM	5.0
60	415679	W48529	Ha. 290200	hypothetical protein AF033561	MSP, gsmain, SS, TM, CUB, NTR	5.0
	426524	AB395663	Ha. 155569	ESTs, Moderately similar to RE	SS, PHD	5.0
	459414	NM_001183	Ha. 6551	ATPase, H transportic, lysos	SS, SS, TM, GDI, Sema, TIG, SS	5.0
	436042	AF284422	Ha. 119178	cation-chloride cotransporter-	SS, TM, aa, permeases, SS, TM	5.0
	410775	AB014480	Ha. 661196	nrlh (E. coli endonuclease III)-	HHH-GPD, SS, TM, REL, PLAT, PK	5.0
65	433350	AB17771	Ha. 61790	hypothetical protein FLJ23338	SS, SS, TM, EMP70, PA28, alpha	4.9
	403300	X03383		HERF receptor tyrosine kinase	kinase	4.9
	426811	BE259228	Ha. 172509	nucleobindin 1	ehand, SS, TM, GFO, IDH, Moca	4.9
	421179	U72664	Ha. 148495	proleosome (prosome, macroph	UM, SS, TM, PMP22, Claudin, P	4.9
	429762	SA46255	Ha. 216354	ring finger protein 5	SS, ct-CHC4, Palm, thioest	4.9
70	419250	AW770105	Ha. 176763	US RNAP-specific protein, 118	SS, TM, 7m, 1, BAJ, ct COX, D	4.9
	426381	BE294216	Ha. 8088	S-adenosylmethionine hydrolase	Adipocyte, SS	4.9
	442103	AA333367	Ha. 8088	similar to S. cerevisiae Sec1p	SS	4.9
	414820	AA371931	Ha. 77422	proteolipid protein 2 (polonic	SS	4.9
	426347	AA454912	Ha. 103407	SAC2 (suppressor of actin muta	SS, Ret, GEF, RA, Ras, GEF, N, hom	4.9
75	423880	BE276111	Ha. 134200	DNF2564186 protein	UPF00120, SS, TM	4.9
	426545	AR24164	Ha. 8935	lymphocyte antigen 6 complex,	SS, TM	4.9
	434044	N28522	Ha. 8935	quinoline phosphate ribosyltran	ORPase, ORPase, N, SS, TM	4.9
	417080	BE392846	Ha. 1063	small nuclear ribonucleoprotei	SS, S19, plectin	4.8
	441455	NZ_0271671	Ha. 7554	zincfin regulated transpore	Zp, SS, TM, Cytidylyltransf	4.8
80	410102	NM_001093	Ha. 65544	endocytic repair cross-comple	HHH, SS, SH3, ant	4.8
	455052	AB864286	Ha. 71962	ESTs, Weakly similar to E36298	SS	4.8
	438270	BE268278	Ha. 28393	hypothetical protein MGC2592	SS, TM, HJC03, cotransp	4.8
	403955	BE267317	Ha. 332640	hypothetical protein MGC31010	SS, TM, ACAT, LRR	4.8
	416976	BE243689	Ha. 308409	major vault protein	vault, SS, TM, laminin, ct C2	4.8
	439547	AJ004832	Ha. 50528	neuropathy target esterase	cNMP_binding, SS, TM, cNMP, b	4.8

WO 02/02235

PCT/US02/19297

	424501	AA70163	Hs.323342	actin related protein 23/3 comp	SS/HH-GPD	4.8
	408244	AA435967	Hs.333388	Homo sapiens, clone IMAGE3957	SS,EF1B0,PGCR	4.8
	432716	A075264	Hs.205180	ESTs	SS,TM	4.8
	414460	L00727	Hs.698	dystrophin myotonic-protein k	phlasee,SS,WD40	4.8
5	433329	BE262943	Hs.9234	hypothetical protein MGC1936	SS,TM,SS,TM,apn,gpdi,C	4.7
	426120	AJ329243	Hs.166887	coprin 1	C2,SS,aminotrat,S	4.7
	432385			E18P0002470297-SEBOX	SS,TM,hemopexin,Somalomed	4.7
	371118	AB017867	Hs.300591	CD3 partner 1	TM,lg,SS,TM	4.7
10	330699	AA302921	Hs.247362	dimethylarginine dimethylaminio	SS,TM,GST_C,hydrolase	4.7
	447131	NM_004585	Hs.17466	retinoic acid receptor respond	SS,TM,phlasee	4.7
	426469	BE545206	Hs.184488	folatin 2	Rand_7,Follin,TM	4.7
	405189			Tmyel Eron	SS	4.7
	404266			NM_024018-Homo sapiens butyro	SS,TM,SPRY,SPRY,lg	4.7
15	457955	A1208996	Hs.121647	ESTs	SS,zf,B_box,SPRY,SS,Nd1	4.7
	413201	BE273378	Hs.13572	hypothetical protein MGC12972	SS,SH2,RhoGAP,SH5,GILT	4.7
	431115	A0015427	Hs.250493	zinc finger protein 219	zf-C2H2,SS	4.7
	442414	BE408758	Hs.8297	ribonuclease 5 precursor	ribonuclease_T2,SS,ribonu	4.7
	416289	AAW403103	Hs.83951	Hernandez-Pudask syndrome	SS	4.6
	436730	AA045767	Hs.6300	bladder cancer associated prot	SS	4.6
20	444586	BE560652	Hs.114147	Rab scaptor 1 (prenylated)	SS,TM,lg,chan,ANF_recept	4.6
	433019	A0206513	Hs.279915	translocase of inner mitochond	zf-Tier10_DDP,SS	4.6
	431522	A025569	Hs.258609	protein tyrosine phosphatase,	In3_Y_phosphatase,SS,TM	4.6
	400846			sorfin-related receptor, LID	ld_recept_L,tn33ld_reco	4.6
25	422154	T79045	Hs.168812	ESTs	SS	4.6
	423211		Hs.95657	hypothetical protein	SS,tag_1,SS	4.6
	439921	AL110209	Hs.6770	LCAT-like tyrosinepholpase	SS,LA,CT,SS,TM,as_pomase	4.6
	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase	phlasee,Furin-like,Recep_	4.6
	426899	AL043221	Hs.172825	KIAA1037 protein	WD40,TPR,SS,TM	4.6
30	408116	AJ051353	Hs.75195	Homo sapiens, Similar to RIKEN	SS,TM	4.6
	412974	R18978	Hs.75195	emopamil-binding protein [lar	SS,TM,SS,TM,TB,Cm,FluJ	4.6
	428510	AW861225	Hs.110613	BANP homolog, SMAR1 homolog	TM	4.6
	414702	L22005	Hs.76932	cell division cycle 34	UQ_con,SS,tyrosin,lg	4.6
	408135	AJ317246	Hs.42557	methyltransferase-like 1	Methyltransf_4,SS,p450,G	4.6
35	445637	WS8429	Hs.8949	hypothetical protein MGC4172	SS	4.6
	452190	H28735	Hs.91688	Homo sapiens clone PP1456 unkn	SS	4.6
	409860	W31092	Hs.55847	mitochondrial ribosomal prot	SS,TM,ssynaptobrevin	4.6
	421140	AA238741	Hs.102133	signal sequence receptor, delt	Herpes_U3,SS,TM,Sema,ph	4.6
	413407	AS365293	Hs.75339	inverted glycoposphate phospho	SH2,GAM,SS,Foln,nc	4.6
40	402463			NM_01462-Homo sapiens s100 ca	ehand,S_100,SS,ehand,S_	4.6
	426402	BE387327	Hs.80475	polymerase (RNA) II (DNA direc	SS,PGAM	4.6
	408339	M34515	Hs.82887	human omega light chain pro	SS,lg,PH	4.5
	417891	W75410	Hs.82887	protein phosphatase 1, regula	SS,TPS	4.5
	425307	BE390657	Hs.30026	HSPC82 protein	SS	4.5
45	423964	NM_004714	Hs.130988	dual-specificity tyrosine-(Y)-	phlasee,SS,Fibritilin,CK	4.5
	432562	BE531048	Hs.278422	DKF2P588J122 protein	zf-C2H2,SS,TM,FG-GAP,Inte	4.5
	427381	W60575	Hs.279771	hypothetical protein FLJ10359	SS,SS	4.5
	422993	NM_018154	Hs.18465	Homo sapiens clone PP1688 unkn	rac,zf,SS,FCG-Fell_Oxy_2	4.5
	424954	NM_000646	Hs.1845	tumor protein p53 (L-Fraumeni	P53,SS	4.5
50	413815	AL040341	Hs.75582	discolin domain receptor fam	FE_Ff_type_C,phlasee,SS,T	4.5
	448963	AA459796	Hs.331247	Homo sapiens, clone IMAGE3610	SS,TM	4.5
	418297	AA157834	Hs.79172	solute carrier family 25 (mb	mb_car,SS	4.5
	421982	D02091	Hs.280534	FABP (beta-ketoadyl-bac-yl car	SS,ab_short,SS,TM,zf-C3H	4.5
	425726	AA488915	Hs.171955	trophinin associated protein (SS	4.5
	414427	L19711	Hs.76111	glycylglycine 1 (dystrophin-ass	SS,TM	4.5
55	433591	AW243994	Hs.5002	copper chaperone for superoxid	rodu,HMA,SS,TM,sspedrin,	4.5
	433997	AW347616	Hs.37003	v-Haas Harvey rat sarcoma vi	rac,SS	4.5
	449029	N28989	Hs.22891	solute carrier family 7 (calb	as_pomases,SS,TM,bzpf	4.5
	432078	BE314877	Hs.24553	hypothetical protein FLJ12541	SS,TM	4.5
60	409560	T08490	Hs.288959	HSCARG protein	SS,SS,WD40	4.5
	412833	AW590547	Hs.298282	ribosomal protein S19	SS,TM,lg,ITAM,Ribosoma_S	4.4
	424153	AJ335721	Hs.213628	ESTs	SS,TM	4.4
	414787	AL049332	Hs.77311	BTG family, member 3	SS,Asn1_proliferat	4.4
	433046	AA225553	Hs.279945	HSPC823 protein	SS	4.4
65	417088	AA541910	Hs.85852	hypothetical protein MGC3169	SS,TM	4.4
	414814	Hs.77307	Hs.77307	farnesyl-diphosphate synthase	polyprenyl_syn,SS,TM	4.4
	418267	BE389537	Hs.83919	glucosidase 1	Glyco_hydrin_63,SS,PH	4.4
	439902	AF174489	Hs.5764	heliose deacetylase 5	Hel_dacetylase,zf-URP,SS,G	4.4
	448947	A197180	Hs.110506	Homo sapiens, Similar to RIKEN	TM,SS	4.4
70	422160	BE176441	Hs.79021	cytosine sulfonic acid decarbox	rac,SS	4.4
	416121	X52762	Hs.23954	isoleucine (cardiomyopathy, dila	Acyltransferase,SS,TM,GDI	4.4
	449717	AA040936	Hs.23954	cerebral cell adhesion molecu	SS,SS	4.4
	425069	AA687465	Hs.258184	potassium voltage-gated channe	SS,akio_kat_nod	4.4
	413380	A9642327	Hs.78323	prohibitin	Rand_7,SS,Rand_7,SH3	4.4
75	429291	AA541837	Hs.112618	melanotransin-1C (neuronal	SS,TM,SSect	4.4
	453415	BE265254	Hs.343258	proliferation-associated 262	Polptitase_M24,SS,TM,Popi	4.4
	425218	AA225085	Hs.198289	Target CAT	SS,Nop	4.4
	447987	BE521544	Hs.157160	hypothetical protein MGC2616	SS,NK,LR,LRNT,LR,LRCT,LR	4.4
	427230	AA157857	Hs.162285	keratin 19	Keratin,bzpf,SS,harnen	4.3
80	448886	AL137291	Hs.22451	hypothetical protein FLJ10357	SS,PH,RhoGEF,SS,anaseA	4.3
	421178	BE267994	Hs.102419	zinc-finger protein	zf-C2H2,SS,TM	4.3
	454031	R38772	Hs.71541	hypothetical protein MGC15577	TM	4.3
	450126	BE016138	Hs.24447	sigma receptor (BR3747) bindin	SS,lg,ph3	4.3
	446537	L86466	Hs.133116	H51 binding protein	SS,TM,MSP,UBA	4.3
	433781	JS5272	Hs.850	IMP (inosine monophosphate) de	IMPDH_C,IMPDH_N,CBS,NPD,S	4.3

WO 02/102235

PCT/US02/19297

433251	AB040965	Ha.32735	KIAA1522 protein	SS,SS,zf-C3HC4,SPRY	4.3
420531	A0652069	Ha.98614	ribosome binding protein 1 (joe	d2P,SS	4.3
432179	X75208	Ha.2913	EgRb1	EPH,ba3,pkkinase,SAM	4.3
448988	Y06763	Ha.22785	gamma-aminobutyric acid (GABA)	Neur_chan_LBD,Neur_chan_m	4.3
428626	A1124572	Ha.323879	inhibitor of kappa light polyp	zf-C2H2,SS	4.3
432966	AL037855	Ha.279861	CGI-31 protein	fibronectin,SS,TM	4.3
428970	BE276891	Ha.194691	retinoid acid induced 3	7m_3,SS,TM	4.3
428953	AA338610	Ha.349183	tumor necrosis factor receptor	TNFR_c6,SS	4.2
401128			C1200054.gql[5729785]ratNP_00	SS	4.2
446899	NM_005397	Ha.18426	potocytin-like	SS,TM,SS,TM	4.2
407151	H25836	Ha.301527	EST 1, Moderately similar to un	SS,TNF	4.2
426613	U96132	Ha.171280	hydroxyacyl-Coenzyme A dehydro	ss,ss,ss,ss,ss	4.2
408616	RS1604	Ha.300842	KIAA1608 protein	SS,DEAD,UDEN	4.2
446616	R65964	Ha.334073	ESTs, Weakly similar to ALU8_H	SS,Zn_cat,Oxpt	4.2
414467	AW603820	Ha.85752	copine 1	SS	4.2
456557	T0192		glycyl 160kDa.1 Stratiogene lung	SS,TM,ssch	4.2
401753			RAH binding protein	SS,Oxid,SH2,STAT	4.2
400563			Target Exon	SS,Pop_M12B_pncop	4.2
430237	A0272144	Ha.236522	DKF2M34P105 protein	abhydrolase,TM	4.2
406101			C11000273.gql[2556107]gbAAK0	SS,TM,TM_1	4.2
421681	BE281303	Ha.299148	hypothetical protein FLJ21801	SS,TM,Vin	4.2
444590	AA457456		hypothetical protein FLJ20435	SS	4.2
408187	AF034373	Ha.43509	statin 2 related protein	SS	4.2
437896	Z83844	Ha.5790	hypothetical protein dJ37E16.5	SS,Hydrolyase,SS,Gal_bnd	4.2
400276			JLHSP000004.43264-2dchdy-dpho	SS,TM	4.2
407394	AF005081		gcf-Homo sapiens ribo-specific	SS	4.2
447407	BE387301	Ha.18528	Sjogren's syndrome nuclear au	SS,HLH,Hsm,GSHp	4.2
410237	A0750589	Ha.61258	argininosuccinate lyase	lyase_1,SS	4.1
415410	AF037322	Ha.278569	sorting nexin 17	PX,k3,pkinase,SAM,EPH_3b	4.1
445757	AA342108	Ha.12271	4-box and leucine-rich repeat	SS,F-box,SS,TM,HSP_pkin	4.1
446388	AA282979	Ha.7758	NPO007 protein	SS,TM	4.1
412825	AW167439	Ha.190651	Homo sapiens cDNA FLJ13625 fs	SS	4.1
439737	A0751438	Ha.41271	Homo sapiens mRNA full length:	SS,C1q,Collagen	4.1
422256	M64673	Ha.1499	heat shock transcription factor	NA,SS,TAF-box	4.1
441184	AA023180		KW40603 protein	hefascine,C,SS,RNA_pol_H	4.1
401722			Target Exon	A_deamin,SS	4.1
411142	NM_014255	Ha.69009	transmembrane protein	Galactosyl_T,SS,Ribosome	4.1
458176	AB61519	Ha.140309	Homo sapiens, clone IMAGE3677	SS,pkinase,pkinase_C	4.1
423216	BE265889	Ha.227314	hypothetical protein DKF2Z044E	SS,serine_catpt	4.1
421537	BE383486	Ha.105547	neural proliferation, differen	SS,TM,Glyco_hydro_47	4.1
421380	D31833	Ha.1372	arginine vasopressin receptor	7m_1	4.1
422702	AJ101373	Ha.119285	chromosome 9 open reading fram	SS,TM,SS,TM	4.1
434142	U47327	Ha.3759	ubiquitin specific protease 5	zf-UBP,UCH,ZUBA,UCH_1,SS	4.1
423896	Z92546		Sushi domain (SCR repeat) cont	SS,TM,ss,Sushi,Somalme	4.1
427407	BE268649	Ha.177766	ADP-ribosyltransferase (NAD; p	BRCT,PARP,zf-PARP,PARP_je	4.1
413749	A1929320	Ha.75816	tyrosine kinase 2	pkinase,SS,TM,jg	4.1
411927	BE274009	Ha.772	glyoxyl synthase 1 (muscle)	Glyoxyl_insrst_1,SS	4.1
433320	D06047	Ha.258079	ESTs, Highly similar to CTNN R	hefascine,C,SS	4.1
433990	AF103501	Ha.16381	hypothetical protein	DAO,SS	4.1
452603	AW410801	Ha.30026	HSPC182 protein	SS	4.1
444986	BE302472	Ha.11314	DKF2P64N1363 protein	SS,GKAP,Band_41	4.1
422556	NM_006245	Ha.118244	protein phosphatase 2, regulat	SS,SS,TM,Ubiquitin_L,Exo	4.1
447347	AA570058	Ha.122730	ESTs, Moderately similar to KI	TM,SS	4.1
428284	AA535762	Ha.183435	NM_005454:Homo sapiens NADH de	SS,TM,Josephin,VM,Joseph	4.1
428551	AA361268	Ha.323847	ESTs	SS,sushi	4.0
417782	T10149	Ha.4243	hypothetical protein FLJ12650	SS,TM	4.0
443939	BE288442	Ha.8661	prolesome (prosome, macroph	SS,SS,TM,SS,TM,LA,CT,ly	4.0
410039	AF207989	Ha.58014	Homo sapiens, Similar to G pro	SS,TM,7m_3,SS,TM	4.0
452715	Z21093	Ha.30352	ribosomal protein S6 kinase, 5	pkinase	4.0
442549	A1751001	Ha.8375	TNF receptor-associated factor	zf-C3HC4,MAP3H,zf-TRAF,SS	4.0
430603	A148164	Ha.247280	HIV associated factor	zf-C3HC4,zf-RanSP,pkin	4.0
427239	BE270447		ubiquitin carboxy protein	UD_con,SS,TM	4.0
402665			Target Exon	SS,TM,jg,DSPC	4.0
413818	BE161405	Ha.79	hypothetical protein MGC15429	SS,KH-domain,W40,Ribosom	4.0
406919	M85339		gcf-Homo sapiens DNA-binding p	SS,m	4.0
412659	AF090011	Ha.74375	discovered 1 (homologous to D	SS,PDZ,DEP,DXD,Dishevelle	4.0
437546	AW074836	Ha.173584	T-box 1	SS,TM,T-box,GTP_GDC,RFCT	4.0
419489	AW411280	Ha.90693	replication initiation region	zf-C2H2,LIM,TM	4.0
410043	D30812	Ha.58157	zinc finger protein 262	SS,TM,zf-KRAB,SS,zf-C2H2,K	4.0
430887	U79458	Ha.231940	VW domain binding protein 2	GRAV,SS	4.0
409449	NM_004408	Ha.166161	dynamitin 1	PX,DEG,dynamitin_dynamitin_2	4.0
448099	BE521839	Ha.51976	Homo sapiens cDNA FLJ12547 fs	SS	4.0
436556	M35568	Ha.5245	hypothetical protein FLJ20643	SS,TM,sugar_r_P1D	4.0
424512	A53802	Ha.145848	integrin, beta 5	integrin_B_EGF,SS,TM	4.0
443446	A023985	Ha.59621	ESTs, Weakly similar to A00815	SS,TM,jg,pkinase	3.9
420065	AW140093	Ha.129926	ESTs	SS,TM	3.9
426536	BE242634	Ha.2055	ubiquitin activating enzyme E1	Thif,UBACT,SS,pkinase,UCH	3.9
421579	NM_002875	Ha.105927	stem cell growth factor; lymph	ketide_c,SS,TM	3.9
427496	NM_003826	Ha.179728	methyl-CpG binding domain prot	SS,HLH	3.9
457820	AA341497	Ha.31408	RAR (RAR like GTPase)	SS,TM,Ribomold	3.9
439998	BE559654	Ha.61790	hypothetical protein FLJ23338	SS,SS,TM,EMP70,PA28_alpha	3.9
438652	A0233599	Ha.6351	cleavage and polyadenylation s	zf-CCHC,zf-COCH,zftransluc	3.9
414303	NM_004427	Ha.85263	early development regulator 2	SAM,SS	3.9
453406	F20596	Ha.4884	calcium/calmodulin-dependent p	pkinase,SS,hexothione_hex	3.9

WO 02/102235

PCT/US02/19297

	414168	AW793296	Ha. 103845	ESTs, Moderately similar to I5	SS	3.9
	451962	F13036	Ha.27373	Homo sapiens mRNA; cDNA DKF2p5	SS	3.9
	418181	U37012	Ha.63727	cleavage and polyadenylation s	CPSE, A,SS,TM	3.9
	402753			Target Enn	SS,TM,cyclin,cyclin_C	3.9
5	418681	AA287786	Ha.23446	Insulin receptor tyrosine kina	SS,SH3	3.9
	412621	L40397	Ha.74137	transmembrane trafficking prot	EMP21,GP25L,SS,TM	3.9
	420631	AW919530	Ha.26355	hypothetical protein FLJ22402	SS,TM	3.9
	438443	AW667635	Ha.261635	ESTs, Weakly similar to A46302	SS,TM,trans	3.9
	431472	AK001023	Ha.256549	nucleoside binding protein 2 (lev4,RIH,ParA,APS,kinase	3.9
10	447800	AL080092	Ha.19610	DKF2P564I1362 protein	SS,TM,SS,TM	3.9
	436686	AW450205	Ha.305890	BC12-like 1	TM,BC2,BH4	3.8
	408815	AW567974	Ha.256485	hypothetical protein FLJ22341	SS,TM	3.8
	441196	BE379202	Ha.77744	NM_001705:Homo sapiens NMDH	Complex1,51K,SNF2,Nucleic	3.8
	433030	AW068857	Ha.279929	gp25L2 protein	SS,TM,EMP24,GP25L,SS,TM,G	3.8
15	408721	BE515274	Ha.47062	polymerase (RNA) II (DNA direc	RNA,POL_M,19K0,SS,COX7a	3.8
	435049	AL122067	Ha.47466	hypothetical protein FLJ20124	SS,pRB	3.8
	431347	AT133461	Ha.251664	insulin-like growth factor 2 (SS,insulin,insulin	3.8
	409835	BE262773	Ha.25584	hypothetical protein FLJ10757	A/Kap,SS,swwa,TS,PN,h3,Co	3.8
20	414134	X50158	Ha.861	mitogen-activated protein kina	kinase,SS,kinase,T-box	3.8
	418090	U57059	Ha.33429	tumor necrosis factor (ligand)	TNF,SS	3.8
	446832	AW245212	Ha.221989	ECST	SS,mm	3.8
	447256	AW583008	Ha.6126	hypothetical protein dJ1141E15	SS,TM,SS,TM	3.8
	448107	O45853	Ha.20313	protein tyrosine kinase 2 beta	Focal_AT,kinase,SS,Pepil	3.8
	426433	L38969	Ha.198875	thrombospondin 3	TSPN,Up_3,SS,TM,SEA,TSPN	3.8
25	431026	AL035661	Ha.265327	hypothetical protein DKF2P751I	SS	3.8
	430956	AT183529	Ha.27016	glutathione peroxidase	GHSP,SS,TM,ABC,trans	3.8
	450998	BC387614	Ha.25797	splicing factor 3b, subunit 4,	SS,TM,suag,r,histone	3.8
	434899	BE513631	Ha.283565	FOS-like antigen-1	b2P,SS,b2P,cofilin,ACF,	3.8
	444734	NM_001360	Ha.11808	7-dehydrocholesterol reductase	ERG4,ERG24,SS,TM	3.8
30	411090	BE155695	Ha.239697	VPS28 protein	SS,TM,CPSE	3.8
	452135	AI452175	Ha.21446	KIAA1716 protein	SS,DXD,POZ,DEP,Dishovelle	3.8
	421339	AA070224	Ha.103561	SRp25 nuclear protein	SS	3.7
	406535			Target Enon	SS,SR,Ribosomal,S19e,lgJ	3.7
35	447261	AA017018	Ha.10021	hypothetical protein FLJ20446	SS,SS,Tenin,PM,PAZ	3.7
	433126	AB021262	Ha.59016	bovine caserin-interacting prote	SS,TM	3.7
	425215	AF030281	Ha.155165	zinc finger protein-10	PHD,SS,TM,dnaI,ERG4,ERG24	3.7
	420536	AL117456	Ha.275438	histone deacetylase 7A	Hist_deacetyl,SS,Hist_doa	3.7
	417988	AW567420	Ha.2599	gc-EST37P-45s MAGE sequences,	SS,TM	3.7
	430890	YS4232	Ha.2699	glycogen 1	Glycogen,SS	3.7
40	427863	AF109712	Ha.191002	MLL septin-like fusion	SS,GP,DOC,SS,TM	3.7
	448606	BE513362		Homo sapiens ubiquitin conjuga	SS,TM	3.7
	421961	AA032993	Ha.109929	likely homolog of rat GRIP, ass	TM,K,trans,trans,HULH,	3.7
	410253	AK000047	Ha.51950	hypothetical protein	K,trans,SS	3.7
	425233	T27981	Ha.155284	E1B-SB100-associated protein 5	SPRY,SPR,SS,TM,SPRY,SP,ap	3.7
45	423583	BE386899	Ha.4188	hypothetical protein MGC10612	SS,Peptidase,C16,TGF-beta	3.7
	415597	A365503	Ha.78805	DKF2P598I024 protein	SS,csp60,TCOP1	3.7
	415525	Y10024	Ha.78877	inositol 1,4,5-bisphosphate 3	SS	3.7
	419552	AJ359899	Ha.53347	arago-associated, migratory on	SS,TM,ADUF,SS,TM	3.7
50	444706	AK000398	Ha.11747	hypothetical protein FLJ20391	SS,SS,TM	3.7
	407381	AA420869	Ha.183110	ESTs, Weakly similar to ALUC_H	SS,TM	3.7
	423432	BE262996	Ha.44067	ESTs	TM	3.7
	444882	AK002162	Ha.12211	GDP-ucose transporter 1	SS,TM,ADUF,SS,TM	3.7
	407777	AA161071	Ha.71465	squalene epoxidase	SS,TM,Monooxygenase	3.7
55	422715	AA332178	Ha.119403	hexosaminidase A (alpha polype	Glyco_hydro_X0,Glyco_hydr	3.7
	422809	Z46023	Ha.118721	slaldehyde 1 (lysosomal sialida	SS,TM,ENR,SS,TM,SET,HSP70	3.7
	414732	AW410976	Ha.77152	mitochondrion maintenance def	MCM,FRP,SS,at-C2H2,KRAB	3.7
	425279	AT191667	Ha.28830	ESTs	SS,COI_hydrolyase	3.7
	419032	W61330	Ha.55643	ESTs, Highly similar to JAK3B	SS,kinase,SH2,insulin,lg	3.6
60	411165	NM_000169	Ha.65089	galactosidase, alpha	Methylase,Ribosomal,L44,z	3.6
	444000	AW050934	Ha.135528	ESTs	SS,HULH	3.6
	441174	BE312775	Ha.284036	Homo sapiens, clone IMAGE:3059	SS,TM	3.6
	423491	NM_012111	Ha.204041	chromosome 14 open reading fra	SS	3.6
	438433	AA018274	Ha.6214	KIAA0731 protein	SS	3.6
	425162	BE514851	Ha.154866	choline kinase-like	Cam_acyltransfer,Choline_k	3.6
65	425971	BE137335	Ha.211594	proteasome (prosome, macropain	AAU,UB,ARC,TM	3.6
	421018	BE190029	Ha.129839	hypothetical protein FLJ14780	at-C2H2,SS,mm,ENTH	3.6
	433604	NM_013442	Ha.3439	stromelin-like 2	Bant1,7,SS,TM,AAA,ctofol_N,	3.6
	451544	AK000429	Ha.26570	hypothetical protein FLJ20422	SS,TM,COX3,SS,TM,SPF-TF	3.6
70	444369	AV648296	Ha.282793	ESTs	SS	3.6
	406660	Y55371	Ha.172550	polymerin-like tract binding p	mm,beta-lactamase,SS,try	3.6
	456503	AW677779	Ha.194613	ESTs	SS,TM,bromodomain,sh,shydro	3.6
	451711	AK000461	Ha.26890	cat eye syndrome chromosome re	SS,SS,TMA4,desminase	3.6
	425394	AA356730	Ha.323949	kangalil 1 (suppression of tumor	SS,TM,transmembrane4	3.6
75	428011	BE287514	Ha.161418	KIAA0152 gene product	Aryl-CoA_dh,SS,shand	3.6
	407627	AA15020	Ha.62620	chromosome 1 open reading fra	SS	3.6
	436437	F12200	Ha.5581	chromosome 21 open reading fra	SS,Sytn_N,Exo_endo,phos	3.6
	419418	X75621	Ha.93033	tuberous sclerosis 2	Rap_GAP,Tubulin,Peptidase	3.6
	440300	K19763	Ha.8569	Homo sapiens, Similar to RIKEN	SS	3.6
	446136	AA026880	Ha.204447	protein kinase related to S.c	protein,PRD	3.6
80	435977	AL138079	Ha.5012	brain-specific membrane-anchor	SS,SS,SS,TM,sh,sh,sh,sh,sh,sh	3.6
	415095	AA234009	Ha.188715	ESTs	kinase,PH,kinase_C	3.6
	447267	AL301413	Ha.17536	DKF2P434E132 protein	SS	3.6
	418054	NM_002318	Ha.33354	lysoyl oxidase-like 2	SHC2,lysoyl_oxidase,SS,TM	3.6
	444554	AA047352	Ha.10927	hypothetical protein R33729_1	SS	3.6

WO 02/102235

PCT/US02/19297

	429098	AF030249	Ha.196176	enoyl Coenzyme A hydratase 1,	ECH_Hspes_V23,SS,Gel-tin	3.6
	430622	BE010971	Ha.247478	Homo sapiens, similar to DNA S	G-path,SS,TM,etqulin,a	3.6
	440675	AW050554	Ha.47863	ESTs, Weakly similar to KCCT1	SS,myosin	3.6
	409678	NM_005632	Ha.55536	small optic lobes (Drosophila)	TM,Peptidase_C2	3.6
5	413097	BE383676	Ha.75196	arkynin repeat containing prot	ank,SS,SS,TM,ph,ase,SH2	3.6
	427579	AA386143	Ha.179699	hypothetical protein FLJ20637	HECT,SS,HECT	3.6
	409154	U12832	Ha.50842	interaction-vicacid protein 35	SS,SS,Phosphatase_L276,KCW	3.5
	446528	BE513248	Ha.172084	Homo sapiens, clone NMAS2327	SH2,SH2	3.5
	444226	AL121105	Ha.11170	RNA binding motif protein 14	rm,SS,apocata,PH,rm,so	3.5
10	409297	R34682	Ha.53066	hsp70-interacting protein	SS	3.5
	411138	156785	Ha.10101	hypothetical protein FLJ22875	SS	3.5
	435169	AF148529	Ha.729881	monomelicoid, alpha, class 19,	TM,Glyco_hydro_47	3.5
	422575	AK005046	Ha.118552	hypothetical protein FLJ20539	TM,SS,TM,SRCR,Glyco,trans	3.5
	403325			C2000-4287-gp1705383[et]NP_05	SS	3.5
15	437895	AB014598	Ha.5988	KIA0666 protein	TM,U1.21,Lipoprotein_5,GBP	3.5
	445320	AB365582	Ha.571800	Homo sapiens mRNA for FLJ00016	SS,myosin	3.5
	426542	AF190746	Ha.170031	cat eye syndrome chromosome re	A_galactinase,SS,TM,Hyalin	3.5
	439873	BE159263	Ha.300638	ESTs	SS	3.5
20	428950	BE311879	Ha.194673	phosphoprotein enriched in ast	DEO,SS,TM,Catecholase	3.5
	421354	AB007884	Ha.103650	KIA0004 protein	SS	3.5
	411094	U33819	Ha.7647	MPC-associated zinc finger pro	SS,Szf,C2H2,LIM,PHD,TFIIS	3.5
	450007	BE027693	Ha.24301	polymersase (RNA) II (DNA dire	NA,SS	3.5
	422888	AL043101	Ha.127401	DKFZP451A153 protein; selectiv	SS,SS,TM	3.5
25	444914	AA049497	Ha.12142	WD repeat domain 13	WD40,SS,TBC,rm	3.5
	420178	D55650	Ha.95669	Juhal giant larvae (Drosophi	WD40,SS,TM	3.5
	418994	AA421401	Ha.172401	ribosomal protein L18	SS,TM	3.5
	414166	AW888941	Ha.57589	N-myc downstream regulated	Ndr,ahydrolase,SS	3.5
	409944	BE257925	Ha.57637	four and a half LIM domains 3	LM,SS	3.5
	421458	NM_003854	Ha.104578	carbohydrate (heparan sulfate	SS	3.5
30	423909	AB02664	Ha.31721	peroxiredoxin 5	Ang-C-TSA,SS,homone_rec	3.5
	427715	BE245274	Ha.180428	KIA1181 protein	TM,SS,TM,KW	3.5
	404946			Target Exon	SS,ubulin,SS	3.5
	417911	AA333387	Ha.82916	chaperonin containing TCP1, su	gp69,TCP1,SS,opn60_TCP1	3.5
	433920	AA045230	Ha.25468	ESTs, Moderately similar to AL	SS,U2,U2,U2,U2,U2,U2,U2,U2	3.5
35	430053	AF052155	Ha.227940	SEC13 (S. cerevisiae)-like 1	WD40,SS,TM,E1-E2,ATPase,C	3.5
	458857	AW024815	Ha.170088	GLUT4 enhancer factor	SS	3.5
	424879	AL114777	Ha.119960	DKFZP77G051 protein	chromo,SS	3.5
	417360	AW567103	Ha.82203	hypothetical protein similar 1	SS,TM,GSDM1_CD39,GSDM1_CD39	3.5
	459441	U23137	Ha.331184	ESTs	SS,TM,GV,acid,PA	3.5
40	428437	BE079537	Ha.169895	ubiquitin-conjugating enzyme E	UJ,con,SS,TM,Armadillo,se	3.5
	427117	BE258946	Ha.173611	Target CAT	complex_1,49kDa,SS,TM,TM,TM	3.4
	422051	AW327546	Ha.111024	solute carrier family 25 (mito	SS,mito_csr,SS,mito_csr	3.4
	422759	AA316582	Ha.246571	ESTs	SS	3.4
45	417220	U00698	Ha.81728	enr19 (C elegans) homolog	SS,szf_cyrc,SS	3.4
	450158	AK001899	Ha.24545	hypothetical protein FLJ11137	SS,Szf,C2H2,SCAN,TFIIS,SS	3.4
	425421	L11669	Ha.157148	tetracycline transporter-like	SS,TM,SS,TM	3.4
	415515	F11327	Ha.167408	ghsHC2A0101 normalized infant	SS	3.4
	427880	AB361119.comp	Ha.181013	phosphoglycerate mutase 1 (tra	PGAM,SS,TM,ubt	3.4
	413503	BE410228	Ha.75410	heat shock 70kD protein 5 (glu	SS,HSP70,homo,scp,hydanio	3.4
50	413014	AW250533	Ha.75139	partner of RAC1 (ratp15) 2	SS,homopexin,Flamin,NHL	3.4
	487555	AA622986	Ha.71574	hypothetical protein FLJ14626	SS,SP,CREF,IBD	3.4
	419432	AK001459	Ha.30375	hypothetical protein FLJ10597	PEP-utilitars,PEP-utilize	3.4
	421086	AW076725	Ha.101408	branched chain aminidoxylase	aminoxidase_4TM	3.4
	428038	AW134755	Ha.192477	ESTs	SS,Exonuclease,zf-C2H2	3.4
55	430352	AW750535	Ha.50742	Homo sapiens cDNA: FLJ23331 f	TM	3.4
	435447	AB017481	Ha.276501	fibroblast growth factor recep	Ugu,phase,SS,SS,gu,phina	3.4
	421310	AW530087	Ha.103315	intracellular lipid in containin	TM,zf-C2H2,SS,PHD	3.4
	420999	AA338903	Ha.100915	peroxisomal biogenesis factor	SS	3.4
	409551	US8048	Ha.183138	picoagglut (type II) N-endop	SS,TM	3.4
60	419727	AW160796	Ha.92700	DKFZP564C43 protein	Heperat_sav,SS,TM,Peptidase	3.4
	421287	BE314724	Ha.103061	ribosomal protein S6 lineage, 7	glucose,am,phase,C,SS	3.4
	411501	AK002368	Ha.70500	KIA04370 protein	SS	3.4
	484741	BE514567	Ha.19574	hypothetical protein MGC5469	SS	3.4
65	407103	AA424881	Ha.256301	hypothetical protein MGC13170	SS,TM,myosin	3.4
	422806	AA449014	Ha.121025	chromosome 11 open reading fra	SS,TM,myosin,CUB,ubiquit	3.4
	481873	N95657	Ha.58203	ESTs, Moderately similar to YO	SS	3.4
	418535	HE1851		glycylser10, r1 Soares fetal liv	SS,TM,homobac,LIM	3.4
	406556	M16714	Ha.181362	major histocompatibility compl	MC,C,U3,SS,TM	3.4
70	435589	AB677783	Ha.21619	HT1014	SS,ahydrolase_2	3.4
	411077	AW177263	Ha.68527	general transcription factor 1	SS,TM,TCF-beta	3.4
	427062	AW232785	Ha.173421	KIA11554 protein	SS,Peptidase_M24	3.4
	421890	AW999486	Ha.21732	ESTs	SS,Szf,C2H2,SPRY	3.4
	412368	AW300508	Ha.75102	alanine-4RNA synthetase	DHAA1,SS,SPRY-synt_25,DH1	3.4
	439496	BE16501	Ha.32343	Homo sapiens, similar to RIKEN	SS	3.4
75	433959	AK001301	Ha.3487	hypothetical protein FLJ10439	WD40,SS,TM,Syntaxin,Synta	3.3
	447578	AA512347	Ha.136585	ESTs, Weakly similar to JCS314	SS	3.3
	441722	AW995054	Ha.173103	FE65-Like 2	SS,TM	3.3
	452245	AA235279	Ha.29173	hypothetical protein FLJ28515	DSRF,SS,myc,F-box	3.3
	454714	AK000344	Ha.26098	hypothetical protein FLJ20337	SS,TBC,FHA,zf-C3H4	3.3
80	410533	BE545789	Ha.346742	hypothetical protein MGC3260	SS,TCF	3.3
	410609	BE289441	Ha.287361	ADP-ribosylation factor relate	arfas,SS,arfas,Stetferrin	3.3
	414775	AAS96236	Ha.172702	ESTs, Weakly similar to (Hsf)	SS,PCI	3.3
	423946	NM_013479	Ha.154540	hypothetical protein MGC10751	SS,TM,MFG,MXP,LS_3_2_2_2	3.3
	429215	NM_005341	Ha.2364	GL-Kruppel family member HNR3	zf-C2H2,ETB,TP2,K,leirs_5	3.3

WO 02/102235

PCT/US/19297

446618	AL110307	Ha.15591	COP9 subunit 6 (MOV34 homolog,	MOV34,SS,zf-C2H2,SCAN	3.3
444888	BE560471	Ha.12101	hypothetical protein	SS,PC	3.3
430041	AW247237	Ha.227835	KIAA1045 protein	SS,TM,7tm,1,tubulin	3.3
416950	AL048706	Ha.80532	dermatopodin	SS	3.3
431203	AW248421	Ha.250758	proteasome (prosome, macropain	AAA,Signa5_4_activat,SS,TP	3.3
427174	Y12059	Ha.278675	tricomodomain-containing 4	SS,comodomain,SS,TM,SNF2_N,	3.3
15674	EE394784	Ha.78595	proteasome (prosome, macropain	SS,proteasome,SS,TM,Cadre	3.3
432142	EE229190	Ha.117246	P450 (cytochrome) oxidoreducta	SS,oxidoreductase,FAD_binding,SS	3.3
145840	NM_005936	Ha.85119	SMT3 (suppressor of mitf two 3,	ubiquitin,SS,UQ	3.3
101045	U32324	Ha.64310	interleukin 11 receptor, alpha	ig,h3,SS,TM,GaIP,UOP_1ra	3.3
409428	NC63580	Ha.54457	CD81 antigen (target of anipr	transmembrane4,cytopl,SS,	3.3
443121	Y12957	Ha.19447	VAMP (vesicle-associated membr	SS,SNF2_domain	3.3
453856	AA804789	Ha.19447	POZ/MLM protein myristic	LIM,SS,SH3_Sort	3.3
430137	NM_005456	Ha.234249	mitogen-activated protein kina	SS,SH3,PD,SS,PD	3.3
446427	AW295863	Ha.119632	ESTs	SS	3.3
400747			Target Enon	ig,h3	3.3
445680	AF167572	Ha.12912	shb1 (G protein) homolog	SS,SS	3.3
452568	AA805634	Ha.300670	Homo sapiens mRNA: cDNA DKF7p5	SS,mm,Ephrin,kinase,ATP	3.3
418558	AW082266	Ha.86131	Fas (TNFRSF6)-associated via d	DEAD,DEG,SS,TM	3.3
401655			Target Enon	SS	3.3
429460	D65263	Ha.203238	phosphodiesterase 1B, cistoidal	PC,SS,SS,POEase	3.3
145448	L13210	Ha.79339	lectin, galactoside-binding, s	SROR,SS,TM	3.3
433038	AF192659	Ha.279309	mitochondrial carrier homolog	TM,mito_car,TM	3.3
440251	AF196016	Ha.332012	Homo sapiens, clone IMAGE3687	SS,TM,SS,TM,IRK	3.3
412922	M07721	Ha.74670	JL2.0 (Drosophila)-like homeo b	SS,homocysteine,SS	3.3
432941	W04803	Ha.279361	hypothetical protein FLJ10241	SS,Phospho_PHLRase_PHL_C	3.3
441244	BE512936	Ha.184052	PP1201 protein	SS,TM,W40	3.3
438175	A1376727	Ha.122110	ESTs	SS,TM,tyrosin,kinase,12	3.3
423024	AA593731	Ha.325823	ESTs, Moderately similar to AL	SS,TM,CD36,CD36	3.3
430120	AW162598	Ha.233594	hypothetical protein FLJ11350	SS	3.3
419571	AW674952	Ha.91146	protein kinase D2	kinase,DAG,PE-binding,PD	3.3
143019	BE281604	Ha.75140	low density lipoprotein-related	tyr,SS	3.3
400299	X07730	Ha.171995	kallikrein 3, (prostate specif	SS,SS,tyr,tyr,tyr,tyr	3.3
435119	BE263801	Ha.233594	ESTs, Weakly similar to S37431	SS,TM	3.2
434700	AL049074	Ha.4099	nardilysin (N-angiotensin dipep	Peptidase,MTH,HCO2_cotran	3.2
422242	AJ281780	Ha.273385	guanine nucleotide binding pr	G-alpha_a,nt,SS,G-alpha	3.2
430480	AL079399	Ha.241543	DKF2959f1524 protein	SS,TM,tyrosin,kinase,Somatol	3.2
452438	BE514230	Ha.235955	JM4 protein	SS,TM,KO,WH	3.2
456939	AA431633	Ha.153897	NM_002488-Homo sapiens NADH d	SS,TM,myo-actin_2b,WHIER,TR	3.2
421009	AL049709	Ha.343357	Human DNA sequence from clone	TM	3.2
11989	X12458	Ha.72980	Protein P3	SDF,SS,TM,g6PD,g6PD,C,hex	3.2
409197	NS4706	Ha.303025	chromosome 11 open reading fra	SS	3.2
147896	AA379770	Ha.62890	defensin against cell death 1	DAD,SS,TM	3.2
148026	BS379727	Ha.83213	faty acid binding protein 4,	lipocalin,SS,lipocalin	3.2
409057	AA702305	Ha.180090	ESTs	SS,TGFP_gropeptide,TGF-be	3.2
437869	W91976	Ha.250834	ESTs	SS,TM,SH3,zf-C3HC4	3.2
413211	AW867107	Ha.109274	hypothetical protein MGCA356	SS,TM	3.2
425980	A392498		isolated 1,4,5-ribophosphate re	SS,CTF,JNF1	3.2
445363	NM_005993	Ha.12570	tubulin-syncl chaperone d	ATP_synth,B,HEAT_PBS,SS,TM	3.2
421943	BE516520	Ha.343912	Homo sapiens, Similar to RIKEN	SS,TM,SS,TM	3.2
433337	Y07604	Ha.93235	non-metastatic cells 4, protei	NDK,SS,adh_short,NDK	3.2
145885	Y07130	Ha.59434	drobin 1	cofilin_ADF,SS,cofilin_A	3.2
141817	BE302000	Ha.72241	mitogen-activated protein kina	kinase,SS	3.2
143891	BE271020		tumor suppressor deleted in or	SS,TM	3.2
449455	T90748	Ha.279408	hypothetical protein	TM	3.2
419193	D29643	Ha.34769	dolichyl-diphosphoglucosylacchar	SS,TM,DOOST_49d,WP7,SS,T	3.2
409701	AA750613	Ha.62854	feritin, heavy polypeptide 1	SS,TM,WDGPT	3.2
436467	AAW450278	Ha.91681	ESTs, Weakly similar to OCHUO	SS,IRNA_synth_1,IRNA_bind	3.2
446334	U52427	Ha.14839	polymerase (RNA) II (DNA direc	SI,SS	3.2
101070	AF279142	Ha.198727	tumor endothelial marker 1 pre	SS,TM,EGF_lectin_c_sushi,	3.2
445411	AA513726	Ha.125645	hypothetical protein FLJ22693	SS,CTF,SS,pczf-COOH	3.2
458018	AL159675	Ha.37716	ESTs	SS,TM,Oxyd,PEP	3.2
426530	U24578	Ha.278825	complement component 4A	SS,A2M,NTR,A2M_N,myr,tyr	3.2
445504	T86566	Ha.12956	Tax interaction protein 1	POZ,SS,TM,PP2X_receptor,FG	3.2
443462	U77846		elastin (extracellular matrix	SS,PDZ,LM,kinase	3.2
432416	BE410937	Ha.2965	emerin (Emery-Dreifuss muscula	SS,EM,SS,Ribonuc_110,AcA	3.2
429652	AS929701	Ha.215588	phosphotransferase 3-kinase, reg	SH2,SH3,RhoGAP,SS,GIT,SH	3.2
429150	AF120103	Ha.197366	smoothed (Drosophila) homolo	SS,TM,Fzrized,7tm_2S	3.2
427729	AG033100	Ha.300646	KIAA1274 protein (similar to n	SS	3.2
148151	AA652638,comp	Ha.83583	acid related protein 25 comp	SS,HEGF,REV,PH,SS,TM,Ribes	3.2
448250	NM_016034	Ha.20776	mitochondrial ribosomal protei	Ribosomal_S2,SS,lipocalin	3.2
431158	AW659138	Ha.135280	Homo sapiens cDNA: FLJ22288 f	SS,Exonuclease	3.2
144252	BE388407	Ha.75875	ubiquitin-conjugating enzyme E	UQ_cox,SS,TM,SAM_PNT	3.2
406307			Target Enon	SS,TM,7tm_2,SS,TM,7tm_2,G	3.2
423322	R55565	Ha.347290	hypothetical protein FLJ22427	SS,TM,Sun,ubiquitin,TEG	3.2
427584	BE410293	Ha.179718	v-erbA avian myeloblastosis vir	N,SS	3.1
149009	AA233601		ESTs, Weakly similar to CA13_H	SS	3.1
431717	BE396150	Ha.6945	KIAA0482 ribosomal prota	SS,TM	3.1
443831	BE1560	Ha.21036	Homo sapiens mRNA: cDNA DKF7p4	RhoGAP,SS,TM,SET,zf-COXC,	3.1
149394	AB011124	Ha.90232	KIAA0552 gene product	SS	3.1
436240	BE386873	Ha.5096	hypothetical protein MGCI0433	SS,TM,EG,COXII,transmemb	3.1
143900	AAW40947	Ha.75612	stress-induced-phosphoprotein	SS,TM,SH3,TM,DnaI	3.1
147900	SA7453	Ha.82527	adenosine monophosphate desamin	A_desaminase,SS,G-alpha,GS	3.1
421819	NM_013403	Ha.108655	zincfin	WD40,kinase,kinase	3.1

WO 02/102235

PCT/US02/19297

423696	23112_1	Z35245 AA333056 AIS70568 AW341487 AIB27050 AW296868 AIT92189 AIO15693 AIT33599 AIS72251 AIB72488 AW193262 A1244716 AIB64375 A126100 AA392444 A1269395 A1602054 AWT72465 AIB67336 AA627604 A161914 A1335977 A1338019
425080	24669_1	A132405 A12314 A128618 A1605468 A116941 AA573152 F08617 A1070726 AW338034 F03024 AAT29145 BE245956 A1093722 AA541730 F08365 A1242755 AA350447 A1635667 T03903 AW081025 AA033711 AA600303 N13995 N12491 TS7002 Z25379 A1306851
427239	27647_1	AW720447 AW409921 BE207288 BE207170 D56355 BE263223 BE408171 BE262243 BE392439 BE292738 BE261776 BE314300 BE267719 BE268715 BE613876 BE296291 BE297065 AA210923 BE407619 H15344 BE622905 AW248281 A1W250313 T19021 AA351115 AA16879 BE269533 BE521955 AA229074
427391	27815_1	W06376 AC001212 AA1155763 AAB78266 AA090872 AB033013 AW249107 AA031890 AA112920 AW336538 N55156 AA326756 AW9662294 AA180280 C05570 C04352 W06076 AW240674 AA034988 AA044781 AA021474 1125212 A1080572 A127583 A951765 AAB55551 A517146 H23835 A1589543 A1215670
428092	286020_1	AW879141 AA421182 A1734104 A1733023 AA330600
428545	303802_1	AW598444 AA330524 AA347898 AA327507 AW391973 AA495763 AA479278 AW635918 T19644 A1204484 A1B834745 A1B081339 A1B090002 A1306153 W06164 A1281973 AAB584073 AAB583986
430168	313927_1	AW968430 AA408507 AA478223 AA513008 A1762122 A1565412 A1A626542 AA688976
433519	368001_2	BE236301 AA590196 A1150276 A1049006 A131250 A1572668 AW204662 A1090690 A1922941 R496291
438707	46380_1	BE1239 BE518154 AW365394 AW365398 AW365401 A1972653 A907337 AA110504 A1B26142 A467998 A9010594 BE518528 AA1603991 A1990417 A130440 A1B3071 A1712453 AW003408 AW1151568 AA400201 A158740 A1039165 A1W665173 AW042722 A1215122 A1200785
440191	46804_3	BE467373 A1147599 A215120 A0776110 AIB03429 A1262491 A1B08243 A1B01007 AW135212 A1W20513 A1754349 A1004801 A1051273 A1W76918 A1W103289 A14
443402	5981_1	U77846 AA475373 AA363488 AA348194 A126867 AAT72601 AA715367 AAT37787 R54236 A1327271 R77311 AA3339585 BE074254 AAW36712 AW598444 AA330524 AA347898 AA327507 AW391973 AA495763 AA479278 AW635918 T19644 A1204484 A1B834745 A1B081339 A1B090002 A1306153 W06164 A1281973 AAB584073 AAB583986
444590	6116_1	AA457456 AA007921 A1567715 AA579472 T54216 AA373128 F35533 AA722113 T64403 A1653378 F28806 AA599589 AA047537 AAO22499 AWA04532 F35782 A1554180 A1183767 AIB09352 AA160379 AA481676 A1165031 A1148988 A1174482 AA686833 A1674395 AA481440 A1314985 A1688771 A444
446625	64558_1	BE240743 AA436542 A1W024744 A1W242177 A1975476 A1W385165 R07536 R73462 A1W654529 T54442 A1399896 R50703 R48743 A1769893 A1B63005 AA317806 AA678000 A1B18963 A1568207 AWA471273 R73463 A1335104 A1590161 A1A68257 A1B54604 H21954 T25141 A1A56793 A1W0074 A1W028253 A12
448606	77158_1	BE513362 AA447862 H72036 A1333964 A1B81334 A1W139128 AA532579 A102421 A1363600 A1W960628 A452148 C06192 AA336707 AA080008 A1B012712 BE267439 BE269576 A1B76207 A1A52895 A1620631 A1A538126 A1A45827 A1W412861 A1A68401 A1W130326 AA40513 A4588685 A1B53229 A133246
448677	775217_1	A1560769 A1B57497 A1W151454
450788	648440_1	A1738410 A1W160305 A1B71725
452180	921991_1	BE378541 A1B53251
453412	966254_1	A1J003290 A1J003288 A1W276947
455857	137021_1	T70192 BE147698
456928	138389_1	BE170313 BE160746 BE158290
457022	274445_1	AW377258 BE067438 BE067511 BE067515 BE067467 BE067514 AA397442
46	TABLE 21C:	
	Key: Unique number corresponding to an Eos probest	
	Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (G) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22. Dunham, et al. (1989) Nature 339: 598-595	
	Strand: Indicates DNA strand from which exon were predicted	
	NL position: Indicates nucleotide positions of predicted exons	
45		
	Key	Ref
	420450	8389428
	400563	9844011
50	400747	732330
	400846	9186025
	401097	9595518
	411128	8659792
	401655	9090903
55	401727	8134856
	401751	9828651
	401772	9695243
	423265	9454516
	402463	9796896
60	402665	8077133
	422793	6138340
	422916	7406502
	403028	7570577
	403325	8440025
65	404256	9367233
	405189	1220907
	405325	6094961
	405356	2155224
	405486	946898
70	405101	9124019
	405307	8570399
	405536	7714747
75		
80		

TABLE 22A:

Key: Unique Eos probest identifier number

ExAcn: Example Accession number, Genbank accession number

WO 02/102235

PCT/US02/19297

UnigeneID: Unigene number

Unigene Title: Unigene gene title

Protein Dom.: Predicted protein domain

RT: Ratio of tumor to normal body tissue

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Phylo	Exon	Unigene ID
407223	H95850	
432281	A017842	Hs.237924
410418	D11392	Hs.63325
431773	BE409442	Hs.288557
438424	A018248	Hs.25895
410895	W33191	Hs.23507
453028	A005632	Hs.31442
407722	BE252241	Hs.38041
451721	NM_009465	Hs.25915
416619	U17735	Hs.80205
430397	A024533	Hs.105607
450334	AF035959	Hs.24879
418545	BE245762	Hs.85459
424420	BE814743	Hs.145688
412574	U04106	Hs.74451
430023	AA158243	Hs.227729
444672	Z59530	Hs.11669
413726	AJ276465	Hs.75510
430861	U51336	Hs.5463
420095	BE436562	Hs.195177
431765	AF124249	Hs.265641
422645	LK0027	Hs.118950
413436	AF238033	Hs.63861
422635	A025577	Hs.172724
425865	A050718	Hs.15577
418891	NM_002419	Hs.85445
419138	U45608	Hs.59631
423665	BE355075	Hs.275619
452875	BE27560	Hs.30558
426997	BE520736	Hs.173125
402516		
425760	D17829	Hs.159479
402416	AF024545	
415444	NM_002496	Hs.50443
459133	U40343	Hs.29566
447955	AW979130	Hs.18563
422708	AS017430	Hs.115324
414837	U24265	Hs.77446
425712	AW245825	Hs.211514
425848	AF242709	Hs.159637
451643	ME4547	Hs.234759
447659	AK022154	Hs.19551
426457	AW874667	Hs.165666
421612	AF161264	Hs.106196
421363	NM_001381	Hs.103854
422739	NM_007274	Hs.6575
420958	F09247	Hs.247735
421445	AA913069	Hs.104433
424244	NM_004854	Hs.157199
446325	NM_013272	Hs.14605
406620	AB1105	Hs.144550
425109	AL008637	Hs.196362
425183	AB014604	Hs.157955
444654	K26362	Hs.11615
427640	AF053293	Hs.180015
425123	AF005374	Hs.154655
416006	AA324251	Hs.78950
412942	AL120344	Hs.75074
423355	Z60346	Hs.127510
426351	AW161500	Hs.165611
424558	AF030518	Hs.150595
420029	BE255876	Hs.84446
433573	AF234887	Hs.67562
420719	AL063341	Hs.37166
427325	A128787	
442620	C00138	Hs.8535
458130	A0115811	Hs.5338
449335	A0582193	Hs.50388
406230	AA652431	Hs.15295
423801	NM_015071	Hs.132942
419539	AQ001502	Hs.91753
419298	AA653479	Hs.85890
425108	AA622037	Hs.158468
448133	AA723157	Hs.73765
418735	T18979	Hs.87938
435543	NM_002212	Hs.5215
415115	NM_012152	Hs.258553
423459	ME4590	Hs.27

Unigene Title	Protein Dom.	RT
gryw01812.1	Soares melanocyt	55.9
CG456 protein	mlle_carr	55.7
transmembrane protease, serine	ldl_recept_a,lysin	41.0
pleckstrin homology-like domain	PH	37.1
hypothetical protein FLJ14996		35.3
hypothetical protein FLJ20258	SH3	35.0
RocC protein-like 4	DEAD, helicase_C	28.2
pyridoxal (pyridoxine, vitamin	pkb	28.2
spectrin, beta, non-erythrocyt	specific,PH,CH	27.9
pin-2 oncogene	phosphatase	27.9
bicarbonate transporter related	HCO3_cotransp	27.7
phosphatidic acid phosphatase	PAP2	25.7
arachidonic acid 5-lipoxygenase	lipoxygenase,PLAT	25.1
prostaglandin E synthase	MAPEG	25.1
calpain-4, small subunit (30k)	ethand	24.4
FKBP5-binding protein 2 (13kD)	FKBP	24.3
laminin, alpha 5	laminin_EGF, laminin_GEGF	24.0
annexin A11	annexin	23.1
inositol 1,3,4-trisphosphate 5'	oxidoreduct_nitro	23.0
phosphotyrosine kinase, gamma 2	pknox	23.0
novel SH2-containing protein 1	SH2	22.4
tyrosine synthase kinase 3 alp	pknox	22.4
sphingosine kinase 1	DAGK	22.3
cardiac kinase, brain	ATP-gua_Pkase,ATP-gua_Pi	21.5
Target CAT		21.3
mitogen-activated protein kinase	SH3,phkase,pyridoxal_deC	21.1
retinoid receptor 1 (steroid)	RYOR,ITPR,RyR,SPRY,ion_tr	21.0
mitochondrial carrier homolog	mlle_carr	20.9
DNA segment on chromosome 15 (Euk_proin	20.8
peptidyl/prolyl isomerase F (cy	pro_isomerase	20.8
ENSP00000232587-Bicarbonate s	HCO3_cotransp	20.8
glutathione (N-acetyl)-S-ol	Sulfatase	20.7
Target	EGF,tyrosin_A,tyrosin_Xii	20.0
Target CAT	ker	19.5
cyclin-dependent kinase inhibi	ank	19.2
phosphodiesterase 5A	PDEase	19.2
kinase 4	kinase,kinaseox	19.0
aldehyde dehydrogenase 4 fami	aldehyd	18.8
ENSP0000023327-NADH-ubiquino	oxidoreduct_d6	18.5
aryl-ATP synthetase 2	GST_C,GST_M,Tropomyosin	18.4
breakpoint cluster region	RhoGEF,RhoGAP,PH,C2	18.1
peroxisomal biogenesis factor		17.5
chimerin (chimerin 1)	DAG_PE-bind,RhoGAP	17.3
BDG antigen	ldl_recept_a	17.1
cocking protein 1, G20 (downs	PH,RS	16.9
cytosolic acyl-coenzyme A thio	Aryl-CoA_dh, Aryl-CoA_dh_M	16.8
prolactin alpha 10	cadherin	16.8
Homo sapiens, clone IMAGE-4054	asp	16.8
ELK1 motif kinase	phkase,KA1,lyso	16.7
soluble carrier family 21 (large	kazal,ONTAP_N,ONTAP_C	16.5
myelin, heavy polypeptide 5, n	myosin,heavy,Myosin_XIII	16.4
neutrophil cytosolic factor 4	PX,SH3,ORP	16.3
KIAA0704 protein	PH,Oxidoreduct_BP	16.2
map kinase phosphatase-like pr	DSPC,Phosphatase	16.2
D-serine racemase	MIF,kinase,protein_L2	16.2
phosphomannomutase 1a	PMM	16.0
branched chain keto acid dehyd	E1_dehydrog	15.8
mitogen-activated protein kinase	phkase	15.7
acyl-Coenzyme A dehydrogenase,	Aryl-CoA_dh,Aryl-CoA_dh_M	15.7
second mitochondria-derived ac		15.7
cytochrome P450, subfamily XXV	p450	15.7
polyamine-modulated factor 1	alko_ket_red	15.5
cathepsin B, LAG seven-pass G	7hm_2EGF,cadherin,lamin	15.4
collagen, type IX, alpha 2	Collagen	15.3
glutathione S-transferase Lymf	7hm_1	15.2
Homo sapiens mRNA for KIAA1668		15.1
ras homolog gene family, membe	ras,arf	15.0
hypothetical protein MG31314		15.0
NM_0210743 Homo sapiens NADH d	complex1_24kD	14.7
GTPase regulator associated wi	RhoGAP,SH3,PH	14.0
hypothetical protein		13.6
pyruvate carboxylase	CPase_L_chain,PYC_QADA,H	13.6
programmed cell death 5	DIF12	13.5
folate receptor 1 (adult)	Folate_rec	13.5
Snf2-related GBP activator pro	helicase_CAT_hook	13.5
integrin beta 4 binding protein	efB3	13.3
endothelial differentiation 1,	7hm_1	13.3
glycine dehydrogenase (Krebs	GDCP	13.2

WO 02/02235

PCT/US02/19297

431462	AW583672	Hs.256311	genin-like neuroendocrine pep
444855	BE409281	Hs.12084	Tu translation elongation fact
429464	NM_216240	Hs.126565	CSRI preagin
450787	AB006190	Hs.25475	aquaporin 7
428539	AW410063	Hs.164677	solute carrier family 25 (mito
436014	AF261134	Hs.283741	osome component Rpl46
416886	AA257356	Hs.03234	serine/threonine protein phosph
433867	AK003696	Hs.3616	hypocretin-like 1
411408	U76666	Hs.69549	calcium channel, voltage-depen
433239	NM_002562	Hs.2980	S100 calcium-binding protein A
447887	AA114350	Hs.15949	cysteine 8, apolipin-related c
427446	BE246446	Hs.2157	Wiskott-Aldrich syndrome (cecs
428820	AA436167	Hs.172631	integrin, alpha M (complement
446603	NM_014835	Hs.15519	oxysterol-binding protein-rela
422633	X56832	Hs.118804	onolase 3, (beta, muscle)
448830	BE619268	Hs.18244	mitotic spindle coiled-coil ro
414757	U46522	Hs.77252	fragile histidine triad gene
426553	AW207440	Hs.185973	degenerative spermatocyte (hom
432370	AA308334	Hs.274424	N-acetylnearaminic acid phosph
401542			C15001413-g[1084519]ntRP_
427892	X12830	Hs.193400	interleukin 6 receptor
425999	AW513051	Hs.332981	ESTs, Weakly similar to D3022
422301	A0752163	Hs.114589	collagen, type VII, alpha 1
419720	AF036154	Hs.65756	regulator of G-protein signal
407143	C14078	Hs.332329	EST
421521	NM_005309	Hs.103502	glutamic-pyruvate transaminase
425251	Z22521	Hs.155342	protein kinase C, delta
413354	BE489556	Hs.281873	DNA (cytosine-5)-methyltransf
424241	AF281133	Hs.343563	osome component Rpl41
416714	AF283770	Hs.79530	COT9A unique (linear)seroglobuli
427336	NM_005658	Hs.2134	THF receptor-associated factor
407979	D11928	Hs.76845	phosphoserine phosphatase-like
436319	H90727	Hs.5123	inorganic pyrophosphatase
420748			NM_002122-Homo sapiens matrix
428948	BE514362		FKBP-binding protein 3 (25kD)
401215			C12000457-g[7512178]ntT30
401281			DKFZP586N2124 protein
427397	AB29956	Hs.177656	calmodulin 1 (phosphorylase ki
433496	AA442103	Hs.175364	solic carrier family 2 (flect
409606	AF231023	Hs.55173	cathenin, EGF LAG seven-peste G
424415	NM_001975	Hs.146580	onolase 2, (gamma, neuronal)
447486	AW01064	Hs.18720	programmed cell death 5 (apopt
429528	AF037062	Hs.172914	rotin dihydrogenase 5 (11-c
405371			NM_005659-Homo sapiens LIM do
416282	R68664	Hs.187257	brain link protein-1
452295	BE379938	Hs.28866	programmed cell death 10
433350	AB023168	Hs.241161	ADA4955
430594	AK007090	Hs.248655	hypothetical protein FLJ200783
443814	BE281240	Hs.9857	carbonyl reductase
440242	AW256871		glucose transporter protein 10
447355	BE363675	Hs.334	Rho guanine nucleotide exchang
403843			NM_002100-Homo sapiens corfil
422416	AK001383	Hs.115385	hypothetical protein FLJ10521
400232			NM_001895-Homo sapiens casein
426828	NM_000020	Hs.172670	activin A receptor type II-like
411157	AB23961	Hs.12678	ESTs
422616	BE300330	Hs.118725	serine/threonine synthetase 2
406779	AA412048	Hs.279574	CGI-39 protein; cell death-reg
400389	AL135841		olactory receptor, family 2,
422307			Target Exon
455615	Y15365	Hs.4975	potassium-voltage-gated channel
452434	D30934	Hs.29549	C-type lectin-like receptor-1
402053			C11001722-g[1143628]ntGP_X
418641	BE243136	Hs.88647	z desintegrin and metalloprote
415112	BE270734	Hs.2795	isolate dihydrogenase A
403213			NM_013655-Homo sapiens interse
412158	BE241740	Hs.785	integrin, alpha 2b (platelet g
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (m
438348			C12000613-g[453922]ntRP_0
457679	AF119666	Hs.23448	insulin receptor tyrosine kin
416416	U11700	Hs.84999	ATPase, Ca transporting, beta
419594	AA013051	Hs.51417	topoisomerase (DNA) II binding
422765	AW409701	Hs.1587	bovalentin IAP repeat contain
453323	AF026733	Hs.131438	serine protease inhibitor, Kain
429594	Y15333	Hs.159237	hexokinase 3 (white cell)
438800	AB037106	Hs.6416	seven transmembrane domain orp
402476	AL031685	Hs.12755	Target Exon
442232	AL031685	Hs.12755	KIA0852 protein
425597	U26994	Hs.158324	chemokine (G-C motif) receptor
413431	AW248428	Hs.75356	alkylglycyl-conjugating enzyme E
415200	AL040326	Hs.76202	SWI/SNF related, matrix associ
414874	U26351	Hs.7515	inized 1,4,5-inophosphate re
423524	AF036909	Hs.129738	potassium-voltage-gated channel
457558	AF063855	Hs.279552	G-protein-coupled receptor

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	400471			Target Exon		8.8
	400591			NM_003868?Homo sapiens retina	aldoh	8.8
	423427	A852692	He.157205	branched chain aminotransferase	aminotran_4	8.8
5	410839	NM_000849	He.65581	protein, disulfide isomerase	thiorod,Rho_GDI,gnIR	8.7
	430037	BE409649	He.227789	mitogen-activated protein kinase	phkase	8.7
	405046	A587594	He.428	trans-activated tyrosine kinase 3	tk3_jg	8.7
	414534	BE257293	He.76366	BDL-antagonist of cell death		8.7
	401454			NM_214270?Homo sapiens renal	phkase	8.7
10	409493	BE206854	He.46039	phosphoglycerate mutase 2 (mus	PGAM	8.7
	433333	NM_016521	He.71816	v-akt murine thymoma viral onc	homocbox,phkase,PH,phkase	8.7
	434332	A803758	He.241419	KIAA1337 protein	Palkhet	8.7
	405126			NM_002020?Homo sapiens tegula	Ceet_uncp_of_CA,hormone_	8.7
	419493	AF01212	He.90744	proteasome (prosome, macropain	PCP	8.7
	439669	AW602166	He.222399	CEGP1 protein	CUB,EGF	8.6
15	401134			C12001186p1831833p183142	biopletin_H	8.6
	442286	W31847	He.50335	cytochrome P450 monooxygenase		8.6
	428576	AF119655	He.184011	pyrophosphatase (inorganic)	Pyrophosphatase	8.6
	433494	AB029396		beta-1,3-glucuronyltransferase	Glyco_tran_43	8.6
20	427001	NM_005482	He.173136	dual-specificity tyrosine (Y)-	phkase	8.6
	432278	AJ748017	He.290145	EST 3	cHMP_binding	8.6
	414463	T89078	He.76177	alpha-1-microglobulin/tubulin	lipocatin,Kunitz_BPTI	8.6
	421871	AK0061416	He.308122	glycoprotein, synaptic 2	Steroid_ch	8.6
	447827	U73727	He.19718	protein tyrosine phosphatase,	Y_phosphatase,fn3,jg,MAM	8.6
25	403379			Target Exon	DNA_pol_A	8.6
	446872	X97058	He.16362	pyrimidine receptor P2Y, G	7m_1	8.6
	428587	NM_016103	He.279882	GTP-binding protein Ras	ar/rae	8.5
	420670	AA305079	He.1342	cytochrome c oxidase subunit V	COX5B	8.5
	427221	LI5409	He.174037	von Hippel-Lindau syndrome	VHL	8.5
30	402289			Target Exon	A2M,UA2M	8.5
	420518			C1000029?_GDC111705hNAAC21		8.5
	425906	U52112	He.198331	renin-binding protein		8.5
	437965	AA843222	He.193534	ESTs. Moderately similar to AL	RasGEF	8.5
	433332	AF038536	He.127588	synaptobrevin VII	C2	8.5
35	421191			NM_021733?Homo sapiens testis		8.5
	446893	A701393	He.278728	Raf and Com-related 2 (raf) hom	ras	8.5
	431857	W19144	He.271742	ADP-ribosyltransferase (NAD: p	PARP,PARP_reg	8.5
	457579	A5030816	He.36781	RAS-like suppressor		8.5
	409656	NM_205133	He.289526	HCE 1, prerenal protein protease	Abi	8.5
40	455370	BE247706	He.89751	membrane-spanning 4-domain, s	ras,arf	8.4
	432458	BE276633		RAB6B, member RAS oncogene fam	ras,arf	8.4
	400565			Target Exon		8.4
	401980	X52496	He.3041	Target Exon	Branch	8.3
	432545	AW382198	He.12803	arachidonic acid glyoxylase 2	cycle	8.3
45	445303			interleukin 15 receptor, alpha	sushi	8.3
	404528			peptide YY, 2 (seminalpessnin)	GDA1_CD39	8.3
	428642	D79586		KIAA167 gene product	ank,PH,ArfGap,ras	8.3
	406868	AA505445	He.300097	immunoglobulin heavy constant		8.3
	405473			NM_001059?Homo sapiens acetyl	CPSase_1_chain,bioin_jap	8.3
	406601	U47628	He.86122	protein A	7m_1	8.3
50	415008	NM_002777	He.928	proteinase 3 (serine proteinase	trypsin	8.3
	403258	AJ071644	He.239363	protein phosphatase 2A, regula		8.3
	435463	AJ722063	He.280010	vanilloid receptor subtypes 1	ank_joe_trans	8.3
	453032	NM_002314	He.36566	LIM domain kinase 1		8.3
	437644	AA746575	He.136748	lectin-like NK cell receptor	lectin_c	8.3
55	421707	NM_014621	He.107054	lectinome-2	Lactophlin,OLF,7m_2,Gal	8.2
	414629	AA345824	He.78688	carboxylesterase 1 (monoclelmn	Coelesterase	8.2
	453898	AW025812	He.232770	arachidonate lipoperoxase 3		8.2
	424053	AF057036	He.138620	collagen-like tail subunit (el	Collagen	8.2
	457398	BE255832	He.261871	CTP synthase	GATase	8.2
60	421504	AW402997	He.109052	adaptor protein with pleckst	SH2,PH	8.1
	403495			Target Exon	SRCK	8.1
	453610	AW366882	He.33818	RacQ protein-like 5	DEAD,heikase_C	8.1
	424880	NM_000328	He.153614	rednifin pigmentosa GTPase re	ROCT	8.1
	423847	U16997	He.133314	RAR-related orphan receptor C	hormone_roc_of-C4	8.1
65	403829	M33552	He.56729	lymphocyte-specific protein 1	Cadherin	8.1
	401180			eukaryotic translation elongat	ion_trans,jQ	8.1
	452072	BE759867	He.27744	RAB3A, member RAS oncogene fam	ras,arf	8.1
	426484	AA379658	He.272759	KIAA1457 protein	IP_trans	8.1
	402453			C102456g9(17363439)g9NP_039	7m_1	8.1
70	457310	W28363	He.239782	nucleic receptor subfamily 2,		8.1
	422069	AJ010063	He.343603	tilin cap (telethorin)	globin,cNMP_binding,phkase	8.1
	400275			NM_006613?Homo sapiens seryl-	NA	8.0
	434357	AW732264	He.3828	mevalonate (diphospho) decarbo	GHMP_kinases	8.0
	432229	W28672	He.136747	aspartic carbonylphosphatase 1 proe	FKBP,TPR	8.0
75	413762	AW414149	He.846	FK506-binding protein 4 (58kD)	RHOGEF,PH	8.0
	422933			ENSP0000005284?CDNA FLJ20404	C2,PH,RasGAP,BTK	8.0
	429282	NM_004668	He.193312	RAS protein activator like 1 (RA,S12,VP39	7.9
	456181	138463	He.1030	ras inhibitor	p450	7.8
	431493	AJ071493	He.126873	ESTs, novel cytochrome P450	ABC_tran,SRP54	7.8
80	451558	NM_001069	He.26630	ATP-binding cassette, sub-fam	phkase,DAAG,PE-bind,phkase	7.8
	415758	BE270495	He.78793	protein kinase C, zeta	EPH_1b,phkase,SAM,fn3	7.8
	419270	NM_002632	He.89639	EphA1	7m_1	7.8
	422837	U25441	He.121478	degenerate receptor D3	phkase	7.8
	401118			Target Exon		7.8

WO 02/102235

PCT/US02/19297

426440	BE382756	Hs.169902	solute carrier family 2 (facil
419635	L11329	Hs.1183	dual specificity phosphatase 2
432747	NM_014404	Hs.278907	calcium channel, voltage-gate
403672			OCT12 (4q35)359333p10p11275
437806	AI424921	Hs.122487	ESTs, Weakly similar to A54854
456890	U48213	Hs.155402	D site of albumin promoter (al
424107	AB014506	Hs.139448	kinesin family member 1C
452695	AW170109	Hs.30327	mitogen-activated protein kina
433322	AI571225	Hs.284711	KIAA1535 protein
424198	AB029010	Hs.143026	KIAA1057 protein
402496			Target Exon
425423	NM_005897	Hs.157180	inhibitor of A particle-prom
402211			KIAA0430 gene product
408710	Y10256	Hs.47007	mitogen-activated protein kina
457615	W56321	Hs.111460	calcineurin-modulin-dependent p
402760			NM_021797 Homo sapiens eosino
425428	AL110261	Hs.157211	DUF2P568021 protein
423579	NM_004121	Hs.1675	gamma-glutamyl-transferase-like
413104	L42374	Hs.75199	protein phosphatase 2, regulat
419650	BE280337	Hs.194653	solute carrier family 7 (calo
424774	BE244179	Hs.153022	TATA box binding protein (TBP)
402632			Target Exon
444159	AF116846	Hs.10431	dead ringer (Drosophila)-like
405714			ENSPO00000221137:Olfactory rece
442732	AA257161	Hs.8656	hypothetical protein DGF2p434E
421758	BE376336	Hs.1422	Cardiac-Rhodolol saline sarcoma
415995	NM_004573		phospholipase C, beta 2
405137			Target Exon
402460			C10U12617a[2655973]en[CAAA70
431398	BE616547	Hs.2785	keratin 12
429592	AB029041	Hs.209646	KIAA1116 protein
426225	BE260337	Hs.198273	Target CAT
423015	U18848	Hs.123034	G protein-coupled receptor 12
454373	NM_005133	Hs.285626	RCE1, prenyl protein protease
449188	AA001912	Hs.7035	N-Acetylglucosaminyl kinase
432920	U37689	Hs.3128	polymerase (RNA) II (DNA direc
446143	BE245342	Hs.306070	sec21 homolog
422201	NM_001505	Hs.113207	G protein-coupled receptor 30
440939	NM_014297	Hs.7465	protein expressed in thyroid
435099	AC024770	Hs.4759	flap structure-specific endonu
437161	AA064477	Hs.25391	ESTs
429583	AF148213	Hs.211604	a disintegrin-like and metallo
426286	AF063420	Hs.168913	antithrombin-like kinase 24 (S1
445987	AA098449	Hs.123303	suppressor of Ty (S.cerevisiae
416377	AA179630	Hs.263867	caspace recruitment domain pro
421748	NM_014718	Hs.107809	KIAA0726 gene product
426691	NM_006201	Hs.171834	PCTAIRE protein kinase 1
425680	AB053078	Hs.186613	sphingoglyco-1-phosphatase
411858	BE405714	Hs.444556	hypothetical protein FLJ12116
427010	AW133332		muscle RAS oncogene homolog
457305	BE286048	Hs.238484	RAE10, member RAS oncogene fam
431630	NM_002204	Hs.265829	Integrin, alpha 3 (integrin CD4
457754	AW026394	Hs.4815	medic (peucedanoid) phosphatase
435675	AF213467	Hs.44234	triggering receptor expressed
456488	AW015058	Hs.301946	ESTs, Weakly similar to T30867
426761	AF236119	Hs.193676	GRG2-related adaptor protein 2
430386	C04742	Hs.241583	hydroxase-binding protein 2
422066	AW429275	Hs.343521	malate dehydrogenase 2, NAD (m
445937	AI452943	Hs.321231	UDP-GalNAc6NAc beta 1,4-g
457496	AB530075	Hs.274370	hypothetical protein FLJ20260
402845			NM_001057 Homo sapiens sortil
416931	D45371	Hs.80485	adipose most abundant gene tra
414915	NM_002462	Hs.76391	myxovirus (influenza) resistan
432990	AL030071	Hs.278989	tumor necrosis factor receptor
456128	W32474	Hs.301746	RAP2A, member of RAS oncogene
425842	AF038660	Hs.206713	UDP-GalNAc6NAc beta 1,4-g
401488			Target Exon
462643	AI345001	Hs.62380	menage a trois 1 (CAK assembly
424321	W74048	Hs.1705	lymphocyte-specific protein ty
405187			NM_001057 Homo sapiens sortil
413055	AV655701	Hs.75163	cytochrome P450, subfamily IIE
443496	BE379077	Hs.130849	ESTs, Weakly similar to U30822
419687	AU077005	Hs.92208	a disintegrin and metalloprote
417103	Z33905	Hs.81216	hypothetical protein MG03597
407887	AB020211	Hs.37358	hypothetical protein FLJ11149
456469	NM_005109	Hs.95220	oxidative stress responsive 1
449546	W86248	Hs.58819	ESTs
428926	NM_001702	Hs.194564	brain-specific angiogenesis in
404953			C100020a[127351]2p12p9P0
448401	AL135401	Hs.23557	serologically defined colon c
429982	ME9113	Hs.226795	g/tRNAIle:G-tRNAIle:G pi
421547	AA489908	Hs.1390	proteasome (prosome, macropain
430335	NM_005463	Hs.227777	protein tyrosine phosphatase I
405887	AI157857	Hs.182655	keratin 19

sugar Jr	7.8
DSPC:Rhodaneso_Y_phosphat	7.8
PM2P2_Claudin	7.8
Insulin	7.8
RasGAP	7.7
DeltaGCBZIP	7.7
kinesin.FHA	7.7
chNMP_binding_jon_trans	7.7
Na_Ca_Ex_Catb-beta	7.6
SHCR	7.6
BTB_Naich	7.6
lov_trans_K_beta	7.6
phkase,SAM_decarbox	7.5
phkase	7.5
Glyco_hydro_18,CBM_14	7.5
C1q_Collagen	7.4
G_glu_transposi	7.4
B56	7.4
aa_pemase	7.4
Fz_kirnglu Ig	7.4
AFID_SNF	7.4
7hm_1	7.3
EGF_inhibin_EGF_Xlnk_S_m	7.3
SH2_Rhodolol saline sarcoma	7.3
PHPLC-X-PL-PLC-Y_C2	7.3
	7.3
filament	7.3
Tropoin	7.3
	7.2
	7.2
AM	7.2
ROK	7.2
secY	7.2
7hm_1	7.2
lactamase_B	7.1
XPG_X-XPG_L5_3_exonidea	7.1
	7.1
lsp_1_Fetoplysin_Pep_M12B	7.1
phkase	7.1
S1SH2_Rhodolol_L23_pkin	7.1
	7.1
cadherin	7.1
phkase	7.0
pyridoxal_deC	7.0
	7.0
ras	7.0
ras.arf	7.0
Integrin_AFG-GAP_Rhaid_g	7.0
	7.0
IQ	6.9
	6.9
SH2,SH3	6.9
tyrosin_kinglu.EGF	6.9
ldh_Mh_C adh_short_Soma	6.9
Galactosyl_T_2	6.9
PH	6.8
ldh_incept_La_h3_jd1_rece	6.8
C1q_Collagen	6.8
dynamain_2_dynamain.GED	6.8
TNFR_c5	6.8
ras.arf	6.8
Galactosyl_T_2 Ig	6.7
Glyco_hydro_1	6.7
zf-C3H4C	6.7
SH2,SH3,phkase	6.7
Neprosylin_lsp_1_Pep_M12B	6.7
p450	6.7
NADHdh_2	6.7
disintegrin_Neprosylin_Pe	6.7
TPR_C3H4C.PHD	6.7
FAO_Synth	6.7
zf-C2H2_phkase	6.7
hearcKinase	6.6
7hm_2_lsp_1_GPS_HRM	6.6
	6.6
pro_isomerase	6.6
GST_C_GST_N	6.6
CuIthrin_glu_ch_galactosom	6.6
Y_phosphatase,DSPc	6.6
filamentZIP	6.6

WO 02/102235

PCT/US02/19297

	404946			Target Exon	3Beta_HSD	6.5
	435213	AA092510	Hs.5985	non-kinase Cdc42 effector prot		6.5
	411201	T74584	Hs.5529	ESTs, Weakly similar to CSH1c	A2M_NA2M	6.5
	415364	U94905	Hs.277445	disacetylcholine kinase, zeta (1	ank-DAGK4/DAGK4/G_Pe-ii	6.5
5	428194	T50872	Hs.2001	thromboxane A synthase 1 (gat	p450	6.5
	424681	AA054400	Hs.151706	KIA0194 gene product	holocase_C,PRK	6.5
	417933	NM_002342	Hs.11116	lymphoblast beta receptor (TNF	TNFR_65	6.5
	408905	AV553783	Hs.061	Target CAT		6.4
10	438646	A/973076	Hs.231958	murine metalloproteinase 28		6.5
	431530	X61615	Hs.2798	leukemia inhibitor factor rec	li/3	6.5
	428883	AA439959	Hs.258802	ATPase, (Na/K) transporting, b	Na_K-ATPase	6.5
	404757			Target Exon		6.4
	406370			Interleukin 11	lypsin	6.4
15	436111	NM_014597	Hs.9625	NIMA (never in mitosis gene a)	pkmase	6.4
	424036	R02740	Hs.137555	putative chemokine receptor; G	7tm_1	6.4
	444912	AW247380	Hs.12124	putative prostate cancer virus	lactamase_B	6.4
	454480	W6945	Hs.748	RhoGTP growth factor recep	ly.phkase	6.4
	432269	NM_002447	Hs.2942	macrophage stimulating 1 recep	phkase,Soma,PSI,TIGM_E	6.4
	458716	AA359476	Hs.157099	ESTs		6.4
20	405262			Target Exon	Cacho	6.4
	447245	AK031713	Hs.17860	hypothetical protein FLH10051	E1_dehydrog	6.3
	442297	NM_005202	Hs.69901	phosphodiesterase 4A, cAMP-de	PDEase	6.3
	400694			CT1000125g(G538014)el/NP_05	7tm_1	6.3
25	404446	NM_013365	Hs.7189	pleckstrin homology, Sec7 and	Ph.Sac7	6.3
	430686	L36749	Hs.243116	chemokine (C motif) XC recepto	7tm_1	6.3
	451594	AK030995	Hs.26350	lysophospholipid sulfotransfer	Sulfotransfer	6.3
	438523	BE612990	Hs.5212	single-strand selective monote		6.3
	422714	AB018335	Hs.119367	KIA00792 gene product	DUF221	6.3
30	408924	AW256506	Hs.239513	homodomain-interacting protein		6.3
	414681	AS15629	Hs.76394	enoyl Coenzyme A hydratase, sh	EC04Pepylase_U7	6.3
	413254	U40272	Hs.75253	isocitrate dehydrogenase 3 (NIA	li.phkase	6.3
	419101	NM_004203	Hs.77783	membrane-associated tyrosine-	pkirase	6.3
	449761	AB009986	Hs.23965	solute carrier family 22 (orga	sugar_tr	6.3
35	422221	M21191	Hs.273415	acidase A, fructose-bisphosph	glyoxylate_acyl_aden_E3_	6.3
	414613	AW238400	Hs.76297	G-protein-coupled receptor kin	pkhase,RGS,phkase_C	6.2
	459516	BE010749	Hs.265097	ESTs		6.2
	417985	AA187545	Hs.63114	crystallin, zeta (quinone red	adh_zinc	6.2
	447507	H69996	Hs.16147	PCPT (processing of precursor,		6.2
40	418322	AA264166	Hs.64113	cyclic-dependent kinase inhibi	V_phosphatase,DSPe	6.2
	428443	BE0918106	Hs.184326	CDC10 (cell division cycle 10,	GTP_CDCM	6.2
	423229	AC003965	Hs.125632	protease, serine, 26	lypsin	6.2
	400903	BE244377	Hs.46676	farnesyl-diphosphate farnesyl	SQS_PSY,frmz-alpha	6.2
	429176	AB000462	Hs.107679	SH3-domain binding protein 2	PH.SH2	6.2
45	421565	BB0004	Hs.1023	pyruvate dehydrogenase (E1)an	E1_dehydrog	6.2
	400517	SC0071	Hs.241597	solute carrier family 6 (neuro	SNF	6.1
	435906	AB663379	Hs.110796	SAR1 protein	ar/ars	6.1
	402758			C1001697_g8(12722636)pe/DP_0	Gyoxy_hydro_16	6.1
	434202	BE382411	Hs.3764	guanylate kinase 1	Guanylate_kin,CoaE,Viral_	6.1
	402115			NM_021524:Homo sapiens histami	7tm_1	6.1
50	407801	AC002300	Hs.37129	sodium channel, nonvoltage-gat	ASC	6.1
	404879			Target Exon		6.0
	450739	AT32707		ESTs, Weakly similar to ALU7_H	VIR	6.0
	439658	AB040949	Hs.6733	pacose-enriched phospholip	C2,PL-PLC-X,PL-PLC-X,RasG	6.0
55	415742	BE410243	Hs.78769	thimet oligopeptidase 1	Peptidase_M3	6.0
	453190	AB002384	Hs.32312	KIA00356 gene product	PH,PH-D,RLIN	6.0
	439975	AW320261	Hs.6617	inositol triphosphatase (nucleo	Hamp1_like	6.0
	412800	AV552652	Hs.74668	polymerase (DNA directed), del	homodom	6.0
	432805	X94630	Hs.3107	CDC67 antigen	7tm_2,GPS,EGF	6.0
	416964	T74640		glyco5c7c12.1 Stralagene liver	A2M_NA2M	6.0
60	417483	BE464943	Hs.82208	acyl-Coenzyme A dehydrogenase,	Acyl-CoA,sh,Acyl-CoA,sh_M	6.0
	419755	H18444	Hs.134846	5HT1B-associated protein 3	C2	6.0
	457276	AF235087	Hs.227653	Homo sapiens chromosome X map		6.0
	423906	AJ004422	Hs.135103	cerkasin-alpha	PH/ArGap	6.0
	423118	N68718		glyxy65g02.1 Soares_multipla_		5.9
	427334	R44769	Hs.33191	Homo sapiens, Similar to trans		5.9
65	424959	NM_005261	Hs.159337	activated p21cdc42a kinase	pkhase,SH3	5.9
	453082	H18835	Hs.31608	hypothetical protein FLJ130041	kon_trans	5.9
	421166	AF182277	Hs.330780	cytochrome P450, subfamily IIE	p450	5.9
	422287	F16365	Hs.114546	cytochrome c oxidase subunit V	COX2a_Phage_G	5.9
70	401736			C16300492g(g1c127193)gk/AD05	AMP-binding	5.9
	434755	AA646502		ESTs		5.9
	414962	AF273304	Hs.235376	YPM2C protein	Exonuclease	5.8
	407338	AA173213		g1c366110.1 Stralagene lung	lg	5.8
	446426	BE016316	Hs.260776	interleukine, TNF-interacting an		5.8
75	409896	AK000002	Hs.55979	Homo sapiens mRNA: cDNA DKF2p	ABC_tran	5.8
	450778	U81375	Hs.25450	solute carrier family 29 (nuc	Nucleoside_tran	5.8
	423612	NM_002067	Hs.1686	guanine nucleotide binding pro	G-alpha_arf	5.8
	430845	AF246500	Hs.249056	G protein-coupled receptor 43	7tm_1	5.8
	424741	AF051941	Hs.340824	radioactive dihydrophosphate	NDR	5.8
80	412958	BE391579	Hs.75067	Fas-activated serine/threonine		5.8
	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase [con	GATase	5.8
	423156	H97991	Hs.193313	Target CAT	MoaA_NiB_PqgE	5.8
	414785	X76242	Hs.77115	cyclic-dependent kinase (CDC2)	pkhase	5.8
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NACD de		5.7

WO 02/102235

PCT/US02/19297

420904	AL035954	Hs.100221	nuclear receptor subfamily 1,	hormone_rec_zf-C4	5.7
415953	U19601	Hs.78473	N-deacetylase/N-sulfotransferase	Sulfotransfer	5.7
432074	AL045019	Hs.325462	Homo sapiens cDNA FLJ11214	DEAD盒 helicase_C, dsm, Vira	5.7
409124	AW292809	Hs.60727	N-acetylglucosaminidase, alpha		5.7
428270	BE501549	Hs.107040	ESTs		5.7
435114	AA775483	Hs.288536	mitochondrial ribosomal protein	OOC_AZ	5.7
425211	M18667	Hs.1867	progastrin (peptidase C)	asp	5.7
453054	AB176938	Hs.31547	Target CAT	Target CAT	5.7
420730	NM_002691	Hs.59890	polymerase (DNA directed), dol	ICL	5.7
415117	AF120499	Hs.78016	polynucleotide kinase 3'-phosph	Viral_helicase1	5.7
400986			Target Exon		5.7
413163	Y00815	Hs.75216	protein tyrosine phosphatase,	h3.ig_V_phosphatase	5.7
413588	NM_001610	Hs.75569	acid phosphatase 2, lysosomal	acid_phosphat	5.7
457308	AA110588	Hs.238272	inositol 1,4,5-triphosphate re	ion_transferrin_TPRMIR	5.7
400551	AA514246	Hs.33443	C100019917g(B624920)emb(C)A96	SROR	5.7
433472	BE384319	Hs.64702	phosphoglycerate dehydrogenase	2-Hisid_DH_2-Hisid_DH_C,M	5.7
409531	BE266315	Hs.23111	cytochrome beta1.4-galactosyl	Galactosyl_T_2	5.7
449139	BE266315	Hs.23111	phenylalanine-tRNA synthetase	neur	5.7
450207	T87615	Hs.14716	ESTs		5.7
400256			NM_002850/Homo sapiens ATP-B1	ABC_iron	5.6
430713	AA351547	Hs.2642	eukaryotic translation elongat	GTP_EFTU,GTP_EFTU_D3,GTP_	5.6
420511	U77413	Hs.100253	O-linked N-acetylglucosamine (TPR	5.6
405683			Target Exon		5.6
449181	X96783	Hs.23179	synaptotagmin V	C2	5.6
414457	AB934320	Hs.75159	ATPase, H-transferring, lysoso	ATP-eynt_C	5.6
415153	AL048981	Hs.12185	hypothetical protein MGCI4333		5.6
434863	AW381538	Hs.15807	hypothetical protein MGCI2696		5.6
433135	AA443673	Hs.110477	dolichyl-phosphate mannosyl		5.6
413049	NM_002151	Hs.6323	heparin (transmembrane protease	heparin	5.6
420299	NM_001620	Hs.100194	archaeobacter 5-lysozyme/ac	MAPEG	5.6
422357	NM_001638	Hs.1652	chemokine (C-C motif) receptor	7tm_1	5.5
443759	BE350832	Hs.134729	FXID domain-containing ion tra		5.5
454112	NM_000665	Hs.40034	integrin, alpha 4 (malign CD4	integrin_AFG-GAP	5.5
405594			NM_C19154/Homo sapiens A1Phase,	E1-E2_A1Phase_Hydrolase	5.5
415322	BE015464	Hs.75217	gamma-L-cysteine-lyase	PCPD,Calcium_DH_N	5.5
446765	AAW51473	Hs.16134	serine/threonine kinase 10	kinase,TVA	5.5
411030	BE367193	Hs.67896	7-60 protein		5.5
431498	AK001777	Hs.258551	aspartyl aminopeptidase	Peptidase_M18	5.5
433512	NM_020456	Hs.279510	ATX1 (acidic domain) protein 1, y	HMA	5.5
414907	X80725	Hs.77557	polo (Crosophila)-like kinase	kinase,POLO_box	5.5
424572	M19650	Hs.92909	2',3'-cyclic nucleotide 3' pho		5.5
405617			Target Exon	ehand,Ferrie_redut	5.5
421583	X55079	Hs.1437	glucosylase, alpha, acid (Pomp	treat,Glyco_hydro_31	5.4
415625	T76257	Hs.1259	asialoglycoprotein receptor 2	lectin_a	5.4
448053	AW977382	Hs.15598	2,4-dienoyl CoA reductase 2, p	adh_short	5.4
411574	BE242842	Hs.6780	protein tyrosine kinase 9-like	collin_ADF	5.4
405432			CD1E antigen, e polypeptide	Sulfotransfer	5.4
428521	Z43809	Hs.194638	polymerase (RNA) II (DNA direc		5.4
430337	M36707	Hs.239600	calmodulin-like 3	ehand	5.4
427162	AB011133	Hs.173564	KIAA0551 protein	kinase,PDZ	5.4
414216	D66870	Hs.75822	TFGB1-induced anti-apoptotic f	oxidoreduct_P1, myosin_head,b	5.4
422083	NM_001141	Hs.111226	acetylcholine 15-lipoxygenase,	lipoxigenase,PLAT	5.4
424373	AI133756	Hs.146219	copine VII	C2	5.4
449405	AA001350		gloab3H05.17 Soares_fetal_liv	mito_carr	5.4
400963	D50522	Hs.57729	Kelch-like ECH-associated of pro	BTB,Kelch	5.4
455818	AT32347	Hs.71174	heparinase 21 receptor		5.4
424357	AA961058	Hs.44456	hypothetical protein FLJ12116		5.4
423606	AB011094	Hs.129692	KIAA0522 protein	PhhZIPQ1,Sec7	5.3
432311	BE063090	Hs.274323	similar to sialyltransferase 7	Glyco_transf_29	5.3
450800	AB007831	Hs.24372	ESTs, Weakly similar to G207H	DEAD,GSP1_E	5.3
428716	Y09257	Hs.132621	skin containing monooxygenase	FMO-like,gyr_redox	5.3
402338			Target Exon	p450	5.3
412276	BE262621	Hs.73798	macrophage migration inhibitor	MF	5.3
437957	BE271414	Hs.5947	mel transforming oncogene (der	ras,arf	5.3
424166	BE338835	Hs.152978	proteasome (prosome, macropa	PA28_alpha,PA28_beta	5.3
447765	NM_018011	Hs.155153	C2H43 protein	adh_zinc	5.3
453690	X98607	Hs.286226	myosin IC	myosin_head,IQ	5.2
435327	BE301871	Hs.4867	mannosyl (alpha-1,3)-glycopro	HLH,Myo_N_term,Myo-LZ	5.2
423236	NM_002798	Hs.274382	protein kinase, interferon-ind	dsm,kinase	5.2
445139	AB057846	Hs.122056	lysophosphatidyl-XII	C2	5.2
429214	AB017222	Hs.198265	kinase-like 3	kinasin	5.2
432462	AK000013	Hs.274701	thymidine kinase 2, mitochondr	dNK	5.2
424387	AT739312	Hs.284163	ANKRD21 protein		5.2
400697			gh1Homo sapiens like mRNA	CydydytHans,Adeno_VII	5.2
456321	Y15521	Hs.24812	CDP-4-acylglutathione synthase (p		5.2
412939	AAW41491	Hs.75059	eukaryotic translation elongat	SHMT	5.1
445108	AF039916	Hs.12330	ectomendocytic triphosphate di	GDA1_CD36	5.1
419073	AK372170	Hs.183915	Homo sapiens cDNA FLJ12787	kgap_1,CD36	5.1
409968	NM_001623	Hs.57697	lysophosphatidyl synthase 1	Glyco_transf_1	5.1
442559	AF078037	Hs.324051	RoA, c-src-related inhibitor	SH3_nuk	5.1
424305	BE368095	Hs.112272	histone deacetylase 6	Hist_deacetyl1	5.1
427247	AV504221	Hs.174103	integrin, alpha L (malign CD1	vwa,Integrin_AFG-GAP	5.1
425931	Y14039	Hs.195175	CA3P6 and F1A0D-lac apoptosis	DED,ICE_20	5.1
429849	X52221	Hs.95587	excision repair cross-compleme		5.1

WO 02/102235

PCT/US02/19297

5	45337	R73417	Hs.25391	phylp2g12r1 Soares breast 2N	GSPII_III	5.1
	418910	Z25821	Hs.89466	Homo sapiens, similar to doc2c	ECH	5.1
	425771	BE561776	Hs.159494	Grainyhead, similar to Drosophila	SH2,SH3,kinase,PH,RTK	5.1
	450202			NM_021734 Homo sapiens decouyin	mlto_csr	5.1
	451452	BE590065	Hs.26433	doctylphosphate (UDP-N-acetyl	Glycos_transf_4	5.0
	418231	AA328895	Hs.83848	inosophosphate isomerase 1	TIM	5.0
	425185	NM_014434	Hs.154999	Target CAT		5.0
	407876	NM_004619	Hs.40666	potassium voltage-gated channel	ion_trans,KCNQ1_channel	5.0
	417831	H16423	Hs.82695	CD47 antigen (Rb-related antigen)	lg	5.0
10	404716			NM_007313 Homo sapiens v-erb	SH2,SH3,kinase	5.0
	405020			Target Exon	7tm_1	5.0
	425236	NM_004798	Hs.168212	kinasin family member 39	kinase	5.0
	431778	AB038286	Hs.253706	cysteinyl leukotriene CysLT2 r	7tm_1	5.0
15	422340	AW296219	Hs.115325	RAB7, member RAS oncogene fami	arf/ras	5.0
	438414	NM_001183	Hs.6551	ATPase, H transporing, lysoso		5.0
	425846	AA102174	Hs.159829	myosin XB	myosin_head,DAG_PE-bind_1	5.0
	413599	AJ068239	Hs.75438	signal transducer and activator	adh_short	5.0
	424188	L28277	Hs.321877	quinted chondroclonine rodac	SH2,STAT,STAT_bind,STAT_p	5.0
20	438042	AF284422	Hs.119178	cation-chloride cotransporter-	aa_permeases	5.0
	410775	AB014480	Hs.68196	nth (E-cad endonuclease III)-	Hh-LCPD	5.0
	428734	BE230344	Hs.192223	chlorotic transducin inhibi	WDR4	5.0
	420340	NM_000734	Hs.97087	CD32 antigen, zeta polypeptide	ITAM	4.9
	433075	NM_002959		sortin 1	BNR	4.9
25	403030	XO3363		HER2 receptor tyrosine kinase	kinase	4.9
	426811	BE259228	Hs.172809	nucleophosin 1	ehand	4.9
	401577			NM_000781 Homo sapiens cyclochr	p450	4.9
	409637	AA323946	Hs.55407	Homo sapiens mRNA; cDNA DKFZp4	Collagen	4.9
	428831	BE298216	Hs.172873	S-adenosylhomocysteine hydrola	AzohHyase	4.9
30	433904	U65402	Hs.248124	G protein-coupled receptor 31	7tm_1	4.9
	423502	AF107028	Hs.129783	sodium channel, voltage-gated,	lg,Adeno_E3_CR2	4.9
	421487	AF027406	Hs.104985	serine/threonine kinase 23	kinase	4.8
	402163			NM_004811 Homo sapiens glucoc	FF	4.8
	458748	AW137748	Hs.125902	ubiquitin specific protease 2	UCH-1,UCH-2	4.8
35	424771	BE387151	Hs.153003	serine/threonine kinase 16	kinase	4.8
	405441			Target Exon	Asa_trans	4.8
	437053	AJ077018	Hs.32335	keratin 1	filamen,bZIP,Tropomyosin	4.8
	443044	N28522	Hs.8305	cytochrome c phosphoribosyltran	QRPase,QRPase_N	4.8
	431204	F28841	Hs.250780	cytochrome c oxidase subunit V	cytochrome_c_oxidase	4.8
40	458417	L38531	Hs.51298	Integrin, alpha 8	uTTPase,COX6A_ras,ATP-syn	4.8
	438735	L48489		mannosyl (beta-1,4)-glycopro	Integrin_A,F,G-GAP	4.8
	441455	AJ271671	Hs.7854	zincfin regulated transporte	Zip	4.8
	449848	BE439053	Hs.239626	peroxisomal long-chain acyl-co	sugar_1r,Condensation	4.8
	451584	AJ076689	Hs.132780	hypothetical protein MGCT5729	EGF_laminin_G,LR,LRRT,L	4.8
45	403771			NM_003061 Homo sapiens sll1 (D	SLT	4.8
	403248			ESTs, Weakly similar to 178885		4.8
	410214	L26555	Hs.301698	sialyltransferase 4A (beta-gal	Glyco_transf_29	4.8
	407347	X55985		gH.sapiens SOC-2 gene for insa	sofle	4.8
	422868	AF193864	Hs.119120	E3 ubiquitin ligase SMLU1-1	C2,WV,HECT	4.8
50	439057	AJ004832	Hs.5038	neuropathy target esterase	cNMP_binding	4.8
	431282	NM_008672	Hs.251395	solute carrier family 22 (orga	sugar_1r	4.8
	409525	Y13547	Hs.113597	stearoyl-CoA desaturase (delta	FA_desaturase	4.8
	423658	U65679	Hs.186559	G protein-coupled receptor 23		4.8
	432716	A1782964	Hs.205180	ESTs		4.8
55	414480	L00727	Hs.888	dystrophin myotonia protein k	kinase	4.8
	403287	S36329	Hs.181350	kalikrein 2, prostatic	trypsin	4.8
	423846	AB040848	Hs.154885	DNK2 (DNA replication helicase	UvrD-nucleic,Viral_helic	4.7
	420228	AB014680	Hs.6798	carbohydrate (N-acetylglucosam	Substrate	4.7
	402912			Target Exon	kinase	4.7
	443329	BE282943	Hs.9234	hypothetical protein MGCT936		4.7
60	428120	AA325243	Hs.189887	copine 1	C2	4.7
	433059	AA332821	Hs.247382	dimethylarginine dimethylamino	z-C2-12,BAR,SH3	4.7
	451320	AW118072	Hs.17498	dimethylglycerol kinase, zeta 1		4.7
	447131	NM_004585	Hs.17498	retinoic acid receptor respond	zona_pellucida	4.7
65	431222	X58777	Hs.273790	zona pellucida glycoprotein 3A	C14OR00333/gly1882739/gly18C44	4.7
	404688			protein kinase C, alpha isoen	kinase	4.7
	427804	AL048654	Hs.180671	ESTs	7tm_1	4.7
	450748	A1730393	Hs.247686	ESTs	ehand	4.7
	429397	U03270	Hs.122511	centrin, EF-hand protein, 1	POEase	4.7
70	407978	AW385129	Hs.41717	phosphodiesterase 1A, calmodul	SH3,BAR	4.7
	428713	BE256238	Hs.152163	binding integrin 1		4.7
	456444	AA084517	Hs.31856	ESTs, Weakly similar to KIA114		4.7
	405574			Target Exon	kinase	4.7
	442414	BE408758	Hs.8297	hemocytoblast 6 precursor	nucleotidase_T2	4.7
75	418280	AAW40303	Hs.83951	Hemaphys-Pfaffik syndrome		4.6
	421601	AI060190	Hs.106070	cyclic-dependent kinase inhibi	CDI	4.6
	422795	AB033109	Hs.120866	KIAA1283 protein	kazal,A2M,A2M_N	4.6
	433019	AD086153	Hs.279915	translocase of inner mitochon	z1-Tim10_DDP	4.6
	431522	AW125589	Hs.258809	protein tyrosine phosphatase,	hs_1_v_phosphatase	4.6
	403848			corrin-related receptor, LID	ldl_recept_nld3,ldl_rece	4.6
80	459881	AW028302	Hs.155079	protein phosphatase 2, regulat	B56	4.6
	481172	X81157	Hs.83636	adrenocortical, beta, receptor kin	kinase,PH,LRGS	4.6
	408433	AW162631	Hs.45002	ras-related G3 botulinum toxin	ras	4.6
	439921	AL110026	Hs.6778	L101-like phosphatidylphospho	LACT	4.6
	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase	kinase,Furin-like,Rasop_	4.6

WO 02/102235

PCT/US02/19297

427945	AW137156	Has. 181202	lymphothelial protein FLJ10036	Collagen	4.6
451777	U95210	Has. 459	soluble carrier family 18 (vesi	sugar_tr	4.6
429536	BE259804	Has. 226377	phosphate cytidylhydrolase	Cydylyltransfer, COMBC	4.6
412074	F18070	Has. 75105	acropod-binding protein (star	UO_con	4.6
414702	L22005	Has. 76932	cell division cycle 34	7tm_1	4.6
425795	AJ000479	Has. 159543	endothelial differentiation, G	Relanase, WW	4.6
422454	U45070	Has. 161302	protein (epiglycyl-prolyl car	Methyltransfer_4	4.6
409135	AJ312448	Has. 42357	methylenetetrahydrofolate	cochom, Cofactor, C-term	4.6
452388	AF025300	Has. 264157	cadherin-like 22	Hepes, UL3	4.6
421140	AA298741	Has. 102135	signal sequence receptor, delt	Acytransferase	4.6
434834	AF158774	Has. 324020	1-acylglycerol-3-phosphate O-s	SHC5A	4.6
413407	AJ366293	Has. 75339	invariant glycoprotein phospho	chondr_100	4.6
400463			NM_014824 Homo sapiens S100 ca		4.5
417891	W99410	Has. 82897	protein phosphatase 1, regulat	ICE_p20DED	4.5
421681	AA284622	Has. 195175	CASP6 and FADD-like apoptosis	aminotran_1,2	4.5
426516	BE259800	Has. 170197	glutamic-oxaloacetic transamin	aldo_act_mol	4.5
419693	BE304571	Has. 68529	allo-leucine oxidase family 1,	kininase	4.5
423664	NM_004714	Has. 130688	dual-specificity tyrosine (Y)-	TNFR_c6,death,PH,Xbl,Ph	4.5
427681	AB018263	Has. 180338	tumor necrosis factor receptor	FS_F3_type_C,kinase	4.5
432853	NM_016154	Has. 279771	Homo sapiens clone PCP1569 unk	ABC_membrane,ABC_tran	4.5
413815	AL046341	Has. 75592	disoidal domain receptor fam	mlto_car	4.5
405546			NM_018633 Homo sapiens transp	adh_short	4.5
416297	AA157634	Has. 79172	soluble carrier family 25 (milo	kinase	4.5
421962	D62061	Has. 283354	FabG (beta-oxoacyl-acyl-car	Neur_chan_LED,Neur_chan_m	4.5
415341	R00802		glycerophosphatidyl transfer	aminotran_1,2	4.5
456666	W81526	Has. 116329	ESTs. Moderately similar to GA	iodicu/HMA	4.5
459952	AW327546	Has. 111024	soluble carrier family 25 (milo	res	4.5
407663	AA317089	Has. 597	glutamic-oxaloacetic transamin	death,TNFR_c6	4.5
435891	AAW45304	Has. 5002	copper chaperone for superoxid	UO_con	4.5
453597	AA247815	Has. 37303	W-helix. Harvey rat sarcoma vi	acyl_pemases	4.5
449029	N25865	Has. 22691	soluble carrier family 7 (oslo	7tm_1	4.4
424829	NM_002507	Has. 1827	nerve growth factor receptor (polyphenyl_Lynt	4.4
425362	T28333	Has. 200476	ubiquitin-conjugating enzyme E	PH_Oxydase_BP	4.4
429133	N31854	Has. 187116	soluble carrier family 7 (oslo	HCOO_cotransp	4.4
428076	K01220	Has. 68166	pesterase (Drosophila) homolog	Glyco_hydrol_63	4.4
414814	D14697	Has. 777393	isomeryl diphosphate synthase	ehand	4.4
433281	AB040967	Has. 112034	KIAA1534 protein	kininase	4.4
402915			ENSP00000202567-Bicarbonate i	Hist_deacetyl,5-UBP	4.4
415287	BE386537	Has. 83919	glucosidase 1	Sufl	4.4
430716	BE387257	Has. 247831	Homo sapiens. Similar to myosi	20G-Foll_Oxy	4.4
420674	X66357	Has. 336478	cyclin-dependent kinase 3		4.4
439902	AF174489	Has. 67574	histone deacetylase 6	ATPase	4.4
400223			Exo Control	kinase	4.4
409611	NM_004405	Has. 419	distal-less homeo box 2	homoecor	4.4
412965	L06419	Has. 75093	procollagen-lysine, 2-oxogluta		4.4
435564	AF210652	Has. 16614	SD-deoxyribonucleoside (dN	Acytransferase	4.4
416121	X92762	Has. 75021	telatazin (cardiomyopathy) dia	ion_trans	4.4
433323	A951628	Has. 127007	potassium channel, subfamily K	HATPase_c	4.4
448191	NM_005881	Has. 20944	branched chain alpha-ketoadid	NDK,Arten_glycop	4.4
436417	BE253181	Has. 61667	non-metastatic cells 3, protei	Peptidase_M24	4.4
439415	BE262554	Has. 343236	proliferation-associated 2G4,	7tm_3	4.4
429216	AA232665	Has. 156269	Target CAT		4.4
407433	AF026923		gt-Homo sapiens orphan G-pro		4.4
425955	T96308	Has. 248549	ESTs. Moderately similar to S6		4.4
407230	AA157857	Has. 182285	keralin 19	flament,bZIP	4.3
410187	NM_005516	Has. 95865	3-hydroxy-3-methylglutaryl-Co	RMG_CoA_Lynt	4.3
415406	R61673	Has. 79300	ubiquitin-conjugating enzyme E	UO_con	4.3
447957	NM_014821	Has. 20126	KIAA0317 gene product	Flavin,HECT	4.3
421771	NM_001224	Has. 108131	casepase 2, apoptosis-related c	ICE_p20,CARDICE_p10	4.3
448686	AL137291	Has. 22451	hypothetical protein FLJ10357	PH_RhoGEF	4.3
418821	M33635	Has. 77424	Fe fragment of IgG, high affin	ig	4.3
431066	AA324358	Has. 243227	Homo sapiens DNA control clone	ig,ln3	4.3
429892	NM_003903	Has. 2504	myomesin 1 (skeletinin) (185kD)		4.3
460126	BE018136	Has. 24447	sigma receptor (SH3T147 bindin	INPDR_CAMP,PH_NG5,NPDR	4.3
413781	J05272	Has. 850	hMP (nitroson monophosphate) de	SH2,SH3,kininase,PH,LYK	4.3
406330			NM_005547 Homo sapiens L2-in	GNT14	4.3
429393	AK000284	Has. 183690	hypothetical protein FLJ20277	GalP_UDP_transfer, GalP_UDP	4.3
413954	AL031111	Has. 75941	galactose-1-phosphate uridylyl	EPH1,Edm3,kininase,SAM	4.3
421779	X75206	Has. 2913	EpkB3	coronin	4.3
456529	AF014643	Has. 103072	coronin-46.8	Neur_chan_LED,Neur_chan_m	4.3
446098	Y06765	Has. 22785	gamma-aminobutyric acid (GABA)	zf-C2H2	4.3
429626	AI124572	Has. 323879	inhibitor of kappa light polyp		4.3
423956	AL037895	Has. 275961	CGI-31 protein	thored	4.3
426970	BE278891	Has. 194991	indinole acid induced 3	7tm_3	4.3
428953	AA336810	Has. 346193	tumor necrosis factor receptor	TNFR_c6	4.2
423622	AK001693	Has. 126458	muscle-specific beta 1 integr		4.2
426613	U98132	Has. 171280	hydroxyacyl-Coenzyme A dehydro	adh_short	4.2
426666	AF131636	Has. 170453	tropomodulin	Tropomodulin,kinase	4.2
425179	AJ224442	Has. 155320	putative methyltransferase		4.2
412715	NM_000947	Has. 74619	pinase, polypeptide 2A (58kD)		4.2
459208	R86701		gh-yne66009.1 Soares adult bra		4.2
404879			NM_000607 Homo sapiens glucose		4.2
400836			Target Exon		4.2
439940	Z25470	Has. 248145	metanocortin 5 receptor	Apdipoprotein	4.2

WO 02102235

PCT/US02/19297

405663		Target Exon	Pep_M126_propep	4.2	
430237	A1272144	Hs.236522	abhydrolase	4.2	
425175	AF020202	Hs.155001	DAG_Fc-binding2	4.2	
409067	BE260459	Hs.50267	putative CTR-binding protein s	4.2	
419982	AJ262644	Hs.55610	solute carrier family 30 (zinc	4.2	
428354	ALJ075472	Hs.104141	glutaryl-Coenzyme A dehydrogen	4.2	
437696	Z63844	Hs.5790	hypothetical protein d337E16.5	4.2	
454034	NM_000891	Hs.575	aldehyde dehydrogenase 3 famli	4.2	
410237	A750589	Hs.51258	argininosuccinate lyase	4.1	
451478	NM_012331	Hs.26458	methionine sulfoxide reductase	4.1	
415410	AF031332	Hs.278569	sorting nexin 17	4.1	
405638		Target Exon	Target Exon	4.1	
424349	AF141289	Hs.145560	solute carrier family 7 (calio	4.1	
441164	AB023180	Hs.7724	KIAA0953 protein	4.1	
421518	U63973	Hs.102501	rhodopsin kinase	4.1	
435540	AB032436	Hs.6535	brain-specific Na-dependent in	4.1	
417447	N71703	Hs.283267	EST6	4.1	
409693	AA010233	Hs.55921	glutaryl-prolyl-1RNA synthetase	4.1	
403655		NM_003071	Homo sapiens SWMSNF	4.1	
411142	NM_014255	Hs.63009	transmembrane protein 3	4.1	
437016	AJ076916	Hs.5386	guanine monophosphate synthetase	4.1	
422699	BE410590	Hs.119257	onco1 suppressor (mammary tumor a	4.1	
427202	BE272922	Hs.173936	interleukin 10 receptor, beta	4.1	
421390	D31833	Hs.1372	serpinine vasopressin receptor	4.1	
434142	U47927	Hs.3759	ubiquitin specific protease 5	4.1	
427407	BE236849	Hs.177766	ADP-ribosyltransferase (NAD+ p	4.1	
415749	AQ28320	Hs.75516	tyrosine kinase 2	4.1	
411927	BE274009	Hs.772	glycogen synthase 1 (muscle)	4.1	
419728	U01330	Hs.1274	bone morphogenetic protein 1	4.1	
423914	AF103200	Hs.13289	putative protein O-mannosyltra	4.1	
461355	NM_004197	Hs.444	serine/threonine kinase 1b	4.1	
422656	NM_006245	Hs.118244	protein phosphatase 2, regulat	4.1	
428204	AA435762	Hs.183435	NM_004545	Homo sapiens NADH de	4.1
431985	AF117222	Hs.272261	UDP-Gal-beta-GlcNAc beta 1,3-ga	Galactosyl_T	4.0
424339	BE259442	Hs.8951	proliferone (proliferin, macroph	proliferone	4.0
419039	AF207989	Hs.58914	Homo sapiens, Similar to G-pro	7im_3	4.0
431066	AF026273	Hs.249175	interleukin-1 receptor-associat	kinase,death	4.0
427215	Z12193	Hs.30352	ribosomal protein S6 kinase, z	phkase	4.0
403692		NM_007637	Homo sapiens a disti	Regulatory_inh_1_Pop_M12B	4.0
424549	A1761601	Hs.8375	TNF receptor-associated factor	z-C3H4C1MATH1z-TRAFA	4.0
427239	BE270447	Hs.228923	ubiquitin carrier protein	UQ_con	4.0
461126	AA015779	Hs.154443	ESTs	Y_phosphatase	4.0
425081	X74794	Hs.154443	melanoblastoma maintenance def	MCM	4.0
402171		Target Exon	Target Exon	C2	4.0
402665		Target Exon	Target Exon		4.0
420148	U34227	Hs.95361	myosin VIIA (Usher syndrome 1B	myosin_head,IQ,MyTH,SH3,	4.0
412167	U58487	Hs.73739	5-hydroxytryptamine (serotonin	7im_1	4.0
412656	AF030011	Hs.74376	dishevelled 1 (homologous to D	PDZ,DEP,DDX,Dishevelled	4.0
425760	_U35234	Hs.159534	protein tyrosine phosphatase,	fn3,jg_Y_phosphatase,DSPc	4.0
424288	AW113719	Hs.279882	Phosphatidyglycerophosphate S		4.0
425230	AW1135390	Hs.224170	ESTs	kinase	4.0
408449	NM_004408	Hs.126101	dynamitin 1	PH,GED,dynamitin,dynamitin_2	4.0
423855	AF250228	Hs.136141	ATP-binding cassette, sub-famli	ABC_tran,phnolomC,SRP54,Ca	4.0
422676	O28481	Hs.1670	histamine receptor H1	7im_1	4.0
468639	BE247683	Hs.14611	dead specificity phosphatase 1	DSPc	4.0
407026		C1300717	gill1263/9/hp126195	DEAD,heulacase_C	4.0
405370		NM_005699	Homo sapiens LIM do	kinase,LIM,PDZ	4.0
413954	AA331881	Hs.75454	peroxiredoxin 3	AhpC-TSA	4.0
432917	NM_014125	Hs.241517	PRO0327 protein		4.0
446362	AA641767	Hs.21015	hypothetical protein DKFZp564L_	sugar_tr	4.0
424512	X53302	Hs.149548	integrin, beta 5	integrin_B_EGF	4.0

TABLE 22B:

Play: Unique Eas probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

65	Play	CAT Number	Accession
40191	11824_1	AB09545	AB16201 AA948024 A1278970 AA68806 AA593279 F21973 W95940 AW696644 X59726 AA431579 AA970671 AB66005 AB671835
		BE56516	AA12524 A103001 AA1262322 AW001204 W68289 AA431456 AW468973 BE222544 AA45454 A969503 W95975 A338171
		AA776725	AD000676 A495
415341	1534442_1	R00602	Z42821 F06132
415995	1564_1	NM_004573	AB55578 BE24666 AW500410 A1W40849 AW402206 AA774870 AW530959 AA439523 A1933994 A1W751282 AW374413 AA578823
		H10054	AA310465 F12578 T74300 AA4353176 W9500136 AW6900136 AW6900136 AW6900136 AA124064 AW163096 AA116986 AW769251 A1767111 AA235723
		AA12290	AA466398 A
418994	1099600_1	T74546	T74546
424339	23827_1	BE257149	BE312111 AF219137 NM_015720 BE313658 BE382952 BE752205 BE251553 F12128 T66206 BE255806 BE254484 AA324163 H07952
		AL134164	AB67802 A204971 A1262524 A1W192547 A1952763 A1266471 A1083776
		AW138322	A1W207459 A1513351 NM_012219 AF043038 A051335 A054500 AA970999 BE551105 AA650290 A108039 AA324154
427010	27436_1	AF022090	BE039091 AL118847 AA4558 AF765270 AA45321 A1148538 A1373696 AA324153 BE174826 AA350765
427239	27647_1	BE270447	AW409921 BE207288 BE201770 D56356 BE263223 BE408171 BE262243 BE392439 BE297236 BE261776 BE314300 BE267719
		BE206715	BE133876 BE295291 BE207066 AA210623 BE407519 H51344 BE622905 AA402481 AW205213 T19021 AA355115 AA316879
		BE26533	BE521936 AA290724
427326	277229_1	A287878	AB54160 AA403077

WO 02/102235

PCT/US02/19297

	402760	9213669	Plus	136829-136952,137306-137621
	402823	8217481	Plus	57916-58170,58475-58795,59580-59867
	402912	7263904	Plus	145995-146267,150876-161358
5	402915	7406502	Minus	143-276
	402916	7406502	Minus	361-474,541-687
	403213	7630897	Minus	162572-162735,164442-164540
	403246	7656833	Minus	167438-167606
	403296	7231682	Minus	73532-73562
10	403379	9438244	Minus	117348-117560
	403655	8736093	Plus	65668-65689
	403672	7283266	Minus	96600-96891,96956-97280,97393-97594
	403592	7367304	Minus	53033-53039
	403771	7770492	Plus	112901-113045
	403949	7711972	Minus	1731-1941
15	404199	6010176	Minus	1669-2740
	404527	8152087	Plus	127731-127796,128090-128210,129808-130054,132545-132809
	404528	8152087	Plus	135375-135486
	404596	9568262	Minus	104907-105043
20	404676	9797204	Minus	56167-56342,58066-58186,58891-59048,60452-60628
	404679	9797204	Plus	128964-129002,129691-127011,127774-127893
	404716	9839066	Minus	123146-123417
	404767	7706327	Plus	100933-101063,101580-101782
	404879	5103013	Plus	78346-78473,78663-78893
25	404946	7382189	Plus	134446-134750
	404983	7397324	Plus	16588-17031
	404988	6899755	Plus	39287-39690
	405020	7137674	Plus	106606-107309
	405137	8570507	Plus	158969-159423
30	405187	7225826	Plus	117025-117170,118567-118736
	405202	7230116	Plus	40229-40453
	405282	3810573	Minus	10482-10689
	405370	2078469	Minus	38980-39111
	405371	2078469	Minus	47657-47766,49461-49596
35	405473	9439781	Plus	153074-153343,154501-154596,156879-156996,158863-159061,159910-160053,161109-161229,163035-163131,165163-165229,165828-166003,167375-167552,168236-169354,171127-171281
	405474	8439781	Plus	172005-172175
	405646	1064740	Plus	124010-124183
	405674	3620491	Minus	33200-33649
40	405934	6960456	Plus	161628-161734,162823-163014,164439-164652
	405983	4508157	Minus	21701-21844
	406897	4308923	Minus	56765-57010,57896-59016
	406714	4156179	Minus	42799-43653
	406128	9159110	Plus	50425-50676
45	406370	9266130	Plus	125320-125482
	406432	9266504	Plus	3804-3930,4026-4120,4929-5109
	406441	9280716	Plus	26200-26468
	406458	9756020	Plus	145574-146911
	406495	7711328	Minus	174693-174970
	406496	7711328	Minus	178947-179264,181775-182087
50	406530	7711474	Minus	11703-11900,14711-14829,14920-14984,16232-16448,16916-17087
	406636	7711478	Plus	35196-35367,36228-38476,40080-40216,43522-43840
	406811	8224230	Minus	2117-2257,2436-2540
	406817	8439858	Plus	36430-36562

Table 23A lists about 779 gene up-regulated in ovarian cancer compared to non-malignant adult ovaries. These were selected as for Table 20A, except that the ratio of "average" ovarian cancer to "average" normal ovaries was greater than or equal to 4.0, the "average" ovarian cancer level was set to the 93rd percentile value amongst various ovarian cancer specimens, the "average" normal adult tissue level was set to the 93rd percentile value amongst various non-malignant adult ovaries, the "average" ovarian cancer value was greater than or equal to 200 units.

TABLE 23A:

Pkey: Unique Eos probe(s) identifier number
Ex_Accn: Exemplar Accession number, Genbank accession number
UG ID: UniGene number
Tss: UniGene gene title
Protein Dom.: Predicted protein domain
R1: Ratio of tumor to normal ovaries

	Pkey	Ex_Accn	UG ID	Title	Protein Dom.	R1
70	421296	NM_000686	Hs.103263	perlepin	perlepin_SS	37.8
	437897	AA770561	Hs.146170	hypothetical protein FLJ22969	SS,TM,H-DHHC	29.2
	453028	AB006632	Hs.31442	RecQ protein-like 4	DEAD,Helicase_C,Fork_head	27.6
	441021	AW578716	Hs.7644	H1 histone family, member 2		27.2
75	422510	AA316812	Hs.56370	cytochrome P450, subfamily 1B5	SS,TM,kinase,Ac3g	25.5
	454017	AW022617	Hs.34700	hypothetical protein FLJ22709	SS,TM,myosin_head,RA,DAG_	25.9
	438424	A912498	Hs.25855	hypothetical protein FLJ14996	SS,TM	25.8
	435017	AA336522	Hs.12854	angiotensin II, type I recepto		25.0
	498518	BE364536	Hs.3454	KIAA1821 protein	SS	23.3
	410418	L311302	Hs.61335	transmembrane protease, serine	SS,TM,H1_recept_L,tyrosyl	22.7
80	439524	A936597	Hs.125293	ESTs		22.8
	446374	AA329260	Hs.24756	ESTs, Moderately similar to al		22.6
	431773	BE409442	Hs.268567	pleckstrin homology-like domain	PH,SS,LIM,Protein	21.4
	420839	A1792682	Hs.262950	hypothetical protein MGCI0870	SS,SS,LFFC139,Glyco_Hydro	21.4
	413436	AF238083	Hs.68061	sphingotriase Nuclease 1	DAGKc	21.2

431354	BE048956	Hs.261573	DNA (cytosine-5)-methyltransferase
443760	NM_012058	Hs.5754	activating transcription factor
448133	AA0723157	Hs.73789	Scale receptor 1 (beta)
444202	AL031945	Hs.12785	KIA0258 protein
427640	AF058263	Hs.160015	D-deoxycholate isomerase
419167	AF583535	Hs.94875	ESTs, Weakly similar to A45363
426118	L29472	Hs.1802	major histocompatibility complex
427487	AW152475	Hs.31240	ESTs
420423	AA827718	Hs.88218	ESTs
414755	AW451101	Hs.159489	ESTs, Moderately similar to JC
407893	BE408399	Hs.43521	Homo sapiens, Similar to hypox
408254	BE1417382	Hs.337480	gbcCVA-H10101-01009-032-057 H
442332	AF157815	Hs.337480	ESTs, Weakly similar to A47582
416855	AA297395	Hs.80324	serine/threonine protein phosph
419823	AW271708	Hs.118918	ESTs, Weakly similar to M20M_H
422625	AW504098	Hs.155975	cutlin 4B
401184			C10000997-g106780561p10NP_0
407507	U73799		gbcHuman dyxactin mRNA, partial
400633			C10000690-g13746443g1AAC639
422064	AW452889	Hs.335742	ESTs
425454	D30534	Hs.255459	C-type lectin-like receptor-1
427193	NM_001381	Hs.103854	dosage protein 1, 52kD (clonin
427387	A929685	Hs.177656	calmodulin 1 (phosphorylase ki
431452	AF583672	Hs.258311	granin-like neuroendocrine pep
434796	AAR12046		ESTs
428039	A929377	Hs.177274	creatine kinase, brain
447657	AF523298	Hs.164303	ESTs
424272	AW906859		gbcMRD-ST0020-081159-004-c03 S
455588	AI129303	Hs.74669	vesicle-associated membrane pr
454319	AW477396	Hs.101617	ESTs, Weakly similar to T32527
429527	AA454184	Hs.289014	ESTs
432803	AA554920	Hs.105794	UDP-glucose:glycoprotein glucos
110338	W03445	Hs.38205	gbcza05g11.1 Scanes melanoyr
452833	BE55981	Hs.30736	KIA0124 protein
407363	AF033032	Hs.191125	gbcHomo sapiens clone MCA1.1 my
414413	BE294877		gbcS01174162F1 NIH_MGC_17 Homo
431765	AF124249	Hs.268541	novel SH2-containing protein 1
421694	BE387430	Hs.106880	lysine-like
453685	AF078684	Hs.116958	Homo sapiens mRNA for KIAA1678
418736	T16579	Hs.87908	Sm2-related CBP activator pro
460658	AL137680	Hs.348012	Homo sapiens mRNA; cDNA DKFZp4
419725	U66048	Hs.52683	Homo sapiens clone 161456 brea
418126	D60945		gbcJNH1410049 Clontech human f
408301			Target Exon
416843	AJ251016	Hs.89230	potassium intermediate/small c
433396	A1742071	Hs.133205	ESTs
434333	A13168733	Hs.252154	stromal cell protein
407045	Y10141		gbcH.sapiens DAT1 gene, partial
452651	AW1723191	Hs.213117	ESTs
422418	AK001383	Hs.118385	hypothetical protein FLJ10521
447859	AK002194	Hs.19851	peroxisomal biogenesis factor
420836	AW956453	Hs.204959	hypothetical protein FLJ14885
423036	BE413992	Hs.195177	phenylethylamine kinase, gamma 2
419639	AK001902	Hs.91753	hypothetical protein
429712	AW245825	Hs.211914	ENSP0000023627-NADH-ubiquinol
452554	AW424543	Hs.588006	ESTs, Weakly similar to ALUS_H
441076	W40505	Hs.111197	Homo sapiens, clone IMAGE3343
428860	U38291	Hs.194301	microtubule-associated protein
421901	AB014554	Hs.106299	protein tyrosine phosphatase,
441363	AW450211	Hs.126825	ESTs, Weakly similar to A63002
443601	AW208974	Hs.253394	iron- or heme-binding protein
423682	AW004058	Hs.236720	acidic/less protein
431849	AF070823	Hs.88573	hypothetical protein MGC10911
423652	AK001035	Hs.130681	B-cell CLL/lymphoma 11A, (zinc
404365			Target Exon
425594	U51333	Hs.195237	hexokinase 3 (white cell)
420398	AC231980	Hs.204582	ESTs
434552	AF539818	Hs.325116	Homo sapiens, clone MGC2962,
418351	AW905358	Hs.12469	gbcUH-FE-BNO-ato-4-03-U1.1
427433	BE0270	Hs.177972	chromosome 4 open reading fram
400138	BE289554	Hs.177729	ESTs
425391	AW151050	Hs.189911	second mitochondria-derived ac
467613	AF589859	Hs.173770	ESTs
427502	AB111855	Hs.71933	Homo sapiens, clone IMAGE3161
427215	AL117468		Human clone 23544 mRNA sequen
423354	AL133632	Hs.127808	Homo sapiens mRNA; cDNA DKFZp4
447151	A022813	Hs.92879	Homo sapiens clone CDARP0014 m
431686	AK000020	Hs.272018	hypothetical protein FLJ20013
454291	AW384947	Hs.213534	ESTs, Weakly similar to MUC2_H
430554	AA565410	Hs.226974	human homolog of Drosophila Sc
459302	NM_002314	Hs.355956	UIM domain kinase 1
422795	AW409701	Hs.1578	baculoviral IAP repeat-contain
429844	AK000054	Hs.154255	hypothetical protein FLJ20057
456073	BE464016	Hs.238955	ESTs

SS,PWWP.PHD	9.7
bZIP,ATP,Transf_2,SS,TBC	9.7
Foldase, jcs,SS	9.7
SS,TM,Hs_PH_Exchange/ABC2	9.7
MF,late protein_L2,SS,GS	9.7
SS	9.6
TM,jg,MHC,J_beta,SS,TMA	9.6
ESTs	9.6
SS	9.6
hexokinase2,hexokinase	9.6
SS,SS,ar,ras,h3,ras	9.5
Armonium,transp	9.5
SS,TM,TG-Cb,propeptide,TGF	9.5
Metallophos,Metallophos	9.4
SS,TM	9.4
SS,SS,Cutlin,Cutlin	9.3
SS,Smad1,Notum,Laminin	9.3
SS,TM,HCO3,calresp,CAP_C	9.2
SS,TM,Tm_1	9.2
TM	9.2
iodin,CS,TM	9.2
PHURS,TM,PHURS,lipysin,	9.1
ethand,RnaAD,SS,ethand	9.1
SS	9.0
SS,mph_dna-binding,mph_dN	9.0
ATP-gus_Plasma,ATP-gus_P1	9.0
TM	9.0
SS,TM,inos-1-P,pyrith,Oct	8.9
synaptobrevin,SS,TM	8.9
SS	8.9
SS	8.9
SS,TM	8.8
phkinase	8.9
WC40	8.9
SS,jg,SS,G_glu,transpept	8.8
SS	8.8
SH2,SS,TM	8.7
SS	8.8
SS	8.8
SS,hcface_CAT_hoof,SS,	8.7
SS	8.7
TM	8.7
TM,CaMBD,SK_channel,TM	8.6
SS,TM	8.6
SNF,SS,TM	8.6
SS,Sema	8.6
RhoGEF	8.6
SS	8.6
SS,ras	8.6
phkinase,SS,SNF2_Nucleic	8.6
SS	8.6
coloreded_g0,SS,TM,rm	8.5
SS,PAS,HLH	8.5
SS	8.5
M	8.5
SAM,SS,TM,rm,PDZ	8.4
SS,TM,HSP20,7m_1	8.4
GATA	8.4
SS,MATM124-TRAF-2,C3HC4	8.4
SS,TM	8.4
SS	8.3
SS	8.3
hexokinase,hexokinase2,he	8.3
SS	8.2
SS	8.2
SS,phkinase	8.2
SS	8.2
SS	8.1
SS,TM,ABC,Tran,Glyco_tran	8.1
SS	8.1
SS,TM,LR,aminotran_1_2	8.0
SS,XRCC1_H,PRCT,jadamine	8.0
SS,TM,jg	8.0
SS	8.0
SS,TM,SS,TM	8.0
SS,zf-C2H2,rm	7.9

WO 02/102235

PCT/US02/19297

454246	AW245185	Hs.6996	ESTs		7.9
456635	AW403954	Hs.25237	mesenchymal stem cell protein	4HBT	7.9
422305	A328242	Hs.293438	ESTs, Highly similar to AF1984	SS	7.9
425760	BT1929	Hs.159479	glutathione (H-acceptor)-S-oxid	SS,SS,SS,SS, TM	7.9
413534	BE146961	Hs.21627	gln:QV4410222-011195-019-612 H	SS, TM	7.8
446931	A348856	Hs.21627	gln:BM65a.5.x2 NCL CGAP_L26 Hs	TM	7.8
421726	A9001237	Hs.319088	hypothetical protein FLJ10375	SS, TM, CAT, LRR	7.8
427461	A4551527	Hs.332040	hypothetical protein FLJ10375	SS, TM, CAT, LRR	7.8
448993	A471630	Hs.9018	KIA0414 gene product	Exonless, SS, TM	7.8
443136	NM_001440	Hs.9018	exonless (multiple) like 3	SS, kinase	7.8
427725	U96639	Hs.180533	mitogen-activated protein kinase	SS, TM, DUF289	7.8
409023			Target Ecton	ESTs	7.8
419757	AA733820	Hs.63970	ESTs	SS, TM	7.8
458834	AA566883	Hs.196446	ESTs	SS, SAA, proteins, SS, SAA, pr	7.7
427899	AA828286	Hs.332053	serum amyloid A1	SS, perlepin	7.7
452399	BES13301	Hs.29344	hypothetical protein, clone 24	allFS	7.7
435643	NM_002212	Hs.5215	integrin beta 4 binding protein	SS, TM, Band_7, AAV, cdc-48, N	7.7
431811	AB040972	Hs.301696	hypothetical protein FLJ11550	SS, hormone_rec, zf-C4	7.7
414534	BE257293	Hs.76366	BCL2-antagonist of cell death	SS, kinase	7.7
455885	BE153524	Hs.189455	gln:PMH-H10339-241199-002-C03 H	ubiquitin, LRR, integrin_B,	7.6
427721	A1582843	Hs.189455	RAD23 (S. cerevisiae) homologue	TM, PAP2, TM	7.6
430432	AB037798	Hs.241419	KAA1337 protein	SS, SS, TM	7.6
427273	AW139032	Hs.107376	hypothetical protein DKF2p434N	PAP2, SS	7.6
450334	AF035969	Hs.24879	phosphatidic acid phosphatase	SS, hormone, UPP0160, DUF23	7.6
413654	BE260103	Hs.146950	gln:G01146950F1 NH1_MGC_19 Homo	SS, Fork, head	7.5
410397	AF217517	Hs.63942	DKF2p954157 protein	TM, ABC, tran, ABC, membrane	7.5
439539	BE348326	Hs.121589	ESTs	zf-C2H2	7.5
400286			C160009222/g7499103/pj107209	disintegrin, RAR, integrin, Pe	7.5
416472	AA180765	Hs.340316	ESTs, Moderately similar to AL	LM, SS, SRS, Srs, Metalloph	7.5
418641	BE243136	Hs.85947	a disintegrin and metalloprote	COX5B	7.5
419492	AA243567	Hs.19447	P32-LIM protein myelopo	SROR, TM, Acetyltransf	7.5
420970	AA305079	Hs.1342	cytochrome c oxidase subunit V	PhD	7.4
406495			Target Exon	TM, PLAT, SS	7.4
448043	A458653	Hs.201881	ESTs	fn3, Ig, R3, SS, TM, fn3, R	7.4
401724	M17640	Hs.1757	L1 cell adhesion molecule (hyd	SS, TM	7.3
424263	AW1879141	Hs.1757	ESTs	Kunitz, BPT1, SS, TM, jon, tra	7.3
428092			serine protease inhibitor, Kun	Est, Control	7.3
453023	AW028733	Hs.31439	ESTs	Corona_7, SS, TM	7.3
400137			ESTs	UPP, synthetase, HMG14_17	7.3
436127	W64824	Hs.11655	RIKEN cDNA 2010100012 gene	PMP27, Claudin, SS, TM, PMP22	7.3
412265	AA101326	Hs.86154	hypothetical protein FLJ12457	SS, TFR	7.3
432747	NM_044044	Hs.278907	calcium channel, voltage-gated	SS, Collagen, SS, Collagen	7.3
446859	BE224446	Hs.265317	hypothetical protein MG25262	SS, TM, gln	7.3
407619	AL050344	Hs.37105	collagen, type IX, alpha 2	FAD-oxidase, C_FAD_binding	7.2
429299	AB26463	Hs.347408	hypothetical protein MG213102	SS	7.2
401674			C16001417/g7500349/pj10721	SS, TM, Na, Ca, Ex, Calc-beta,	7.2
412289	AW935967	Hs.170162	KAA1337 protein	CPase, L_chain	7.2
424198	AB229010	Hs.143026	KAA1087 protein	SS, TM, 7m_1	7.2
412173	T71071	Hs.1071	gln:5505.05.r1 Skatogene liver	rm	7.2
438113	A487908	Hs.8882	ESTs	PAF, AH, IL, Lipase, GDSL, SS,	7.2
428669	AB07018	Hs.15977	Target CAT	SS	7.1
439953	AW247829	Hs.0763	protein-activating factor ace	SS, SS	7.1
429241	A377150	Hs.159914	ESTs	SS, SS	7.1
448340	A482910	Hs.32362	ESTs	SS, SS	7.1
406779	AA412048	Hs.278574	CG-39 protein; cell death-reg	W40	7.1
431005	AA449644	Hs.127269	ESTs, Weakly similar to T02345	SS, SS, RNA-synt, 1, GST, C, G	7.1
421273	AJ264146	Hs.101506	U6 snRNA-associated Sm-like pr	Y, phosphatase, DSPc, TM	7.0
409649	AA159276	Hs.55505	hypothetical protein FLJ20442	miro, car, SS, TM	7.0
430281	A1878842	Hs.237924	CG-69 protein	laminin_EGF, laminin_G, EGF	7.0
444672	Z96364	Hs.11669	laminin, alpha 5	SS, cystatin, Coprogn, oxi	7.0
405928			Target Ecton	aminotran_1, 2, SS, TM, LFR	6.9
421321	NM_005309	Hs.103502	glutathione-pyruvate transaminase	HLH	6.9
439905	AW799755	Hs.110953	retroic acid induced 1	SS, integrin_B,3, Calc-beta	6.9
451937	AF119664	Hs.27299	transcriptional regulator prot	SS, TM, aminotran_1, 2	6.9
426075	AW044791	Hs.131322	hypothetical protein FLJ14524	SS, oxidoreductase, SS	6.9
438627	A907335	Hs.123473	ESTs	SH2, SH3, kinase	6.8
438951	U51336	Hs.6453	insulin 1,3,4-triphosphate 5'	SS, TM, insulin	6.8
427158	BC397336	Hs.1422	Gardner-Rasheed feline sarcoma	RCO1	6.8
423228	AL131491	Hs.125511	Homo sapiens mRNA; cDNA DKFZp4	SS, TM, EF1B	6.8
421755			Rag C protein	SS, TM, TNFR, c5	6.7
425798	AA564512	Hs.24301	polymerase (RNA) II (DNA direc	SS, crystal	6.7
431771	AB187771	Hs.257170	ESTs		6.7
426315	AA684219	Hs.348137	Homo sapiens, clone IMAGE3542		6.7
440317	BE561888	Hs.12769	gln:01340030F1 NH1_MGC_6 Homo	SS, RA, RasG, RasG, GFN	6.7
438657	AB279112	Hs.130783	Forsmanin cytochrome	ras, arf, SS, PDE, ace	6.7
452072	BE258857	Hs.27714	RAS3A, member RAS oncogene fam		6.7
439398	AF161536	Hs.284292	ubiquitin-cytochrome c reducta		6.7
423106	N52572	Hs.13702	ESTs, Moderately similar to AL	TM	6.7
453101	AW652776	Hs.54943	ESTs	SS, TM	6.7
420307	AW502669	Hs.66219	ESTs	7m_1, SS, TM	6.7
415056	AB004662	Hs.77867	adenosine A1 receptor	SS, TM, voltage_CLC_QCB	6.7
454262	AW612232	Hs.254835	ESTs		6.7
409227	A906105	Hs.130323	Homo sapiens, clone IMAGE3960	SS, zf-C2H2	6.6
413908	BE40996	Hs.323613	Homo sapiens, clone MGC2687		6.6

WO 02/102235

PCT/US02/19297

457274	AW074193	Hs.227152	mannan-binding lectin serine p
419157	A423440	Hs.23871	ESTs
41424	A222869	Hs.23873	ESTs
412464	778141	Hs.22826	ESTs, Weakly similar to 155214
430168	AW968343		DKFZ434I735 protein
455035	AW681734		gb:MR2-CT0222-01190-007-e10 C
422682	W05238	Hs.84316	ESTs, Weakly similar to T31613
453307	AW732847	Hs.70573	PKC-2-related HT protein
450593	AF129085	Hs.25197	STIP1 homology and U-Box conta
420319	AW406289	Hs.96593	hypothetical protein
413131	M64730	Hs.250616	isocitrate dehydrogenase 3 (NA
413297	A4851771	Hs.3076	ESTs
410082	AA081584	Hs.158311	Musashi (Drosophila) homolog 1
441307	AW071696	Hs.200065	hypothetical protein FLJ14225
454682	AW18029	Hs.289770	gb:MR3-ST0220-15129-027-b10 S
407289	A4460205		ESTs, Weakly similar to 136022
422637	U25441	Hs.121476	dopamine receptor D5
407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin
417810	D028419	Hs.82609	hydroxymethylglutamate synthase
445333	BE537641	Hs.44278	hypothetical protein FLJ12538
402197			Target Exon
419390	AW071162	Hs.90207	hypothetical protein MGC11138
447754	AW073310	Hs.163833	intron of HER4
444684	N26362	Hs.101515	map kinase phosphatase-like pr
421190	U05051	Hs.102482	muscle S, subtype B, tracheobr
419672	A1909884	Hs.270823	telomerase X, 1
430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)
413343	BE382026	Hs.334346	hypothetical protein MGC13045
417852	A2505062	Hs.82749	transmembrane 4 superfamily na
403126			KAA1003 protein
413055	AV65701	Hs.75183	cytochrome P450, subfamily 11E
427812	AA770424	Hs.89192	ESTs
457761	AW401809	Hs.4779	KIAA1190 protein
453096	H02807	Hs.31659	thyroid hormone receptor-associ
426048	A190883	Hs.134478	ESTs
407223	I196850		gbyr3b2b1.1 Scores melanocyt
445634	A1624849	Hs.344612	ESTs, Weakly similar to NEL1_H
441197	BE244638	Hs.168	steryl regulatory element bind
421707	NM_014921	Hs.107054	actinomyosin 2
435760	AB029012	Hs.4690	KAA1089 protein
432383	NM_016558	Hs.274411	SCAN domain-containing 1
427326	A1287878		gbyr23DG.AT1 NCL_GAP_Lym6 Ho
417425	A1271888		cyclin K
419444	NM_002496	Hs.80443	Target CAT
457978	AA776638		gb:ae77g04.51 Stratagene schiz
410445	AA159530		gb:ae77h01.91 Stratagene hnt n
413657	W19144	Hs.271742	ADP-ribosyltransferase (NAD+ p
407143	C14076	Hs.332329	EST
408724	A1685842	Hs.294143	ESTs, Weakly similar to T22914
436685	W28661	Hs.5288	Homo sapiens mRNA; cDNA DKFZp4
411583	A1701489	Hs.205742	ESTs, Weakly similar to ALUA_H
415802	A5026986	Hs.85600	mitogen-activated protein kina
414927	T35587	Hs.198476	ESTs
434314	BE392521	Hs.3787	RAB26, member RAS oncogene fam
414187	BE287901	Hs.103845	ESTs, Moderately similar to IS
424415	NM_001975	Hs.148590	enkephalin 2, (gamma, neuronat
406407			Target Exon
447365	BE383676	Hs.334	Rho guanine nucleotide exchang
417900	BE250127	Hs.82906	CDC20 (cell division cycle 20,
442297	NM_008202	Hs.85801	phosphodiesterase 4A, cAMP-spo
426440	BE38276	Hs.109902	soluble carrier family 2 (beta
418256	AW843318	Hs.12271	I-box and leucine-rich repeat
431543	AW996919	Hs.250788	adenylate cyclase 1 (brain)
430344	AA476827	Hs.171012	hypothetical protein FLJ22349
428539	AW410063	Hs.184877	soluble carrier family 25 (mito
403938			Target Exon
456950	AF111170	Hs.306165	Homo sapiens 14q32.1 Jagged2 gen
451481	AA300228	Hs.298606	hypothetical protein DKFZp434n
434357	AW732284	Hs.3828	neurokinine (phosphopeptide) decarbo
443563	AL040355	Hs.9573	ATP-binding cassette, sub-fam
433333	AA016521	Hs.71816	v-akt murine thymoma viral onc
430800	AW963067	Hs.274348	HLA-B associated transactin-3
409034	A1684149	Hs.172035	hypothetical protein similar 1
421542	AA411807	Hs.115954	ESTs, Weakly similar to KIAA11
431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp4
409608	AF231023	Hs.55173	cadherin, EGF LAG seven-pass G
423464	NM_016240	Hs.128866	CSRI1 protein
427379	AA552860	Hs.133664	ESTs
443867	NM_034729	Hs.89033	Ac-like leucoposable element
450122	BE313765	Hs.343443	ESTs, Weakly similar to 136022
404807			Target Exon
445303	AW362198	Hs.12503	interleukin 15 receptor, alpha
443631	AK018822		Homo sapiens cDNA FLJ10960 fis
412091	RO6185		gbyr4K03.1 Scores fetal liv

WO 02/02235

PCT/US02/19297

448536	W74413	Has.15251	hypothetical protein	SS	5.8
432686	BE359575	Has.27969	mitochondrial carrier homolog	SS	5.8
422383			ENSP00000005204:CDNA FLJ20404	SS	5.8
413041	BE061580	Has.61622	glt:MR0-ET0249-051295-301-cst E	SS, TM	5.8
414356	AW50505	Has.335147	glt:U-HF-SHO-als-a-10-U-ILr1	SS, TM	5.8
402916			ENSP0000020507:Glyceraldehyde I	SS	5.7
459133	U40343	Has.29655	cyclic-dependent kinase inhibi	ank, SS, Adip, comp, sub	5.7
404757			Target CAT	TM, Cst2	5.7
408079	BE063422	Has.56851	hypothetical protein MGC2666	SS, TM	5.7
411219	AW532917	Has.110665	glt:QV2-T10003-161199-013-h06 T	SS	5.7
421871	AK001416	Has.306122	glycoprotein, synaptic 2	TM, Steroid, cl_SS	5.7
434067	H18913	Has.124023	Homo sapiens CDNA FLJ14310.1a	SS	5.7
416789	AK020076	Has.70741	hypothetical protein FLJ10116	SS	5.7
445582	BE272696	Has.15356	hypothetical protein FLJ20254	hormone, SS, ptk6	5.7
407117	AA146625	Has.10084	gluc271c07.s1 Stratiagene pancr	SS	5.7
444855	BE490281	Has.10084	Tu translation elongation fact	GTP, EFTU, GTP, EFTU_D3, GTP_	5.7
421543	AA000519	Has.100605	hypothetical protein FLJ20612	TM	5.7
407757	BE04914	Has.16215	hypothetical protein MGC3595	SS, EFTG, domain, GST_C, GST_	5.7
419125	AA642452	Has.130881	B-cell CLL/lymphoma 11A (p1nc	SS	5.7
437141	BE354917	Has.31097	hypothetical protein FLJ21478	SS, TM, Glycose, transf_4	5.7
408905	AA055763	Has.661	Target CAT	SS	5.7
450787	AB006190	Has.25475	aqueous 7	MP, SS, TM	5.7
432436	D45276	Has.187959	ESTs	SS	5.7
428367	AB007867	Has.278311	plexin B1	Sema, PGL, TIG, SS, TM, TIG, Se	5.7
422708	AB017430	Has.119324	kinase-like A_	kinase, Junc, connect, SS, TM, r1	5.7
417442	AA139940	Has.124039	ESTs	ESTs	5.7
432751	AF152089	Has.278911	interleukin 17C	SS	5.7
432004	BE018302	Has.2894	placental growth factor, vascu	PDGF, SS	5.7
454151	AA047169	Has.154008	hypothetical protein FLJ22755	SS, TM, Glycose, transf_4	5.7
456145	BE259427	Has.21446	KIAA1716 protein	SS, DDX, POZ, DEP, Dishevelle	5.6
417677	NM_016055	Has.82389	CQ-118 protein	SS	5.6
451558	NM_001089	Has.26630	ATP-binding cassette, sub-fam	ABC, Iran, SRP54, SS, TMECH	5.6
408795	AW749126	Has.170345	hypothetical protein FLJ13710	hormone, reczf-C4	5.6
407204	R41593	Has.142337	ESTs, Highly similar to ALU1_H	SS, Histone, histone	5.6
428248	AF044824	Has.30792	hool2 protein	ICBP, SS, Nuclep-TSA	5.6
439343	AF086161	Has.114611	hypothetical protein FLJ11805	SS	5.6
458271	AL045834		glt:DKFZp-GM4116_r1.434 (synony	SS, PG, xyl_kinase, PGKa	5.6
401609			c18001614g17801278emb1CAB91	SS	5.6
417827	U27227	Has.19718	protein tyrosine phosphatase,	Y_phosphatase, h3, Ig, JAM, J	5.6
409125	R17268	Has.343557	axonal transport of synaptic v	SS, Kinasin, P1, FHA, Kinasin	5.6
450437	X13956	Has.24998	hypothetical protein MGC10471	SS	5.6
415514	F11301	Has.138329	ESTs	SS, TM	5.6
437926	BE363805	Has.300616	small GTP-binding protein	SS, TM, TPR	5.6
406663	U24683		immunoglobulin heavy constant	SS	5.6
421678	AA419006	Has.106730	chromosome 22 open reading fra	SS, TM, UBA, R, Rhomboid, SS, TM	5.6
422472	R59598	Has.279938	mitochondrial carrier homolog	mito, car	5.6
414918	A219207	Has.72222	hypothetical protein FLJ13459	SS, TM, ehand	5.6
434906	BE410573	Has.252356	Homo sapiens, clone IMAGE:4953	SS, TM, Endo_endo_phos, ENR, A	5.6
414757	U48822	Has.77752	fragile histidine triad gene	HIT	5.6
436014	AF251134	Has.283741	exosome component Rps46	RNase_PH, RNase_PH_C, SS, TG	5.6
421696	AF035306	Has.106890	Homo sapiens clone 23771 mRNA	SS	5.6
408015	AW136771	Has.244349	epidermal differentiation comp	SS	5.6
445571	A070291	Has.145502	ESTs, Highly similar to FOR4 M	SS, TM, ehand, ehand	5.6
411813	NM_014931	Has.72172	KIAA1115 protein	SS, TM, Y_phosphatase	5.6
425098	AW285348	Has.8038	ESTs	SS, TM	5.6
428720	W53691		glt:ES101239 Subtracted Hippoca	SS, TM, Junc, pycnogene, PLAT, a	5.6
433986	AW035512	Has.232770	archidonate lipoygenase 3	SS, TM, Na_sulph, symp	5.6
449225	R39108	Has.6777	ESTs	SS	5.6
423233	BE048021	Has.11057	ESTs, Highly similar to T4C95	SS, TM, ehand, ehand	5.6
432536	BE258332	Has.278362	male-enhanced antigen	SS, TM, AAA, Ribosomal_L2	5.6
402155	BE614290		myosin 10	SS, SS, TM, H1, H1, TM, zt-CCCH	5.5
402544			Target Exon	SS	5.5
436041	AB03516	Has.272891	hippocad-like protein 4	SS, ehand, TGF-beta, TGFb_p	5.5
422013	N92896	Has.293354	ESTs	SS, TM	5.5
442451	AA08006	Has.129616	ESTs	SS	5.5
427898	AA168058	Has.98170	ESTs	SS, TM, DUF60, lysin, CUB, a	5.5
405640	BE397032	Has.14468	hypothetical protein MGC14226	SS, TM	5.5
427747	AW411425	Has.180555	serine/threonine kinase t2	SS, TM, SS, TM, synspirov	5.4
441466	AA089811	Has.127785	ESTs	SS	5.4
421630	NM_002204	Has.265829	integrin, alpha 3 (antigen CD4	integrin_A, FG-FAP, Rhad, g	5.4
415976	R43144	Has.21919	ESTs	TM	5.4
447374	AF263462	Has.18376	KIAA1319 protein	SS, Myosin, h1, M	5.4
431275	T56871	Has.100411	ESTs	SS, H1H	5.4
4454343			CYC215111g150530229g15044308	SS, ADC, Iran	5.4
431461	BE299871	Has.256310	likely ortholog of mouse ZP2 ZP	SS	5.4
421779	AB79169	Has.108219	wingless-type MMTV integration	SS, wnt, SS	5.4
418678	NM_001327	Has.167379	cancer/testis antigen (NY-ESO-	SS, TM, Cst2	5.4
457310	W25363	Has.239752	nuclear receptor subfamily 2,	SS	5.3
417193	AB22168	Has.285390	hypothetical protein FLJ22795	SS	5.3
432545	XS2406	Has.3041	tracheal-DNA glycosylase 2	SS	5.3
456673	AZ79811		Homo sapiens, clone IMAGE:3563	SS, cys1n, SS, cyclin	5.3
409164	AA700639		glt:ag0002r.1 Stratiagene HNT a	SS, TM, Hist, H1, H1, signal, tubu	5.3
442296	NM_007275	Has.8106	ling cancer candidate	SS, TM, Glycose, hydric, 56, Glyc	5.3
438670	AZ78803	Has.123428	ESTs	SS	5.3

WO 02/102235

PCT/US02/19297

400257		ENSP0000000452:BAD protein (B	
449514	AW570440	He.23642	
427336	NM_005658	He.2134	
414551	AB15639	He.76394	
447960	AA954377	He.26412	
430605	AJ245433	He.247323	
456849	AA522354	He.153177	
430513	AJ012008	He.241586	
424437	BE244700	He.147490	
427815	BE072019	He.12851	
417903	NM_002342	He.11116	
420476	AW575863	He.136232	
400605	BE251944		
436325	AL390088	He.7393	
444439	AA458883	He.143545	
412915	AW057727	He.74523	
415891	NM_002419	He.89449	
430323	U40714	He.235307	
432396	AW295956	He.11900	
457643	AW138211	He.128748	
422922	NL004658	He.193212	
426225	BE250337	He.198273	
412104	AW205197	He.240951	
449750	H26886	He.32326	
427225	AG557596	He.131035	
432000	AG202156	He.241181	
421658	794048	He.301760	
426928	AF037062	He.172914	
426924	AJ015405	He.95859	
455976	AB558996	He.195347	
402632			
413762	AW411479	He.648	
418451	A907117	He.90535	
455165	R65162	He.7175	
422366	W21872	He.7007	
413963	BE346834	He.278194	
447596	A789966	He.199630	
425858	AA364923		
440511	AF132849	He.7236	
452651	AAW44943	He.257152	
412890	AW955852	He.74598	
449903	NM_014835	He.155519	
402654			
449590	AW245890	He.21753	
431515	NM_012152	He.258583	
427204	AA405404	He.215725	
425169	AW292500	He.126514	
412840	BE250701	He.819	
440539	A1142076	He.135652	
443814	BE281240	He.9857	
434243	AA626082	He.200358	
435605	AF151515	He.4973	
417116	Z43916	He.7634	
403055			
420856	BE513294	He.20739	
402584			
405334			
419493	AF001212	He.90744	
413764	BE162704		
409189	F00991	He.50689	
449933	AL137859	He.297214	
409139	A1681917	He.3321	
459672	AK002016	He.114727	
420842	A083958	He.50601	
421009	NM_013375	He.109528	
419857	AJ077005	He.52208	
434396	AJ006973	He.9482	
400933			
458143	H11097	He.61960	
427527	A1909557	He.153261	
414265	BE410411	He.75984	
433933	A1754389		
452302	AF173867	He.28906	
409936	AW974648		
409846			
425976	C75094	He.334514	
452969	W92792	He.77575	
413163	Y00815	He.75216	
434962	AJ021574	He.4261	
418572	A1751740	He.86172	
440889	NM_014297	He.7496	
453446	BE269996		
412159	U726598	He.9271	
435999	AW276511		

SS,hormone_rec,zf-C4	5.3
SS,PX,art,lipocalin,PHD2	5.3
MATH,SS,MATH,AGM,NA2MANT	5.3
EQ,lipocalin,UT,SS,TM	5.3
SS,TM,CN,N,CN,N,CN,N3	5.3
SS,TM,G-patch,ubiquitin,a	5.3
SS,TM	5.2
SS,TM,GST_C,ubiquitinase	5.2
CUT,homeobox,helix-lactama	5.2
SS,TM,7m_1	5.2
TNFR,c5,SS	5.2
SS,ILH	5.2
SS,TM	5.2
SS,Synapsin,C,SS	5.2
SS,TM,PAF-AH,II	5.2
	5.2
SH3,kinase,prolineact_deC	5.2
DUF101,SS,IRNA-synth,1b,IR	5.2
SS	5.2
	5.2
C2,PH,RasGAP,ETK,SS,C2,PH	5.1
WD40	5.1
SS,TM	5.1
SS,ras	5.1
SS,SS,TM,PX,PH,PLD,c,ames	5.1
PH,SS,TM	5.1
ehand	5.1
adh_short,SS,adh_short,TG	5.1
SS,TM,lectin_c	5.1
EST	5.1
Fz,fringile,jg	5.1
FHEP,TPR,SS	5.1
Sec1,SS,TM	5.1
SS	5.1
	5.0
SS,TM	5.0
SS,TM,Peptidease_M10,ln2,H	5.0
SS,TM,MAGE,Albomom,S17	5.0
	5.0
homeobox,SS,ehand,heaxol	5.0
Oxytelor,EP,SS	5.0
laminin,Albomom,He	5.0
WD40,SS,TM,KOV,H,H	5.0
7m_1	5.0
SS,SS	5.0
SS	5.0
homeobox,SS,homeobox/home	5.0
SS	5.0
SS,TM	5.0
SS,TM,SS,TM,ABC_tran,ABC,	5.0
SS,TM,Ramant,UF,Isa	5.0
	5.0
katal,SS,TM,jg,kinase	4.9
E1,E2,ATPase,Hydroxase,SS	4.9
SS,TM,MIP	4.9
Target Exon	4.9
PC1,SS,CDK5,activator	4.9
SS	4.9
	4.9
SS,TM,ank,EGF,switch,MATH,	4.9
SS,homeobox	4.9
SS,PK,PK_C,myosin_head,Rh	4.9
SS	4.9
	4.9
disintegrin,Reprolysin,Pe	4.9
VIIS,GAT,TM,Heme_oxigenase	4.9
ICE_p20,ICE_p10,CARD,SS	4.9
SS,kinase	4.9
SS,TM,jg	4.9
	4.9
SS,TM,SS,TM,SH2_Y_phospho	4.9
SAND,SS	4.9
SS,Adap_pomp,sub,CYF	4.9
Wt_momt,a,ln3,ln4_mce	4.9
SS,TM,kinase,SH2,SH3,BNR	4.8
	4.8
fn3,jg_Y_phosphase,SS,T	4.8
homeobox	4.8
lactamase_B,SS,XRC1,N_BR	4.8
	4.8
h2IP	4.8
	4.8

WO 02/102235

PCT/US02/19297

418910	Z25821	Hs.89466	Homo sapiens, Similar to dodo:
437300	AL040594	Hs.25063	PROG461 protein
426615	AA408678	Hs.6473	glzn0401.1 Scores_1000_NH
421453	AA234652	Hs.104555	neuropeptide FF-analog peptide
408616	AA076248	Hs.147562	glzn010c1.1 Stratagene pancr
444744	BE384732	Hs.147562	ESTs
412575	AA113177	Hs.20673	glzn020c5.1 Stratagene pancr
425542	AF038660	Hs.20673	UG-Catals-GH44 beta 14-9
435995	BE260415	Hs.348198	hypothetical protein FLJ20522
451555	AK001171	Hs.326422	hypothetical protein MGC4549
456153	AW972270	Hs.144054	ESTs
455340	AW801435	Hs.7004	glzn0401.12-270300-031-310 N
457260	AW212279	Hs.7004	ESTs, Moderately similar to AL
432311	BE083000	Hs.274323	similar to sialyltransferase 7
409555	NM_005133	Hs.288626	RCE1, prenyl protein protease
424919	BE314461	Hs.153768	U3 snRNP-associated SS-40a pr
416528	Hs.6052	Hs.337921	ESTs
415137	AA634034	Hs.72451	Homo sapiens PAC clone RP5-108
417334	AA337572	Hs.157240	hypothetical protein MGC4737
451920	AA224483	Hs.27239	DKFZP680G524 protein
413549	NM_002151	Hs.823	heparin (heparan)sulfate protease
458988	AW110431	Hs.283670	CGA-119 protein
408994	M21305	Hs.283670	FGFENs predicted novel secrete
451595	AW965089	Hs.20996	ESTs
449728	AA927671	Hs.107635	ESTs
453245	T59601	Hs.339761	ESTs
432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZ4
430037	BE409640	Hs.227789	mitogen-activated protein kinase
442796	AA902546	Hs.31844	hypothetical protein FLJ12586
425251	Z22521	Hs.155342	protein kinase G, delta
415014	AW654094	Hs.24651	ESTs
440088	BE558977	Hs.183222	hypothetical protein FLJ22638
418837	U48263	Hs.89040	preproenkephalin
412239	AW583350	Hs.61273	hypothetical protein MGC2650
445975	BE246446	Hs.15595	ubiquitin-activating enzyme E1
453968	AA947843	Hs.62711	High mobility group (nonhistone
446241	AW811064	Hs.62711	gbM22-STC11-211099-008-c06 S
441455	AJ271671	Hs.7854	zinc finger regulated transport
450549	AJ877594	Hs.423	time-related tyrosine kinase 3
429210	AA222065	Hs.198269	Target CAT
425437	AK000482	Hs.181730	hypothetical protein FLJ20241
408813	AL039971	Hs.251216	Target Exon
431239	AL004832	Hs.5038	hypothetical protein DKFZp434A
435057	AL048891	Hs.12185	neurotrophin target esterase
451933	AL048891	Hs.12185	hypothetical protein MGC14333
424619	BE387282	Hs.207443	hypothetical protein MGC01048
432968	BE814192	Hs.273969	melanoma-associated antigen re
425159	BE289339	Hs.152695	mitochondrial ribosomal prot
414084	AW168771	Hs.71574	hypothetical protein FLJ14528
424964	AW161271	Hs.153961	ARF1 (actin-related protein 1,
431410	AW299534	Hs.105739	ESTs
435988	AW151481	Hs.111577	integral membrane protein 3
432351	AJ270313	Hs.127762	hypothetical protein MGC12982
428120	AA325243	Hs.198897	copine 1
416877	BE386285	Hs.85658	hypothetical protein FLJ23435
426970	AK061500	Hs.165188	hypothetical protein FLJ13852
434948	BE276334	Hs.32148	AD-015 protein
458715	AK060573	Hs.16725	hypothetical protein FLJ10111
439551	AA700946	Hs.16725	ESTs
426538	BE270918	Hs.164028	Homo sapiens, clone IMAGE3534
444416	AW288205	Hs.11156	hypothetical protein
426331	BE228216	Hs.172673	S-adenosylhomocysteine hydrola
444596	BE590682	Hs.11417	Rab acceptor 1 (prenylated)
439685	AW956781	Hs.253937	ESTs, Weakly similar to FXD2_H
447402	HS4520	Hs.18480	hypothetical protein FLJ20452
450184	AW1096	Hs.237937	Homo sapiens, clone IMAGE3447
426068	AF029776	Hs.166154	jagged 2
458255	AA53244	Hs.239500	hypothetical protein MGC13114
403182	BE314877	Hs.24553	Target Exon
432076	BE543070	Hs.24553	hypothetical protein FLJ12541
459167	BE543070	Hs.24553	ESTs, Weakly similar to CAT13_H
452747	BE153855	Hs.61460	lg superfamily receptor or LMR
444633	AF111713	Hs.286218	junction adhesion molecule 1
434171	BE247688	Hs.347549	KIA02846 protein
427155	AW049152	Hs.347549	crinoid (crin) mating type in
432622	AI671225	Hs.284171	KIA1535 protein
425959	AF078037	Hs.324051	RelA-associated inhibitor
452900	AW373011	Hs.54558	hypothetical protein FLJ22222
437563	AJ217284	Hs.144958	ESTs
432234	AA531126	Hs.115903	ESTs
433135	AA443873	Hs.110477	dolichyl-phosphate mannosyltra
447495	AW401804	Hs.18720	programmed cell death 8 (apopt
452857	BE672814	Hs.256519	ESTs, Moderately similar to SS
427834	AA656101	Hs.258513	hypothetical protein FLJ11887

WO 02/102235

PCT/US02/19297

	418963	BE304571	Hs.59529	aldo keto reductase family 1,	aldo_ket_red	4.0	
	437340	AL353935	Hs.135917	hypothetical protein DKFZp761D	TBC22P1,MD40,VD40	4.0	
	455928	BE170313		SS	gCvA,HT0535-040500-193-g02 H	4.0	
	400507			Target Exon	SSJhomobox	4.0	
5	424826	AF207089	Hs.153357	procollagen-trypsin, 2-omega1	2OG-Foll_Oxy_Glycos_kinas	4.0	
	438143	BE500981	Hs.269552	ESTs	SURF1,SS,TM,SURF1,SURF4	4.0	
	431713	Z15093	Hs.3196	orf61		4.0	
	412550	RG2452	Hs.26370	glycylglycyl7,1 Scores infant hr		4.0	
10	TABLE 23B:						
	Pkey: Unique Ecol probed identifier number						
	CAT number: Gene cluster number						
	Accession: Genbank accession numbers						
15	Pkey	CAT Number	Accession				
	408215	10476_1	BE154230 AA3307674 H135629 AA338536 AA190603 AA761006 A1800061 A1813258 AW276647 BE221253 A1348910 A1965301 A1020078 A1359617 AA655391 A10510210 AA446461 A1355345 A1349638 A1343640 A275061 M78746 AA262795 AW250002 A033758 A1934519 AW272086 N26520 AA626639				
	408294	1050553_1	BE141732 U15823 A141331 AV1178416 AW1178430 BE141343 BE141296 BE141702 BE141265				
	409114	110365_1	AA634021 AA126205 AA0457771 AA102169 AA035530 AA022163 AA115915 AA085147 A1128905 AA063336 AA079206				
	409164	114348_1	AA108529 AA1547107 ALD32020 AA081598				
	409938	116091_1	AW974548 AA652153 AA649671 AA075582				
	409960	116270_1	BE261344 AA715641 AA318134 A134972 AA1319849 YV04622 A12191655 AYW87892 A130778 BE314003 A1903248 AYW96008 AA385346 AA205977 C20243 AA133057 AA070870 AA377385 AA1316795 A18191560 BE003050 A19370280 A19370244 T69530 AA719292 A1857692 AA62639 A1059520				
	410445	120374_2	AA198630 A143885 AYW61629 A232482				
	411219	1236055_1	AW832917 AYW532913 AYW832905 AYW832788 AYW832915 AYW832776				
	411674	125374_1	AW861123 AYW861125 AYW86117 AYW861116 AYW862706 AYW865798 AYW866774 AYW865787 AYW865787 AYW865782 AYW865789 AYW865772				
30							
	412091	1276564_1	R0165818 AYW601892 AYW601892 AYW601892				
	412173	1280570_1	T107107 AYW62279 AYW68906				
	412576	130769_1	AA111577 AYW694515 AA1113947				
	413534	1357587_1	BE145961 BE145780 BE146758 BE146057 BE146774 BE146963 BE146907				
	413564	1367722_1	BE260120 BE140535				
	413764	1387163_1	BE162704 BE162705 BE162732 BE162702 BE162694				
	413837	139563_1	A19616355 AYW163255 AYW163535 A1925959 BE73979 A132920 AYW517329 AA584408 AYW157522 A892196 AYW303514 T24436 A175658 AYW1458107 A191045 A1925582 A865824 A192604 A1940953 A1943963 AYW29522 AYW64650 AYW20613 A113529 A340691 A9128336 A1912439 A19530619 A2729				
	414143_1	1434696_1	BE294477 BE294759				
	415128	1523606_1	A45625 C50146 C50146 D063536				
	417920	182028_1	BE7719221 BE771921 A1424233 A4471354 BE171081 A2453462 A4470113 A824337 Z14470 AYW504757 N15568 A104700 A2578548 AYT414130 AA0309197 AWT80349 AYW664465 AYW647553 AYW51643 AA469643 AYW474826 A447156 A1926817 AYW53659 AYW62245 AYW62241 A804095 AYW41945 AYW429153 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949				
45	422155	21235_1	AW991452 AYW476153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 AYW429153 BE29859 AYW192077 AFW87714 R05553 AFW83107 A190214 N1,012527 BE259447 BE253088 AAW39771 H05949 AYW41945 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453446 067533_1 BE290995 BE297115 BE270415 BE206214 BE206526
454682 122876_1 AW615023 AW815322 AW815158 AW813333 AW816156 AW813302 AW813344 AW813172
455335 1240762_1 AW651734 AW651676 AW651603 AW651713 AW651722 AW651616 AW651731 AW651618 AW651648 AW652215
5 455340 1263504_1 AW601435 BE094527
455557 1325974_1 AW656835 AW659507
455600 1336777_1 BE061653 BE060850 BE060657 BE060168
455655 1330305_1 BE153524 BE153676 BE153853
455628 1303899_1 BE170313 BE158336 BE158280
10 456573 201205_1 A270811 A301071 A214696 A275613 AA588460 AA287255 BE171665
457268 310453_1 AW272270 AA461542 AA460615
457378 144890_1 AW776538 BE435540
457186 503710_1 AW62409 AA007424 A2729523 A2002762 N33163 BE045678 AB683332 AW173559 A3002326 220793 Q25504 BE326283
458167 52063_1 BE504370 A2743453 AB00556 A2002876 A1702163 A300626 AW072219 A3069402 A1349557 AW179361 W78140 AAC65893 AAB74152 A304380
15 A303098 AW054657 AB070008 AW207658 AW665508 AW300595 A1152992 A5628019 A274063 AA506522 N52547 AW054727 AW205667
AW136707 AW13761
A045934 AL039332 H55631

TABLE 23C:

Play: Unique number corresponding to an Eos proboscis

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al. (1999) Nature 402:485-495

Strand: Indicates DNA strand from which exons were predicted

NL_position: Indicates nucleotide positions of predicted exons

Play	Ref	Strand	NL_position
400460	6389428	Plus	35559-36295
400607	9857656	Plus	3112-4159
400333	8705148	Minus	187599-188138
400945	5108605	Plus	34426-34612
400923	7537836	Minus	94518-94659
400933	7651935	Minus	106330-105503
401210	7712287	Plus	166656-167133, 165760-166877, 171563-171733
401254	9797154	Plus	135810-135927, 133367-133504
401278	9795536	Plus	98428-98573
401609	7705041	Minus	5877-11597
401674	7686903	Plus	138766-138927, 139157-139298, 139440-139599, 139960-140159
401724	7656694	Plus	150063-150241
402197	6576115	Plus	195456-195565
402365	5454515	Minus	70528-71165
402353	9529588	Plus	15813-20084, 20163-20263
402400	9945145	Minus	60123-60322
402632	9531299	Plus	101168-101419
402884	9225562	Plus	47580-49191
402516	7406502	Minus	351474, 541-657
403055	8748904	Minus	105532-110225
403128	7331426	Plus	122884-123018, 123134-123283, 123372-123695, 123779-123940, 124095-124256
403182	9638273	Plus	102169-102546, 102545-102726
403938	7711705	Plus	48636-48822
403945	7711988	Minus	32141-32263
404036	6567700	Minus	65247-67525, 112537-114003
404333	5862821	Minus	137548-138024, 138111-138300
404343	9638093	Plus	122864-122931
404344	5838093	Plus	127865-128384
404365	5964577	Plus	50151-60315, 50899-51098
404651	9797073	Plus	33374-33675, 33769-34008
404757	7706327	Plus	100593-101033, 101590-101782
404827	4165210	Minus	124246-124422
405334	3135285	Plus	139386-135856
405346	2581263	Plus	101882-102171
405384	2381075	Minus	43259-49451, 45136-46252
405371	2078469	Minus	47657-47785, 48461-48608
405554	6960486	Plus	161628-161734, 162823-163014, 164439-164652
405928	7717155	Minus	2923-3209
406230	4768468	Plus	71716-72515
406244	7417725	Plus	39472-39595
406301	8575666	Plus	57251-57494
406487	7711306	Plus	82039-82902
406495	7711326	Plus	174661-174978
406613	2957166	Plus	9029-5147

Table 24A lists about 117 genes down-regulated in ovarian cancer compared to non-malignant adult ovaries. These were selected as for Table 23A, except that the numerator was set to the 75th percentile amongst various non-malignant ovary specimens, the denominator was set to the 96th percentile value amongst various ovarian cancers, the numerator was greater than or equal to 75 units, and the ratio was greater than or equal to 2.0 (i.e., 2-fold downregulation in tumor vs. normal ovaries).

TABLE 24A:

Play: Unique Eos proboscis identifier number

Ex_Acct: Exon/Accession number, Genbank accession number

UG_ID: UniGene number

Title: UniGene gene title

Protein Dom.: Predicted protein domain

RI: Ratio of normal ovaries to tumor

WO 02/102235

PCT/US02/19297

	Pkey	Ex. Acc#	UG ID	Title	Protein Dom.	R1
	428232	BE272452	Hs.183109	monocamine oxidase A	Amino_oxidase,gyr_redox,F	16.9
	433593	AT732637	Hs.277501	ESTs	SS	10.8
5	444631	AV652066		general transcription factor I	SS,Glycican	8.7
	451573	AW130351		ESTs	SS	8.3
	426570	BE242256	Hs.2441	KIAA0022 gene product	heixin_c,SS,TM	7.5
	453510	AG59482	Hs.42151	ESTs	SS	7.9
10	410255	AA741357		aldogen (enactin)	SS,EGF,ldl_recept,lyl,lyro	6.9
	438549	BE389801	Hs.21858	trifluoride repeat contain	SS,serpin,SS,WD40,FYVE	6.5
	407999	AA048217	Hs.105370	ESTs	SS,Pop_MIT2L,propep,Reprol	6.2
	414541	BE253116	Hs.76362	aldehyde dehydrogenase 1 family	aldohd	6.0
	449438	BE6113051	Hs.24554	Homo sapiens cDNA FLJ11540 fs		5.7
	441422	RA3777	Hs.21364	ESTs	SS,TM	5.1
15	413351	AZ223328	Hs.75335	glycine amidinotransferase (L	Amidinotransf	3.9
	429022	Z56986	Hs.27865	ESTs	SS	3.6
	423044	AA320829	Hs.57266	prolactinrhin 18		3.6
	416030	AA376580	Hs.75595	alcohol dehydrogenase 5 (class	adh_zinc,HCV_NS4a,TM,adh_	3.5
	428554	AA437061	Hs.14060	prokinectin 1 precursor	SS	3.4
	436772	AW575588		metallothionein 1E (functional	SS,TM,TM_2HRM	3.2
20	415162	AF035718	Hs.79051	transferrin factor 21	HEH	3.1
	427794	AA705186	Hs.59070	ESTs	SS	3.1
	433072	AJ528037	Hs.158632	ESTs	SS	3.1
	418318	UA7732	Hs.84072	transmembrane 4 superfamily me	transmembrane4	2.9
25	410059	NM_007038	Hs.58324	a disintegrin-like and metallo	Reprolysin,1_Pap_MIT2	2.9
	431533	AT18797	Hs.132954	ESTs	SS,TM	2.8
	420303	AA258282	Hs.278435	KIAA1474 protein		2.8
	438780	M64936		gluHomo sapiens retinoic acid		2.8
	427881	AA410292	Hs.104761	ESTs	SS,wtl	2.8
30	437342	AW563267	Hs.235438	hypothetical protein DKFZP781K	Sec7/PH	2.8
	453826	AW570890	Hs.253821	ESTs	SS,Pop_MIT2L,propep,Reprol	2.7
	418444	AJ602869	Hs.85155	butyrate response factor 1 (EG	z-COOH,SS	2.7
	453787	AB011782	Hs.35094	extracellular matrix protein 2	wvc,LRR,SS,LRR	2.7
	413624	BE177016	Hs.75445	SPARC-like 1 (matril, herve)	kazal,SS,kazal	2.7
	413305	Hs_200428	Hs.325511	Homo sapiens cDNA: FLJ21175 #	laminin_5,laminin_EGFJam	2.7
35	414504	AW059181	Hs.115175	sterile-alpha motif and leucine	SS,plkasin,SNM	2.7
	435857	NM_015310	Hs.6783	KIAA0942 protein	Sec7/PH	2.7
	421635	NM_012082	Hs.106300	Foetad of GATA2	SS	2.7
	442496	US4617	Hs.8354	Homo sapiens pyruvate dehydrog	HATPase_c,HATPase_c	2.6
40	410404	AJ58454	Hs.84015	protein S (alpha)	EGF,laminin_5,gli	2.6
	452958	AA883525	Hs.40527	ESTs	SS	2.6
	449648	AW205807	Hs.253469	ESTs	SS	2.5
	435519	AJ218950	Hs.125461	hypothetical protein FLJ11536	SS	2.5
	433650	AJ373949	Hs.275610	hypothetical protein FLJ10463	SS	2.5
45	424319	AW561025	Hs.95752	ESTs, Weakly similar to ALU8_H		2.5
	420174	AI824144	Hs.109740	ESTs		2.5
	421709	AA159394	Hs.107056	CED-6 protein	PID,Herpes_UL5	2.4
	417822	AW259163	Hs.82318	WAS protein family, member 3	WH2	2.4
	453555	AW058427	Hs.342874	transforming growth factor, be	SS,TM,zona_policuda	2.4
	405468	AJ959712		phosphatidylinositol transfer	SS,PX,PH,PLDc,PH,PLDc,PX	2.4
50	400829			C11000244:gt11056030pepMP_0	SS,TM,SS,TFHD_3,WD	2.3
	453125	AW779544	Hs.115457	hypothetical protein FLJ22055	ras	2.3
	437862	AW578107	Hs.5884	Homo sapiens mRNA: cDNA DKFZp5	HLH	2.3
	425482	AA911852	Hs.46783	Homo sapiens cDNA: FLJ2282 #		2.3
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	Acyl-CoA_dh	2.3
55	403247			Tergel Exon		2.3
	441916	AA935571		ESTs		2.3
	422746	NM_004484	Hs.119551	glypican 3	Glypican,SS	2.3
	416777	AF146760	Hs.78844	DKFZP564M1415 protein	SS,GTP_CDCSS	2.3
60	409403	AA685024	Hs.6634	Homo sapiens cDNA: FLJ22547 #	SS,TM	2.3
	416956	AA234531		KIAA0785 protein	SS	2.3
	410071	AW468163	Hs.58488	catenin (cadherin-associated p	Vinculin,Stathmin	2.3
	419461	AJ452001	Hs.266656	nuclear receptor subfamily 2,	hormone_rec,cf-C4,hormone	2.3
	426319	AL023754	Hs.195068	similar to calcium/calmodulin	SS,plkasin	2.2
65	452123	AI287615	Hs.36022	ESTs	SS	2.2
	453385	R39224	Hs.267597	CHM2 gene		2.2
	416157	NM_003243	Hs.342674	transforming growth factor, be	zona_policuda,SS,TM,zona	2.2
	409637	U14966	Hs.180546	ribosomal protein L5	Ribosomal_L10p	2.2
	414466	AA345211	Hs.76205	cytochrome P450, subfamily XA	p450	2.2
70	408115	NM_016651	Hs.48950	hepatohepatic carcinoma novel	SS	2.2
	428329	AJ654145	Hs.375628	programmed cell death 4	MA3LRR	2.2
	450572	AJ054347	Hs.2017	ribosomal protein L38	SS,TM	2.2
	405546	AB020015	Hs.54886	phospholipase C, epsilon 2	C2,PH,PLC-Y,PLC-X	2.2
	410209	AJ583951	Hs.65548	hypothetical protein PR01635	SS,TM,Fork_head	2.2
	445900	AW655345	Hs.125265	ESTs	SS	2.2
75	447806	WQ3616	Hs.10432	ESTs, Weakly similar to I36022		2.1
	441712	AW351627	Hs.75948	KIAA1288 protein		2.1
	450525	AJ768885	Hs.295727	ESTs, Weakly similar to ALU8_H	SS,BAG,UPF0001	2.1
	444181	NS2545	Hs.142940	ESTs	SS	2.1
	427195	BE271718	Hs.173602	KIAA0603 gene product	SS,TM,TBC	2.1
80	436955	AJ160015	Hs.125489	ESTs	SS,TM,RasGEF,actin,RasGEF	2.1
	408443	N336337	Hs.10336	ESTs	SS	2.1
	448274	AJ289307	Hs.67317	Homo sapiens cDNA FLJ11775 fs		2.1
	426354	NM_000490	Hs.163490	disintegrin [muscular dystrophy	ZZ,CH,WW,spectrin,bZIP,SS	2.1
	443506	AA343631	Hs.7513	ESTs		2.1

WO 02/102235

PCT/US02/19297

444815	AA151539	Hs.1227	amino-terminal, delta, deleted	SS,ALAD	2.1
426728	AA757718	Hs.93561	hypothetical protein FLJ10512	SS,TM,Soma.PSLip	2.1
434245			HLA-D27101*	Heterogen, C,Ab3,SS	2.1
436420	AA434366	Hs.31595	ESTs	SS,TM,MPF22, Claudin,SS,TM	2.1
410096	AL117664	Hs.58419	DKFZ562042 protein		2.0
414476	AA301687	Hs.76224	EGF-containing fibulin-like α	EGF,TLLSS	2.0
424137	AA335765	Hs.10562	ESTs	ESTs	2.0
467959	AA017472	Hs.107265	hypothetical protein DKFZ559H	SS	2.0
444862	A1261556	Hs.143929	ESTs	SS,TM	2.0
426066	T94607	Hs.185572	ESTs	PH,Chaperonin	2.0
435680	A1684710	Hs.201645	ESTs	SS,ATP-synth_C	2.0
424651	A485206		ESTs	SS	2.0
432939	AL038924	Hs.276849	KIAA0436 gene product	α-C3HC4myosin_head,DIL	2.0
449088	A1654048	Hs.196556	ESTs	SS,MACPF,sushi,IL1_recept	2.0
428442	NM_014699	Hs.10432	KIAA0876 protein	BTB,trans	2.0
415577	L3651	Hs.81296	integrin, alpha II	TIMintegrin_A,FG-GAP	2.0
450435	A1685975	Hs.201805	ESTs	laminin_3,laminin_EGF,lag	2.0
450666	A1654223	Hs.16026	hypothetical protein FLJ23151	SS	2.0
421295	BE326214	Hs.93613	ESTs	TM	2.0
432467	T03667	Hs.233898	Human DNA sequence from clone	SS	2.0
406554	BE016682	Hs.46721	UCC1 protein	SS,Ependymin,SS	2.0
412611	AA732036	Hs.164478	hypothetical protein FLJ21939		2.0
453355	AW265374	Hs.31412	myopodin	SS,TM,Caveolin,Caveolin	2.0
424666	AW558576	Hs.130651	catenin 2	SS,TM,MP,M	2.0
458147	AW752597		gbcL3_C70214-161299-045-606 C		2.0
447566	N50432	Hs.102648	ESTs	ESTs	2.0
414496	W73853		ESTs	SS,TM,kinase_F5_F8_type_	2.0
425618	AW119112	Hs.9052	Human sapiens cDNA: FLJ22042 fl	SS,TM	2.0
415186	NM_020162	Hs.78658	carboxypeptidase Z	Zn_carboxypeptidase_Z	2.0
422157	AW572295	Hs.112318	6.2 kb protein	SH	2.0
450253	AL133047	Hs.24715	Human sapiens mRNA: cDNA DKFZp4	SH9	2.0
418919	AA232635		ESTs	SS,OUF2	2.0
444846	A871055	Hs.148477	ESTs	SS,TM	2.0
418781	T41190	Hs.8404	ESTs		2.0

TABLE 24B:

Key: Unique Eos probe/identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

40	406488	100303_1	A1509712 AL039257 BE000369 AA376876 N75269 AA345359 AA349053 AW960062 R76169 R70638 AA64770 A137687 A138002 A782396 N47613 AG052495 AA74112 AW494680 AA68865 R79114 AW242826 N58955 AA050313 A1379461 A1607102 AA417043 A165444 A16535286 AW267099	
45	410295	11902_2	AA741357 A167000 W75967 H50728 AV568709 AA988187 AL037804 W67847 BE016553 AW033258 N78610 N31548 A1032084 N38278 AW075272 A1032081 R35753 W93372 AA700790 A1030987 N62965 R62468 AW580252 AL036760 A1052219 R39521 W0704 AA088621 A1249109 W68776 W93274 A416	
50	414498	145292_1	W73853 AA928112 W77887 AW889237 AA148524 A1749182 A1754442 AC338392 A1253102 A1079403 A1870541 A169341 H197536 AW188022 A1827669 W72718 A1051402 A1188071 A1335900 N21488 AW770478 W92522 A1691028 A913512 A1144448 W73819 AA604358 N28900 W95221 A1868132 H98	
55	418919	180423_1	AA232635 A1073703 AA233330	
55	418956	180692_1	AA224831 A1070002 A1060216 AA779957 R43415 AA402777 AA666394 AA30616 AA779469 A1672390 A105981 A1094453 AA826397 AA355994 A1668257 A1602456 A1987751 AA232893 A1346880 A1356232 AA235138 F31396 AW079597 H16405	
55	424651	241861_1	A1453208 AA732315 AA344619 AA904035 AW952967 AA488889 AA635644 BE245127 AA689978 AA761574 H28767 AA910061 A4837086 AA765495 W76175 A1515225 AA740692 AA743152 A178562 H88963	
55	436772	426564_1	AW75568 AA31053 N67094	
55	438790	46901_1	H64396 AKC25512 A1323967 BE061777 AA089966 BE169930 T41175 AW594524 BE590415 AA121893 A1269283 T40311 A1684569 AA257011 A1075277 A1241318 BE327710 AW576215 AW90269 AA884990 BE327514	
60	441916	526799_1	AA936371 AA971518 A157262	
60	444931	82657_1	AW62066 AA419580 T55512 T55561 A151265 N49536 H87921 AW264447 AA428067 AA364094 AW556586 D62854 A15341453 AA424962 A1684615 A161693 A1871252 A1376942 A1740496 AA452836 A1277917 A11454141 AA456147 A1704595 A1030975 A1245574 A433703 A1202208 A1269965 A138	
65	451573	875688_1	AW130351 AW33698 A1030973	
65	458147	488021_1	AW752597 AW648781 AW846062 AW648493 AW752699 AW752604 AW567200	

TABLE 24C:

Key: Unique number corresponding to an Eos probe/identifier
Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" (Dunham, et al. 1999) <http://www.sanger.ac.uk>
Strand: indicates DNA strand from which exons were predicted
N_positior: indicates nucleotide positions of predicted exons

70	40347	756933	Plus	152716-152816
75	40347	756933	Minus	78626-77140
75	404245	7406725	Plus	36019-36262,37073-37613,38546-38314,40355-40651,42738-43026,43391-43696,45658-46030,51110-51415,52779-53072,54648-54935,55201-55500,55926-56240,56355-56672,57076-57401,59966-60026,62600-62926,63363-63686,66693-67025,68180-68497,68909-69232,71372-71695,720

Table 25A provides UnigeneID, UnigeneTitle, Key, and Exonmap Accession for sequences in Table 26. The information in Table 25A is linked by SEQ ID NO: to Table 26.

Table 25A:

Key: Unique Eos probe/identifier number

PCT/US02/19297

SEQ ID NO: Sequence identification number for sequences in Table 26

SEQ ID NO:
SEQ ID NO: 1-2
SEQ ID NO: 3-4
SEQ ID NO: 5-6
SEQ ID NO: 7-8
SEQ ID NO: 9-10
SEQ ID NO: 11-12
SEQ ID NO: 13-22
SEQ ID NO: 23-24
SEQ ID NO: 25-26
SEQ ID NO: 27-28
SEQ ID NO: 28-30
SEQ ID NO: 31-32
SEQ ID NO: 33-34
SEQ ID NO: 35-38
SEQ ID NO: 39-40
SEQ ID NO: 41-42
SEQ ID NO: 43-44
SEQ ID NO: 45-46
SEQ ID NO: 47-48
SEQ ID NO: 49-52
SEQ ID NO: 53-54
SEQ ID NO: 55-56
SEQ ID NO: 57-58
SEQ ID NO: 59-60
SEQ ID NO: 61-62
SEQ ID NO: 63-64
SEQ ID NO: 65-66
SEQ ID NO: 67-68
SEQ ID NO: 69-70
SEQ ID NO: 71-72
SEQ ID NO: 73-74
SEQ ID NO: 75-76
SEQ ID NO: 77-78
SEQ ID NO: 79-80
SEQ ID NO: 81
SEQ ID NO: 82-87
SEQ ID NO: 88-89
SEQ ID NO: 90-91
SEQ ID NO: 92-93
SEQ ID NO: 94-95
SEQ ID NO: 96-97
SEQ ID NO: 98-99
SEQ ID NO: 100-101
SEQ ID NO: 102-103
SEQ ID NO: 104-105
SEQ ID NO: 105-107
SEQ ID NO: 108-109
SEQ ID NO: 110-117
SEQ ID NO: 118-119
SEQ ID NO: 120-121
SEQ ID NO: 122-123
SEQ ID NO: 124-125
SEQ ID NO: 126-127
SEQ ID NO: 128-129
SEQ ID NO: 130-131
SEQ ID NO: 132-133
SEQ ID NO: 134
SEQ ID NO: 135-138
SEQ ID NO: 139-140
SEQ ID NO: 141-144
SEQ ID NO: 145-148
SEQ ID NO: 149-150
SEQ ID NO: 151-152
SEQ ID NO: 153-154
SEQ ID NO: 155-156
SEQ ID NO: 157-158
SEQ ID NO: 159-160

Key: Unique Eos probe set identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

272

WO 02/102235

PCT/US02/19297

TABLE 25C:

Phy: Unique number corresponding to an Eos protein

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1996) Nature 402:489-495

Strand: Indicates DNA strand from which exons were predicted

Nt_position: Indicates nucleotide positions of predicted exons

Phy	Ref	Strand	Nt_position
404977	3738341	Minus	43081-43229
405040	5295298	Plus	1553-1712, 1878-2140, 4252-4385, 5522-6077

Table 26

Seq ID NO: 1 DNA sequence

Nucleic Acid Accession #: NM_006115.1

Coding sequence: 236..1765

1	11	21	31	41	51
GCTTCAAGGT	ACAGCTCCCC	CGACGCCAGA	AGCCCGGCTT	GGAGCCCTTC	AGCACCGCTC
CGGACACCCC	CACCCGCTTC	CGAGCGGTGA	CCGTGTCAACA	GCAACTTTCG	GGTGTGGTGA
ACTCTCTGAG	GAAAAACCAT	TTTGATTATT	ACTCTCAGAC	GTGGCTGGCA	ACAGGTGACT
GGAGCTTGA	AATCCAGAGG	TTGGAGTCC	TGAGGCGAC	CTAGTCCCT	TGAATATGA
ACCAAGGCGT	TTGTGCGT	CCATTCAAG	CCGATACATC	AGCATGAGTG	TTTGACACAG
CCCAACGAGA	CTGTGGAGC	TGGCAGGCA	GACCTCTGT	TAAGATGAG	CCCTGGCCAT
TGCCGCCGCT	GAGTGTCTGC	CGAGGAGCT	CTTCCCGGCA	CTCTTCATGG	CAGCCTTTGA
CGGAGACAC	ACCCAGACAC	TGAGGAGTAT	TGGTGAAGC	TGGCCTCTCA	CTCTGCTCC
TTGTGGAGTG	CTGATGAGG	GAGACATCT	TGACTTGGAG	ACCTCTAAG	CTGTGCTTGA
TGACTTGTAT	GTGCTCTGT	CCAGGAGGT	TGGCCCGAG	AGGTGGAAC	TTCAAGTCTG
GGATTACGCG	AGAACTCTC	ATCAGACTT	CTGACATGA	TGCTGTGAA	ACAGGCCGAG
TTGTGATCTA	TTTCCAGAGC	CAGAGCAGC	TGAGCCCAT	ACAAAGAAC	GAAATATAGA
TGTTTGTAGC	ACAGGACATC	TGGGAGGAT	TTCTCTCTAC	CGGGCAGCA	TGATTTATCT
CCCTCAAGGA	GTTGCTGTG	ATGAATTGT	CTCTACCTC	ATTGAGAAC	TGAGGCGAAA
GAAAAATATA	CTACGCTGT	GCTGTAGAA	GCTGAAGAT	TTTGCAATG	CCATGACAGA
TATCAAGATG	ACTCTGAAA	TGTTGCGCT	GGACTCTAT	GAGATTGAG	AGTGACTTG
TACTGTGAG	GTACGACAT	TGGGAGAT	TTCTCTCTAC	CGGGCAGCA	TGATTTATCT
GGCTAGACTC	CTCTCTCTCC	ACATCCATGC	ATCTCTCTAC	ATTTCGCCG	AGAGGAGAA
CGGATATATC	GGCCGTTGA	CCCTCAAGT	CTCTCAAGT	CAATGCTCG	AGGCTCTCTA
TTGAGAGCTC	TTATTTTTC	TTAGAGGCG	CCGAGTCAG	TTGCTCAAGC	ACTGATGAGA
CCCCCTGGA	ACCTGTAAGT	CTGAGTCTG	CCGCTCTTG	GAAGCGAGT	TGATGATCT
CTCTCAAGT	CCGAGCTGA	GTCACTAAG	TGCTCTGAGT	CTAAGTGAGG	TGATGCTAG
CGATGTAGT	CCGAGGCCC	TCCAGCTCT	GCTGAGAGA	GCTCTGACC	CCCTCCAGGA
CCGCTCTT	GATGATGTGT	GGATCAAGTA	GTACGACCT	CTTGGCTCTG	TGCTCTCCCT
GGACCATGC	TCCCGACTTA	CACTCTAAG	CTTCAAGAG	ATTCTCTCT	CCGATATCC
CTGCAAGT	CTCTGACAC	ACTCATCCG	CTGACAGAT	CTCCGACAG	TGCTATATCC
TTCTCCCTTG	GAGAGTTATG	AGGACATCA	TGTTACCTCT	CACCTGGAGA	GCTTGTGCTA
TTGTCATCCG	AGGCTCAGG	AGTTGCTGT	TGAGTTGGG	CGGCCAGCA	TGTTCTGCTG
TAGTGCACAC	CCCTGTCTCT	ACTGTGGGA	CAGACCTCT	TATGCCCGG	AGGCTCATCT
GTGCTCCCT	TGACGCTTA	ACTAGCTGG	TGCGATATC	AAATGCTCA	TTGTCATAC
TTGACACTA	AGGCGAGAT	GTGATGAT	CTTGAGACA	CAAGGCGCC	ACAGTTCTAG
ACAAATGTT	AGTTGAGTG	AGAAACAT	GTTCAGTGA	GAAAAACAT	TONGACAAAT
GTTCAGTGA	GAAAAAAGG	GAAATGAG	GATAGGCGA	TTTGTAGTG	AGAGGTTAAT
GTGATCTTG	GGAAGATGA	TTTATAGA	TTAGAGAGT	ATCTCAAT	TCTAAAGGA
GATTTGCTG	TGGAGATAC	ATGATAGGT	TATCTCCCT	GTAGACTGT	GTAAAGAAC
TGTTGAAAT	AAAGGAGAC	ATGTGAGAC	AAAAAAGAA	AAAAAAGAA	

Seq ID NO: 2 Protein sequence

Protein Accession #: NP_006106.1

1	11	21	31	41	51
MERRLRGSI	QSRVISHSVN	TSPRLVELA	QGLLKLDEAL	ALAALELLR	ELLPFLPMAA
FDGHSHTLK	LVVQAPFTC	LPFLVLMKQ	HLILTFKAV	LDGLDVLQA	EVPRFRHLQ
VLDLRHNSCH	DFWTVNSNR	ASLVSPEPE	AAQVTFKRR	VDGLSTAEQ	FFIPFVFLVD
LFLKAGSDE	LFSVLIKVK	RKKVLRLLC	KKLKIFANPH	QDIKILKMW	QLDSIDELVE
CTWKLPTLIA	KFSVYLQMI	KERLLLSHI	HBSYISPEK	ESQITAQPTN	QFLSLQCAQA
LVYSLFLFR	GRIGLILNV	KVPLTSLIS	HLGLSBSVW	HLGLSBSVW	LVYSLFLFR
LTVSDFEPLQ	ALLERASNL	QSLVDFSGI	TDQLLALLP	SLHSQSILT	LSFYNSGSI
SALQSLQLIL	IGLSLTHVL	VYVPLESYD	IHDTLHLRL	AYLHARLRL	LCELGRPSMV
WLSANPFCIC	GDTFTYDFP	ILPCPFMFW			

Seq ID NO: 3 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 264..782

1	11	21	31	41	51
CCCTCTCCA	GTACACCCG	GAGCTGACT	GCTCCACGA	CAGCTGAGC	ATGAGGAAC
TGATCCGCG	ACTAATTTT	CTTAAATTT	AGACTTGAC	AGTAAGACT	TCAACTGAC
TTCTCTGAC	TGAGACTGT	TTCCATGTA	TACTCAAGT	CACGTAGCT	TCCACACCC
TCCGCTGCG	ACTACTGAG	GACGAGCTG	CTGCTAAGT	CTGCAAGCT	CTTGACCTC
AACTATTAC	CAGAGGACTC	ATCACTGCA	CAGAGTCA	GAGAGTCTG	CATGCTTAG
TGATCCGCT	GTGTGCTCT	TTCTCCGAG	AGCTCTTCT	CACGCCATC	AACTACTGTC
TGACAGAGCA	CTGCGCCAC	AGAGTGAC	AGCATAGCA	AGCGGCGAT	CTCCAGCTC
CGAGGCGAG	CTGCGCCAC	CATCACTCA	CTCTGTTCA	AGGATGAG	GAGACTGAG
CGAGAGAGA	CATCCATAT	TCTGATCCC	TTTACAGCA	TGACAGCAC	ACACCTCCAG

WO 02/102235

PCT/US02/19297

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5  ATACCTTGGG  TAGCTCTCTG  AGTTGCTCTC  CTGCTCTGCA  GGCACAGAG  GATGTGGATT  600
    ACACACAGAT  GGTCTTTTCT  GACCTCTGGG  AACTAAAMAA  TGACTCTCCC  CTGACTATG  610
    AGCAATAA  GAGATGCA  GATTATGTCA  ATCTACCTC  AGAAGACAC  AACCTCAAT  720
    TCTGTATTT  TGTCACCTCT  GCCTCTCTCG  AGCCAGCGCA  ATATGATCAA  GTGGCATGT  780
    GANTTCGAA  TATTTTAAAT  GGGTCTCAAT  TCTCTATGGA  TTCTTACATT  TAATTGTAG  840
    CGGAATGCCA  TTTTCCCCC  TTAACAGAG  CATGAGGCTC  ACAATCTAT  GGGACAGGC  900
    CAAAGCAT  TTGAGTGA  AATCTGAT  ATACACAGAG  GTCTTCAGA  CCATGACAT  960
    TCTGCTCTGT  ATCCGAJAJA  GCTGTTCGT  CTCTAAJAC  AAJACAGG  CTGGCTGGG  1020
    GGAAGAGGCC  AATGCCGCCG  CAAGAAGGT  TGAATAGTA  TGTTAGAAG  AACTTTCAG  1080
    TAPAGTATGA  GAACATATGA  GTTCATCAG  AGAGATAGTA  GTGAGTCTC  TCCCGAGGA  1140
    AATTTTAA  AGATCTGAT  CAGCTGTCT  TGTGATAT  CAGTGTAT  CAGTGTAT  1200
    TGACTTCTCT  TTGACTCTCT  TAATTATGG  CAATAACCA  CTCTTTAA  AGTTTAAAT  1260
    AATAAGCA  CCACACCA
  
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15  Seq ID NO: 4 Protein sequence
    Protein Accession #: B05 sequence
    1      11      21      31      41      51
    MLETYMEVNR  GLVIATVSLF  LQACFLTAIN  YLSRRHMR  SRILKASGL  QVTFPSFOHI  60
    HFAVYKME  TQTERDIFMS  DLVHSDST  PSLSDGSS  SPACQATED  VDTYQVPSD  120
    PGLKIDSLF  DYENIKEITD  YVNVPERIK  PSFWTFVNP  LSEPAVDQV  AM
  
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    Seq ID NO: 5 DNA sequence
    Nucleic Acid Accession #: AB051390
    Coding sequence: 34...2457
  
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25  1      11      21      31      41      51
    AGCGCCCGG  GCACAAAGTT  GGGGCGCGG  AAGATGAGGC  GTGCGCCGCG  GCGCCCTGAG  60
    CTGAGCGCGA  CTGCGGCACT  GCTGCGCCCT  GCGCTGCCCC  TGGCGCGCG  CCGTGCTTC  120
    TCGACGAGA  CCTGTGACCA  AGTGGCCTAG  TCGAGGGCT  ACTCGAGCG  TATCTCCCT  180
    GCGGACGCGA  CGCGCGCGGA  GGGTACACC  GAGTTTCAGC  TCGCGGTGGA  GGGGAGACCC  240
    GCTCTCGA  AGCGGACCA  GACTACGCG  GTACACCTT  TCTCTGCTC  TCCCTCTCT  300
    TCTGAGGAT  TCGACATTAAT  TCGCTCTGAG  GAGACAGAG  AGGTGTAT  GAGAGAGAC  360
    CATCTGGA  CCTTCAGAT  CATAGACGAA  GAGAAJACT  AGTTTATGAG  CAATTGCCCT  420
    GTTCACTGA  CTGAGACAC  TCGACGGAG  AGGACCGGGA  TCGAGCTGTT  TTGGATAGCA  480
    CCACGCGG  GAGAGGCTG  CTTGATCTG  AAGGCGGCA  TGTACAAA  ACCCATAT  540
    TATTTTCAG  ATGAGTGA  TCTGACGAG  TGTACATGT  AGACATCT  CACATTTAT  600
    GGGTGTACTG  ACMAACCAT  CTTAGACTCG  TGTGCGTGG  GAACTGCCAA  GTACAGACTC  660
    ACATTTTAT  GGAATTTGTC  CGAGAAGACA  CACCCAAAG  ATTACCTCG  TCGGCGAAC  720
    CACTGTCTG  CAGTATCGG  AGGATCCAC  TCCCAAGATT  ATTGATCTG  GGAATATGGA  780
    GATATATGA  CGAGAGGAG  CAJACAGAG  GTGAGATTG  GCTCACTCT  GAAATAGAG  840
    GAGAAATTC  GAGACAGAG  TGAATGGTC  CTGACCTCA  TCAAGGCCA  ACCGCCATG  900
    CGAGCTGGC  AGCTCTCAA  GTGAGAGCA  GCACCTCTG  TGAATTTTC  GTGGACAGA  960
    AGCGGCAAT  TATATCTCT  GTGACAGT  GTGGGCGCTA  TGTCCGACT  GAGCTATGG  1020
    TATCTGCA  AGATCTGCA  CAGACAGAA  TGTGCTGG  TCCGAGAGT  GTGGCAGAG  1080
    CTGATCTCT  GGGAGCTG  CAGCCACAC  GGGGTGACT  ATGATCTCC  CAJACACCT  1140
    ACCATTTCCC  AGGAGAAAT  CGGCGCCCT  ACCAGACTG  ACATCTCA  GATCTCTTC  1200
    TATGACCCAG  AGGTGTGCT  CATCATGAA  GTAGAGAGT  TTGTCTAGA  GAGATATGGA  1260
    CGAGAGGTG  AACATGCAA  TATTTGACT  GACAGTCTG  ATGATATGT  AGCTGACTG  1320
    GTCTCGAG  AGAAGATGA  AGATACACT  CTGAAACT  GATCTCTCT  CACTGTGCT  1380
    CCATGTCTG  CCGTCACTC  CTCCACTGT  GAGAAAGCA  AGAGGATCG  ACAGCGCAT  1440
    CTGAAAGCAC  AGCTGACCT  CAGGTTCCT  TCGCTTACA  CCGAGGACT  CAGCGCTCG  1500
    ATGAGCTCT  GTCTCATGA  CGAGAGGAG  TCGACTCTG  CAGTCTGGA  GTGATCAGC  1560
    TGTCTCTCT  GAGCATCTC  CTGCGCTG  GAGATAGT  CCGCGGAG  GTATCTGAG  1620
    CAGTCTCCG  AGGACGCTC  GTGTGTGAG  CTGCGACTG  AGGAAAGGA  GAGTGCTGAG  1680
    GTCAAGCGG  AGTCTCTCT  CAGCAGCTG  CTGATGACG  ATGGGCGGA  GTGGACAG  1740
    TGTGGGCCA  CTGCGGCTAT  GGGATGAG  GGGGCGCAG  CAGTATGAA  GATGAGGCC  1800
    CAGATGCT  CAGTGTGCA  AGGACAGCA  TCAAGGCTA  AGAGTGCAT  GATTCGAGCA  1860
    TCGCACACA  TCCATGTCT  CTCTGTCCA  TGTCTGAGT  GAGTGTACT  CAGCTGACC  1920
    TCGCGGAGG  CGATGTGAC  CGACACAGG  AGTCTCAAT  CTCTGGAGA  ACTTGAGAG  1980
    TCGATGAG  ATCTGAGCA  GTTGGAGAG  TGCATCTCT  CTGATGCC  CATTTAGT  2040
    GACTCAGG  AGTGTCTG  TGTATCAGT  CATGTGGGA  AGGCCAGT  2100
    ATTCGAAC  GATATGCA  AATGAGCT  GAGTTGAG  GTGACCTG  CCGAGACT  2160
    GTGACGAA  AAGATGCG  CATCGGAAA  TCGTTCGAA  ATCCATCAT  CCAJAGCTA  2220
    CCGTGAAGG  AGGCGCGAGA  GAGCGGGGG  AGTTGACG  TGAAGAGA  GTCTGAAGG  2280
    GAGCTCTCC  GAGTGTGAT  GATGAGGAG  AGCGAGAT  AGAGATGAT  CAGCAATG  2340
    TCGGAGTG  GATCTGGA  AGTTACAT  ACTTAAJCA  AGAGATCAA  AGCTCCGCA  2400
    TTTACAGCT  CAAAGACAG  GAGGAGATC  AGAGCATGA  ATGTTATCT  TTGTAGCAA  2460
    GGTATGACT  TCGCCAGCT  TGACTCTAG  ATTCAGAGT  CAGCAATGG  TGTATATT  2520
    GCTTUTTAA  GAGATTTAA  ATGTGTAG  CTAGTTTCA  TTTTCAAGT  GTGTGTGCG  2580
    CAGTATCT  CAGTGTGCA  CAGCATCTC  TTTCTGATC  TTTCTGAT  GTACAGCT  2640
    AGTGGGCGC  CTCACTCT  AGCCAGCTC  TTTCTGAGA  GAGTATGT  CAGCAGCTT  2700
    GCTAGAGCT  GAAACATCT  CTTCTGAGC  TTCCACTCG  CAGAGAGA  CGGAGACTT  2760
    GACCTACTCT  ACATGAGG  CGAACATGT  CTGATGAT  CATGTCTGA  GTCCAGGTT  2820
    GCGCGGCT  GAGACATCT  ACAGAGGAG  AGCGAGAT  CAGCACTCT  TCACTTGG  2880
    CCTTTCAT  GAAACATGT  TTTGCCACT  GTCTTAGT  GAGACTTAG  GTCTCTG  2940
    CAGTCTCT  AGTCACTAT  AGTCTTGG  GAGAAAGGA  CCGGTAGAC  TTGAGAGCA  3000
    AGCTTAGT  TGTGTTCT  TTTTCTTTC  CAJACAGTA  TTGTCTGAC  3060
    CCGTATAT  GTTCTGCA  GCGCATCT  CTGCGGCA  CAAATAA  TAATATAAT  3120
    TATTTAAAT  TAGCTAGCT  ACTTTTACA  CCGTAGATA  ATAAAGCT  TAGATGTAT  3180
    TTTTCTCT  CTTTGGGG  TCGAGAGAG  TATGTACAT  TCTCTGGA  AGCGAGCT  3240
    CTGACCTTT  TGTCTAAA  TCTCTATTG  AACACAGA  AGGAGAGA  AATGTGCTC  3300
    TTTAGAGC  AATTTCTCA  TTTTAAAA  TCTTCTCA  GAGCTCTGA  CTTTCAAGT  3360
    TCGAATGAG  TTTTTCGA  GAGACATCT  TTTCTGAT  AACTTTCT  TATCTGCT  3420
    85  AGAGCCCT  CAGTGTGAT  CTTCTAGCA  AATAACAT  CTGTACTTCA  AACTTATTT  3480
  
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WO 02/102235

PCT/US02/19297

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AOTCATGAA  TTTTATATOC  AGAGAGAAA  AGTTACCGAG  ACAGAAAAA  AATCTAAGG  3540
AAAGCRATAT  TATGCGATTA  AGCTGAGCAA  GCMAATTCBG  TGGAAAGTCA  AGCCTTCAG  3600
TCTYCACAC  CAGCCTCTGT  GTCTCTCCG  AACTCATGAG  GAATGECAC  AGTTTACAC  3660
TGCCCTCCCA  GCMAATTAFA  GCACACACGA  TTCCGCGAGA  CTGACCCACA  AGGAGTAGTG  3720
TAAAGGACA  TTTTCTCATG  TGGTTCATC  AGCAATTTTT  CTCTCCCAT  TTATTTGTA  3780
AAACTATGTT  TTTATCTTCT  TTTTATAGG  ACTTATTAAT  GCTTATCTCA  AAGATGTAT  3840
ATTGTGAGA  CACATCAAT  GCTCTGAAA  CACTACGAT  TGTATTAAA  CACTCTGAA  3900
TATTTCCAAA  TACACATAG  TATAGTCCG  AATATGTACT  TTTACATCA  CAGACMACT  3960
TCAATAAAA  CTCACTGTGT  CTTTCTATC  TTTAAGCTAA  GTAAGTGTTC  AGAAGTTCCT  4020
TTTTTATAT  GTCTCCACAC  TCCATCATTT  TCAATATTAAG  ATAGGCTTAT  TGTCTCCCTG  4080
TCTTGGAGC  GACCTTATAT  AGCTCTCTGA  ACTACCTCTG  GCTTATCAAT  GTTTTATAT  4140
CTTAAAGAA  GTCTCTTAT  CCAAAAAGG  CACATATATA  AGAAGACATA  GATTATATTA  4200
TTTATTACT  TGGGGGAAA  AAGTCTCTCA  GTGAGAAGA  CCAACTTTG  CAATGTGTT  4260
CTAAGCTATC  TATCTATCT  TCCGCCCATG  ATAAAGTCTT  TTAAGCTGTG  TACTCTTAAT  4320
CAGAGACAG  CCAACTCAT  GTCTACATG  GTCTATGCT  CCAATTTGG  GATCTTTTAA  4380
ATTCCTGAT  TTGAGATTT  AAACATGTT  TATAGCTTA  GAATGGTAA  GTGACTCTT  4440
GTGTGATTT  TATTTTGT  TGTCAATGG  GAATTTATA  GAAGCATCA  GTCTCTTCT  4500
TACCAAGTC  TGTTAGGTC  GTTTATAGT  CTTTTGCTA  ACAATCAT  TTGGAATAA  4560
AGATTTTTTA  CTACAAAAAT  G

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Seq ID NO: 6 Protein sequence
Protein Accession #: BAB18461
1      11      21      31      41      51
25  MLRLPAPLKL  SRTPALLALA  LPLAALAFS  DETLDDKPKS  EYCSRLIRA  QGTREGYTE  60
    FSLRVGDFD  FYKPTGYTRY  TLSAAPPST  RPTLLIALRE  NRECDKEED  AGTFQIIDEE  120
    ETQPMSCNP  AVTSCSTPRR  TRIGVFNIA  PACTGCVLLK  ASIVKRIITY  FQDSGLTKK  180
    LCEQDFTGG  VDEKELDC  AGTAREPLT  FIGHNRKTI  POUTPRHAK  HSLVIGSHS  240
    KTYLREYGG  YAEQVVGVA  ELQSPVHSE  ELPQGEDEVL  TVIYKAKPQ  AMQPLNRAA  300
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    KQECNMDEP  HTIPLCLPS  SEWSDCVTC  OKOMRTQRM  LKSLAELGDC  NEDLRQVENC  660
    MLPECTIDCE  LTENQMSSE  HKRQCKXVI  RTRMIOHEP  PDGACPEVT  CRKCRIRK  720
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Nucleic Acid Accession #: NM_022454
Coding sequence: 205..1449
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Seq ID NO: 8 Protein sequence
Protein Accession #: NP_071899
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    LQFPGGPTA  GPPLLRUNG  GVRDQGLD  APPLDPLP  TPTSPLEW  DRDFAPAL  240
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WO 02/102235

PCT/US02/19297

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Seq ID NO: 10 Protein sequence
 Protein Accession #: Q9H8V3

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 85 PVVLCNQKG EPLFSCRFPL YCTGQHLVL CFTGFRKKE LVRILVLIH NQVTRKDFN 180

WO 02/102235

PCT/US02/19297

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 HAPFLINQAE PRUCBQSVVS LLIIPFQWLP SWALLMLLA KRTADNRHFK STYLSAIGSS
 KRYVTHLHED KRNYEAKQRI FDVVVEYDCC PANLLSHRS LVQRVETISL GRPCDQRQD
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Seq ID NO: 11 DNA sequence
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	CAGGGGCGGG	GAGGACGGGG	GAGTGCGGGG	GGGCGGCGCC	CCGCCGCCAC	CGACAGCCCC	240
	CCCGGACGGC	GGGCGACGGC	CGCGCGCGCG	CGCCGCCCGC	CGCTCCCGAA	CGACGCGCCC	300
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85	FWYTGREVV	ATPAREIISA	ABHFSMIRAS	RNKSAGAFGV	APALPQQTIT	RVRYVRYVVG	240

WO 02/102235

PCT/US02/19297

10 LVUGPKGATI KRIGQQTHY IITPRSRDEDP VFEITGAPGN VERASREIST HIAVKTGKIL 300
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Nucleic Acid Accession #: Bos sequence

Coding sequence: 1..2982

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 35 TTTGTGCCCC AAGACCTGCG AAATCTTCAG GTTCTCTG GAAACCAAGC TCGTAGAAC 1380
 AGTATGCGA CAATTACTCT TCTCTCATG CTGATGAATA ATTACCAAG TCTGACATG 1440
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 40 TCAGCAATG GTCGCTCTGT CAAGACGSG AGATTGAATG AAGCACTG TACGTCTGAC 1740
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 ATGATGCTG TGAATGCTT TACATATATT GGTGTGSGC TTTCACTAAT TTTCTGTCA 1860
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 60 CACATGTTA ACAGAAAGA AGATTCTG ATGTGGAAAG GCGTATGCG TCTCAGAAG 2940
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Seq ID NO: 14 Protein sequence

Protein Accession #: Bos sequence

65 1 11 21 31 41 51
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 GTLGVLSLS ELKRSELMTK LQTSISTYFI MCATAEAGST LACTPTIKLN NTRMCAVET 180
 70 ALBVKIRRM RHCCCEVRI CESSPELEK LQCDQDPIV CLADPRRPF FSSGGLIV 240
 FRATVLSGP KATSRAPFP YSPFHNVPF PIGELPLP GRAPFASGE AIDMPFSET 300
 ISSPMPJTV SGTTPPVKAS FSPPTVSAPV NKNITSAFPV GTDIVNTSSI SDNQLVQLM 360
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 75 SPSCALAVR NFNASRITIT FVADPAPML VSELPAPEN SIGTITLPS LKNNLPARM 480
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 ILVYHQGLC ISVAVPLIFV LVSFTDMLG RARHNYLALV KPVHTIKRY LKPTICVWG 720
 80 FVTVVITLL TIRKNGIGG SVKFTWFGSP DDFVHMAA VYIIVWQV CTFLVLRSG 780
 FIVVLQLEK IEXKQLGAG NTKSICDLAS IAGLTFLGI TWGFAFFAG PWNVTMYLF 840
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Seq ID NO: 15 DNA sequence

WO 02/102235

PCT/US02/19297

Nucleic Acid Accession #: Bos sequence
Coding sequence: 1..2904

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	TTCAAGATAT	TCCTTGTCAT	CTATGTCTCT	CATGTCCTTC	TGTGTAACATC	CTCTGAGAGA
	GATACATATA	ATTCTGGCTT	GTGCACAGCA	CCGAGAGTTA	CTTTAAACCT	ACTCTGTCTA
	AGATCAACAG	AAAAACTTAA	ATCATCTATA	GTAAAAACCT	TCATGCTCTC	AGGCGTCAAA
	CCCCAGACAA	ATACTGCGAA	TTTGTCTCAT	ATTTGCAATG	ACTCGACATG	TTTTAGAGCT
10	GGAGTCATGT	TGTATATAGA	TAAGAAAGCC	ACTGTGCCCC	AGATTCACCA	TATAACAGAT
	GGACGCTTAA	CTGGAGGAGC	GTCTCTAGAT	GATTAACAG	CTCTTAATGT	TACATTCAG
	ATAAAACTGA	ATAATACAAAT	GAATCCATGT	GTCTGATATG	TCGCTTTGGA	AAGAGTAANG
	ATTGACACAA	TGGAACTACT	CTGCTGTCTC	TCGAGGATAC	CTCGCCCTTC	CTCCCCAGAA
	GAGTGTGAAA	AGCTTCAGTG	TGACCTGGAG	GATCTCATTG	TCGTGCTTCG	TGACATATCA
15	CTGTGCCCAC	CTGATGCTTC	CAACCAATATC	ACTCTAGGAG	GACTCTGAGC	CAGTGTGCT
	TCGAGCTGCC	CCAAAGTACG	CTCTTTTGCT	GAGCCCTGAG	ATTATTCACC	TGTGACCCAC
	AATGTTCCCT	CTCCATAGG	GGAGATTCAA	CCCCCTTCAC	CCGAGCCCTC	ACCTCCCATTA
	GTCTTCGCC	CTGCATATGA	CATGCCCCCA	CAGTCTGAAA	CGATCTCTTC	CCCTATGCCC
	CAAAACCATG	TCGTGGGCGC	CCGACCTCTC	GTGAAAGCTC	CATTTTCTCT	TCGCCACGTG
20	TCCTGCCCTG	CGAATGTGCA	CATCTACGAC	GGACCTCTCG	TCGAGACAGA	CATGCTACAC
	ACCGACGATA	TTTCTGATCT	TGGAAACCGA	GTGTGTGCGA	TGGAGAGGCG	TCGTGCTGTG
	GGCGACCTGG	AGCCTTAACCT	CCGCGAGAGAA	GATCTACCAO	AACTGACAGC	ACTCTCTCAT
	TCGCCGCTGG	ACATGCTGCG	CCCTCTGGCT	CAAGAGATGC	TGAAAGTAGT	GGATGACATT
	GGCTCTACAC	TGACTCTTCT	AACACGACAT	ATGATCTGAA	CTCTCCCTTC	TTTGCTCTGT
25	CGTGTATACA	GAGTGAATCG	CAGTAGTTTC	AACACRACTA	CCTTTGTGGC	CCAGGACCTC
	GGAATCTCTC	AGGTTTCTCT	GGAAACCCAA	GCTCTGAGA	ACAGTATTGG	CACAAATTACT
	CTTCTCTCAT	CGCTATAGAA	TAATTTACCA	GCTCATGACA	TGGAGTAGCG	TTCCAGGGTT
	CTGATCAATT	TTTGTGAGAC	ACCTGCTTTG	TTTGAGAGAT	CTTCCCTGGA	CAGATCTCTC
	CTGATCGACT	ACCTCATATC	ATCGAGTGTG	GGAACCTGGA	CCGTGACGGA	CTTGAACAGA
30	CTGATCGACG	TCACATATAA	GCACATCAAC	CCGAGCCGAG	ATGAGTAAAC	AGTGAAGATG
	GTAATTTGGG	ACTGTGGGCG	AAATGGTGCG	AGAGGAGGCT	GTGTCAAGAC	TGGCTGGCTC
	TCGAAAGACA	GGTCTGTGTA	TGACACACAT	TCGTGACAGC	AGCTCTGCGC	AGCTCTGCGC
	GTCTCTGCG	ACTATCTGAG	GGACCTGTGG	CTGCGCTGCT	AAATGAGGCG	CTTGAGCTTC
	ATTACATATA	TGGTGTGGG	GCTTTGATCA	ATTTTTCGTG	CAGTAGCTCT	TGTAACTTAC
35	ATAGCTTTTG	AAAAAGTCCG	GAGGGATATC	CCTTCAAAA	TCCTCATCCA	ACTGTGTGCT
	GCTCTGCTTC	TGCTAAAGCT	GCTTCTCTCC	CTGAGACTGG	GGATTCCTCT	GTATAGAGTG
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	TGGATGGGCG	TAGAAAGCAT	CCATATGTAC	CTGGCCCTTG	TCAAAGATT	TAATATCTAC
40	ATCCGAAAT	ACATCTTAA	ATTCTGAT	GTGGTGTGGG	GGGTACGAGC	TGTGTGTGTG
	ACGCTATCC	TGACTATATC	CCGAGTAAC	TATGGGCTGT	GATCTCATAG	GAATATCCCT
	CAAGTCTGCT	CGAGTCTGCT	CTGCTGAGC	ACACACATCA	CATTAAGCTG	CATTAAGCTG
	GTGGATATAT	TCCTGTGAT	ATTTTTCG	AACTGACGCA	TGTTCAATGT	GGTCTGTGTT
	CAGCTCTGTC	GAAATTAAGA	GAGAAAGCAA	CTGGAGGAGC	AGCGAARAA	CAGTATTCAA
45	GACCTCAGGA	GTATGGTG	CGCTTACTG	TTACTGTGGA	TAAGCTGGGG	CTTGTGCTTC
	TTTACTGGGG	GGACATAGTA	GTGACACTAT	GTGCTGAGT	TTGCTCTCT	TAATACCTTA
	CGAGGATTTT	TCATATCAT	CTTTTACTGT	GTGGCCGAAG	AAATGTGCG	GAGCAATG
	AGGCGATATC	TTTGTGTGG	AAAGTTAAGG	CTGGCTGAAA	ATTCTGAGT	GAGTAAATCT
	GCTCATATAG	GTTTAAGAG	CGACAGCTGA	AACCAAGAG	TGTCGAGCTC	TTCAATATCC
	TTACAGTCAA	CGAGTACTTC	CACTATATCC	ACCCACACTC	TAGTGAAGTA	TGATATCTCA
50	GTACAGACGA	CGGGAATGG	AAATGCTTCT	ACAGAGACGA	ATGGGCTCTC	TTTTAGTGT
	CAGAAATGAG	ATGTTGCTCT	TCACAGATTC	ACTGGAAAA	AGCAATGTT	TAACGAGAG
	GAGAGTCTCT	CGAATGGGAA	AGGCCATATG	GCTCTCAGAA	GAGCTCAAA	CGGGGAGAGC
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Seq ID NO: 16 Protein sequence
Protein Accession #: Bos sequence

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	GTGLVGLSL	ELANTACTP	IKLNTNMAC	AVIALSRVK	IRHMHCCCS	VRIPGSPSE	160
	ELBLGLCQJ	DFVLCGLHP	RSPFSSBSG	IPVPRVAVI	GVVPAICFA	EPFVSSFTI	240
	MYFSPFIEQ	PLSPGSPAP	ASSPAIDWP	QSEIISLSP	CTVNSGTPP	VKAFSSFTP	300
	SAPANNVTS	APPVGTQIV	TSISIDLENQ	VLQMKXALS	GLSLFNLAGE	MINOVSLHL	360
65	SPFNLAPLA	QLLKVVDI	GLQNFSPIT	ISLTSPELAL	AVIRWASFF	NITTFVAGP	420
	ANLQVLEPQ	AFQNFSTYT	LPSTLNNLE	AKHMLASVY	QVFTFETAL	FOQLEHLS	480
	LENVISRSV	ANLVNMLH	NVTVLEHIN	PSQDELTVRC	VNQLGRNGK	RSGHSDNGCS	540
	VKDRINLETI	CTCSHLSCF	VLLDLSTSV	LAQHMALZF	ITYTGCGLES	IFSLVTLVY	600
	IAFEKIRRDY	PSKILQLCA	ALLMLNLV	LDGIALYEM	QSLCISVAVF	LHYFLNLSFT	660
70	WGLEAFPHY	LALVNVFTY	IRKTLFECF	VGMGVFVAV	TILITLSPN	TGLSBSFTF	720
	NSGSPRCHI	IRHATVFTY	VGFVCPFL	IVSVFTVLM	GLCRLEKQ	LEQRRTSLQ	780
	DLRSIAGLTF	LLGITWGFAP	FAMFQVNVTF	MYLFAIENF	GGFIFITFY	VAKENVRQK	840
	RLYLCQGLR	LAENSDHKT	ATNGLEKQTV	NGQVSSSHS	LQSSSHSHS	TLLVNDICS	900
75	VHSGNGMAS	TERNGVSFV	QNGDVCLDF	TQKQMFNEK	EDSCNGKRM	ALARTSKRS	960
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Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: Bos sequence
Coding sequence: 1..2811

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	GATACATATA	ATTCTGGCTT	GTGCACAGCA	CCGAGAGTTA	CTTTAAACCT	ACTCTGTCTA	180
85	GTACTCTTAA	GCTTACTCCC	TTCAACAAGA	ACAGGCTGCA	ACCCGACGAG	AAATATCTCC	240

WO 02/102235

PCT/US02/19297

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 20 GCAATCTCTC AGGTTTCTCT GGAACACCAA CTCTCTGAGA ACAGTATGCG CCAATATCT 1380
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 45 TGAAGAGAT GGTCTCTCT TATGTTTCA CAGAGCATC TGTCTCTCA CAGTATCT 2700
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Seq ID NO: 18 Protein sequence

Nucleic Acid Accession #: Bos sequence
 Coding sequence: 1..345
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 LSLSELKRSE LNKTLQLSE TYFIMCATAS AQSLANCTP IKLANTMNA AVIAALERVK 180
 IRPHEIOCCS VRIPCSSPSE EELKQLDQL DPVLCLADHP RGPFFSSQS IPFVPRATVL 240
 SQVFRATSPA EPPVSPSVTH NVSPFISGLQ PLSPQSPADI ASSPAILDMFP QSETISBPML 300
 55 CTWVSPPFP VNASPSPTV SAPANWITS APFVQYTH TSSLSLEHQ VLQMSALSL 360
 GLEPFLAGE MINQVSRLLI SPPMLAPLA QRLKLVDDI GLQMLSNIT ILS7SPSLAP 420
 AVIRNASSFP NITTFVADPQ ABLQVLSLTQ APENSIGIT LPSSILANLP AHMELASLR 480
 QPNFEPFPA PQGSLNLSLS LISVLSSESV ANLTVMLRTH NVTVLHRLN PQGQMLVTRC 540
 60 VPKGLKWDQ RQWMSVRLT VQRLNLESTI VQRLNLESTI VQRLNLESTI VQRLNLESTI 600
 ITYICGLSLS IFLSVLTVTY IAFKPIRSDY PSKILQLICA ALLLLMLWFL LBSMLALYKM 660
 QGLCISVAVF MYFLVLSPTV WHGLEAFHYH LALAVFNTY IRKYLKPCI VGMGVPAVVV 720
 TILITLSPDN YLGSYGRKFP NGSFDDFCWI NNHNVFVITV VGVKPIFLL NVSMPIQVW 780
 CTGCIKKKQJ LQAKRKESIG DRLSIALGTF LLGITNGFAP FAWGPVWVTF MYLPAIFWTL 840
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Seq ID NO: 19 DNA sequence

Nucleic Acid Accession #: Bos sequence
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 75 TCAAGAGAG CAGAGATCA TACATGATCT ACATGATAA CTTCTATATC TCTCCGCTCT 300
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 GGTGAGATCA TGTTTAAATA TGATAAGAAA AGCACTATTC CCGAGANTCA ACATATAAG 420
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WO 02/102235

PCT/US02/19297

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TCATTTCCT CTCGCAACCT GTCTGCCCTT GCGAATGTCA ACACATCCAG CGCACTCTCT 1080
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Seq ID NO: 20 Protein sequence:
Protein Accession #: Bos sequence
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GEINPQYKE SVTPGKHIT HTLRLVLEL SELRESLSEI TLTLESITFI IMCHAPDRA 180
TLMFTTTL NVTWACAL AALERIRIP MSKCCSVRI KPSSSEILG KLQCDLQPI 240
VCLADIRPFP PFSSQSIPV VPRATVLSGV FKATSPFAEP DYSVFTHVPE SPIQEIQLS 300
PQPSAIASS PAIDMPQSE TISSPMPQTH VSGTPPVVA SPSSFTVSAP ANVNTISAP 360
VGTDIVTBS ISUMBLVQLG MEKALSAGSL EPHLAGMDIN QVSKLHSP DMIAFLAGEL 420
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50 HSIQTILES SLMONLPAND MELASRVQFN FFETPALPD PSLNLSLIS VYISSSVNML 540
TVRLNTRNT VILGHINPDS DELTVRCVFN DLGRNGRGRG WSDNGSKVAD RLINRITCT 600
SILTSFVLL DLBRTEVLPA QPAUQTITV IGGOLSEITL SYTLVITAF EKRIRDYFRK 660
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55 AVFTITVGY PCIFILLAS MPFVLVQLC RIKKKQLGA QRKTSQDLR SIAGTLFLGS 840
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NBSWSTACN QLAKGTVAQG VSSSSSSSLGS SSNSFNETTL LNKWCSVIA SGRKSTASR 960
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Seq ID NO: 21 DNA sequence
Nucleic Acid Accession #: NM_005756.1
Coding sequence: 37..3117
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TCCCGTGAGG AAGATACCTGA TAATTCCAGT TTGTCACACC CAGCTGCTRA ATTATCTGTT 300
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70 GCTTCGCGCC TCAACAGCCA GAGAAATATC TGAATTTGTT CATCTATTG CAATGACTGA 480
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GAGCTACACA AAAGCTCGCA AGCTCTGAGT GAGACTGCTC TATAGATGAG TCTTCAAGA 660
75 GAGGCTCAAA GGCATATCAA TTGTAATCTC ACATATAAAC TAAAGATATC AATGATATGA 720
TGTGCTGAAA TACCGGCTTT TGAAGAGGTA AGAGTTGCGC CAATGAAACA CTGCTGCTGT 780
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80 GCTGAGCTCT CAGATTTATC ACCTGTGAGC CAAGATGTC CCTCTCAAT AGGGGAGAT 1020
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CCTTGAAAG CCGTCACTCT CTTCCGCGAC GTTCTCTCC TCGGAGATGT CAGCATCTG 1200
85 AGCGACACTC AGTATGAGCA AGCATATGTC AACACGACCA GTATTCTGA TCTGTGAAC 1260
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 SGLVFPVFA TVVLTGTLT STAPGPFPS VTEVSPVPS EITLAPSPS AFLAGSAIL 300
 MPFGSETISS MPQHTVSGT PDPVKAFFSS PTVSAAPAVN TTSAPVQCTD IWTNVSIDL 360
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 75 FCLVNOVFA VVGLITLITIS FPGVGLSTG ETPGSPSTG CHIRHNAVTF TPVQCTVLT 780
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 Coding sequence: 67..363
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Seq ID NO: 24 Protein sequence
Protein Accession #: NP_001556.1
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25 MKQTALLICK LIFLFLSGIT GVPLSRVTRC TCISISNQPV NPSRLKLELI IPASQPCPRV 60
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Seq ID NO: 25 DNA sequence
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GAACCAAGCT TTGAGCCGGA GGATGAAGAC AGCGAAGAG ATGACATTAT CATTGAAGAC 900
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Seq ID NO: 28 Protein sequence
Protein Accession #: NP_063658.1

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LQWGLRHPF TSLNLSLRLS QSLNLSLWMT SYVSPSPSP LHSLEHRLAD DNALTEIPVQ 180
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EYELIYSHY QQLLELRLT LANKLILBI PRAPLETFSL ILLELSHLLN SPFFLTGSL 420
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DLHKGALMF QAGDRDLLED FLDDFEEDLK ALHSGQSPFS GPPFKPEHL LQGLHLRIGV 540
NTIALVALTC NALVSTVFR SPLIISPIKL LIGVIAVYRN LQVSSAVIA GVADTFPSF 600
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LLVVVPLPAC LNPLIYLIFM PFHKEDLVSL RQATVYVTR KPSLSIMSHS DQVREQSCGS 840
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Seq ID NO: 29 DNA sequence
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Coding sequence: 135..1472

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CGAGGATTC CAGCCCTGTA TTGATGAGC TGAACATGAA CGAATTCAG TTACAGAGNC 1020
GAGAGCGAGC TCTCAAGCA AGAAGAGAAA GATTTAGACA GAGAGACAGC GAGCTTTGTT 1080
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TSLAAGCGAG ACGAGATCT GCGATCTGCT ACGCCAGTAG AGAGACAGAC AGCTCTGTAC 1440
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GCTCCCATGA CGAGCTGCT TGTGTATAGT CAGCATGATA TTTCGGAATT GGTTTTACTG 1560
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Seq ID NO: 30 Protein sequence
 Protein Accession #: NP_002488.1

1 11 21 31 41 51
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 TLALKECHER SDGHTYVLR DLKPANVFLD GKGNVWLKDE GLARILNEHT SPFAKFWQTF 180
 YTHSPBQHR MSYKESKIDH SGCILLYELC ALMPPTFAPS QKELAGKIE GKPRIPRY 240
 SEIHEITS MLANDIEHF SVBILNLEW TAILVDFGR EHLERSGES GEPSSGDS 300
 FYLEELKLE QLQSEBRL KARRERLEQ DQELCVERL ABDLKLRAN LLNYSILKE 360
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Seq ID NO: 31 DNA sequence
 Nucleic Acid Accession #: NM_020242
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WO 02/102235

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Seq ID NO: 32 Protein sequence
Nucleic Acid Accession #: NP_064627

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 QPSSEHPIHF NLGVTPLRST EPLPSLIDE KKPAGAGGSI LCKGCTFSTY NBDIYDLDS 180
 ASAGLYLRKH IKGVFVFGVA VEQVFTSAE AYQVLSGWR NRRVATSMN KERSRHAFV 240
 TITISMERKS HEIVNIRSL LHLVDLAGSE RQKDTNAGFN ELKAGNINR SLSCLOQVIT 300
 ALYGVDRHQ RHVCTDRSHL FTLLBDSLGG HAHTAILNV HIGSRCFSEP LGLTAFATCA 360
 KLIHVAIVN EGVCTCTGGL GATVPLRGG LAGLSTGPT PHSITPDQK KTHVNEYPCA 420
 AMLFFKSSBO SKESLSIKVT QLEBLTWKE KFQENQMHV KFFSDQIIRL EKANESRSG 480
 FLPSBQRLLL SELNLSIQTU KQIEMHPRV AKYAMERHS REENRLRLI EPRVKAQBMQ 540
 AGTKALEKA FSEI8GHERS DNGQCAFSPK AQKECLFEN TBLKALQLQ IOTELNHSRG 600
 HTEFPEFRI KXALRLEKAL ENLLKATCAK KQDVRQLKAK HRAITLITL 660
 TPTKATKRS RVPVLLSPEM GSPGSLVTGN SILELNDILN FVPVPPENBQ AFPSALISEL 720
 QVQMSALQ AKLIDSEEHKN LKLOHRVDKL EHNSTQMOEL PSESRIDWTK QOHELLSQBL 780
 VLEBQLQSTQ TKNDFLKSEN HOLVVLHISA DEKLESVKLE YSPFCTINQEK EPNRLSRHM 840
 RVOLGLDRL LBNELILBER ACLOSDYMG TQEMETLDT LSHLNDPKK EHTLSKAE 900
 HMLSLDAK BBNKLSIQF EEDNSESSEK ILKVLAVRBO EKOKETAKE QOMAKVOKLE 960
 BSLLATKVI SLEKSRDSD KVVADLMMQ IQSLRTSVC KETIDTLQK ELKDINKYLE 1020
 SALVDEESER VLIKHQVDTI LDLEKTLER LSESDIRHM LCELDLHATE QIANHTESK 1080
 KESLLSQTAQ BELTKRALL QSLGHRLNK KEVBOAKNE INFMRLQHE VDSABEDQ 1140
 SPKPTPHRT ILKALLTGT QTEGDRASK TACTVTCMA TQSCNLMGC AMLCTCMA 1200
 MENLEBSQO LIRKMLLQO QLEDSIQKE NSDQHPDQO QLWNBESBI KERLAKSKIV 1260
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Seq ID NO: 33 DNA sequence
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Coding sequence: 1..257

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Seq ID NO: 34 Protein sequence:
Protein Accession #: A810633.1

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ALQEPDDAD YTCMARANCK KFAVHLISFA OFELSGCHVK KSVLLQKAV ERGAVPLRL 180
EIALRNLMLO KKLGLSESE KHLGASTVLV AQSFTSGSLG HLQNNHNSCD SROQTTHARE 240
LQENHMFOD AETGVNRLRL QTNSTQSCSP FGVAVVULNLN SHCIVKID SDVPCFMHQ 300
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ESSLALKEE TRVQEPFV ESKQKQWCK RSECEINQF AASHHWIPI ELARKVHTQ 420
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Seq ID NO: 36 Protein sequence:
Protein Accession #: NP_005814.1

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DYALGALGAL DLPGHFPVBS ARVLLPRLVS CPRLDDQDQ EAAKALQGG GPYGFPSFT 240
EYTHMALGG LLYPLQFTI RSPQCTVAA WKPSSKQPS WQRPSTLI RPTFARVTV 300
ACPSSGKARE IDESLIFYKK WELGACVDAA LQATQMERN AITPTTQLD VLHKLDSLY 360

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GRGLQKDTL DTITATPYNG LCLSPSEELS SVPSSEINAV RQKIDATCDR SOLIDVLYPKA 480
ELARQNRHS TYTPRQSLF GQATFTEELA LQCNVWHLV ATFMELCTIA VLIDVIAVQ 540
KILSHVBEEL KAEBSREIRF DHILRQBDQD LDTLGLRLQGS GIPMOVLVLD LSVQBALGGT 600
FCLIGFGPVL TVALLIAAST LA

Seq ID NO. 37 DNA sequence
Nucleic Acid Accession #: NM_013404.1
Coding sequence: 89..1975

10
1 11 21 31 41 51
TGCCCGGCCA CTCCTCTCTG CTGTGACGGG CGACACAGAG GTACACCGGTG GACCCACGGT 60
GCTCCTCCCTCG CTGGGATCTA CACAGACCAT GGCCTTGCAA CGGCTGACC CCTGTGGTCT 120
CTGTGGGAGC CGCCTTGCCA GCTCTCTGTG AGCTCTGGAT GGGTGCAT CC 180
15
CGACAGGACC CTGGTGGAG AGACAGGAGC GGAATCTGCG CCGCTGGGAG GAGTCTCAAC 240
AACTCCGAT AACCTGCTG GACTCTCCCG TCGTACGAG CAGTCTGGGA CAGTCTGGGA 300
GGTGTCCGCG CTGACAGCGC AGCTGTTCGG GAGCTGGCTG GTGGCGCTGG CACAGAGGAA 360
TGTCAAGCTC TCACAGAGC AGCTGGGCTG TGTGGCTCAC GCGCTCTCTG AGCCCCCGGA 420
GGACTGGAGC GGCCTCCCAT TGGACTGGCT GCTATTCTTC AACCCAGAGT GGTCTCGGAG 480
GCCCGAGGCG TGGACGCTT TCTTCTCCG CATCAGAGAG GCGATGTGGT ACTCTCTCC 540
GAGGAGGGCT CCGCAGGAC AGCGGCTGCT GCGTCCGGCT CTGGCGTCTC GGGGTGTGGC 600
GGGTCTCTCG CTGACAGAGC CTGATGTGGG GCTCTCGGGA GCGCTGCTT GCGACTCTCC 660
TGGCGCTTT TGGGAGAGT CGCGCGAGT GCTCTACCC GGGTGTGGA GCTGCGGGG 720
20
AGCTCTGGAC CACAGACGAC AGGAGGACG CAGGCGCTCT CTGACGGGCG GCGGACCCG 780
CTACGCGCT CCGTCTGAT GCTCTCTCTC CAGATGAC GCTCTGGGCG GCTGTCTGCG 840
GCTCTGGCG CAGCCATCA TCACGACCAT CCGCAGGCG ATCTGTGCCG GGTGGCGGCA 900
ACCTCTCTCT GCGAGACCAT CTGCGCGGCA GCTCAGAGG ACGATCTCT GCGCCGAGT 960
CGCGCGGAGA GTGAGAGGA CAGCTCTCTC TTGCGGAGC AGGCGCGCG ACGTACGGA 1020
25
GAGCTCTCTC TTCTACAGA ACTGGGAGCT GAGAGGAGT GTGATGTGGG AGTGTGCG 1080
CAGCCGATG GACCGGTGA AGCGATCCC CTTCACCTAC GAGGAGCTGG ACCTCTCAA 1140
GQNTAACTG GATGAGCTCT ACCCCAGAGG TTACCCGAG TCTGTATCC AGACACTGG 1200
CTACCTCTTC CTCAGATGTA GCGCTGAGGA CATTCGAGT TGGATGTGA GTCCTCTGGA 1260
GACCTCTG GCTCTGAGG AGTCAAGGA AGGACAGGA AGAGTCTC AGCTCTCTC 1320
30
CGCGCGCTTC CTCAGAGGTC CCACTCTGAT GACCGCTTT GTGAGGGA GGGCGACCT 1380
AGACAGGAC ACCCTAGACA CCGTACCGC CTTCACCTCT GGGTACTCT GCTCTCTCAG 1440
CGCCAGGAGC CTGAGCTCG TGGCCCGCG CAGCATCTGG GGGTCTGAG CCGAGAGCT 1500
35
GCGCATGCT GAGTCAAGCT CCGTCTGAT GCTCTCTCTC AGGCGCGCG TCTCTCTC 1560
GAGCATGAC GGGTCTGAGT ACTCTGTGA GATCGATCC TTCTCTGGT GCGCCCGCAC 1620
GGAGGATTG AAGCGGCTCA CTCACAGGAA TTGAGGATG GACTTGGCCA GCTTCAAGA 1680
CGCGCGGCG GATCGGTGTC TGCGCTGAC TTGTGTGAG GTGCGAGAA TCTCTGAGAC 1740
40
CGCATGGG GCGCTTAGG CGAGAGGCG GCGCCCGCG GCGCGAGCT GATCTCTCAG 1800
GCGCGGCG CTGCGGTGG ACACTGTGG CTGTGGGCT CAGCGGAGA TCCCGAGGAG 1860
CTACTGGTC CTGACCTCA GCGTGGAGA GACCTCTCG GGGAGCGCT GCTCTCTAG 1920
ACCTGAGCT GTTCTCACG TCGTGGACT GCTCTAGCG TCCACCTGG CCGTAGGCGC 1980
45
CGATCTCTT GTCGACCCA GCGCTGCG GATCCGCG CTGGCGAGA CAGACAGCG 2040
GTGTCGCG GTCGACCCA AGAGAACTG GATCTGATTA ACGGAGACT GCGCCGTGCA 2100
GACACT

Seq ID NO. 38 Protein sequence
Protein Accession #: NP_037536.1

50
1 11 21 31 41 51
MALQRLDFCH SCGRSPSLI FLFLSLGNV PARTLAGET TESAPLOGLV TPRMTSSLE 60
PROLLAFCT EYGLSTSEV RELVALAGK NVLESTGLA CLAIRISFP EDLALPLDL 120
55
LLFLNFAFS GPQACTRFS RITKANVELL PRGAPERQEL LPAALACHGV RGLSLAEAV 180
RALQGLACL PRFVABESR VLLPRLVSCP GFLDQQESA ARAALGGGP PYOPSTHVS 240
STMDALRGL VPLQPIIRS IPQIVAAWR GRRSPRSMR QPERTLRPR FREVERTAK 300
PGRKAREED SLLIFPKWE LEACVDAAL ATQWRWMAI PFTTQGLV KLHLDLPTQ 360
60
QYFVSIGL GYLPLRPSF DTPRWTEEL ELKALAEV RHEHMPQL RPLPQVAT 420
IDRFVGRQG LKDLTLLIF AFYFGVLCSL SFPEELSVP SSIWVRPQD LKRTDPRQLD 480
VLYFKARLF QNMNGSEYF KIQSLFQAG TEDLKLQSQ NVSNLAIWF KLRTDVLPL 540
VLAEVKRLG PHVEGLAER HRPVRLWIL RQRQDLDTL GLQLQSGIWF GYLVLDELVSQ 600
ETLGRFTCLL GPQVFLVLA LLASTLA

Seq ID NO. 39 DNA sequence
Nucleic Acid Accession #: NM_001508.1
Coding sequence: 1..1162

70
1 11 21 31 41 51
ATGGCTTAC CAGCTCTCC GCGCAGGAC TGTCCCAAA TCAATGATCA GATCATGTC 60
CCGAGATTG AGGTGACAC CTGATCAAA ATCACTCTA TCTGGGTGA CCGATATAC 120
TGTGTAGGS GCTCTCTGG GACAGAGTC ACATCTGGG TCAACAGGT GCTGCGAAG 180
75
AAGGATACT TGCACAGGA GGTGACAGAC CACATGTGA GTTGGCTTG CTGCGAAG 240
TGTGTCTTC TCACTCGAT CCGCATGAG TTCTACAGA TCACTGGA TCCCTCTAC 300
ACCTCAGCT ACACCTCTG CTGCAAGCT CACACTTTC TCTTGAAGC CTGACACTG 360
CTGACAGCT TCGCTGTGG GACGCTGGG TTGTGGCTT AGATCCCAT GATCTGAT 420
TTCAGGTCA AGCTGTGTC GCGACTTGC CAGGTGAGC TCGTGTATG TCTGTCTG 480
GTACCTTCG CCGGTGTGC ACTGCTCTG CTGTTTGCA TGGTACTGA GTACCCCTG 540
80
GTGAGATGC CGGACGAGC GGTCTCTAT CTGACCGCT CAGAGACCG CCGACAGAC 600
GAGCCAGAG CCGTCAATG ACACACTCT ACACACTCT CAGCCCGTG GACCTCTTC 660
CGTCTGAGA TCTTCTGCC CTCTGTGGT TACTCTGCG TCTCTCTCT GCGCGGCTG 720
ATGTGCTGGA ACGATGAGC GGTCTCATG AANAAGGCA AGGCTCTGCT GCGCGGSGAG 780
AGCGCGCTC CGCACTGAG GAGTCCGAG AGCGAAGGA CAGAGACCG CAGMGCGAC 840
ACATCTCTC GATCTGTGT GATCTGTGT ACATGTGGG TATCTGTAT GCCACAGC 900
85
ATTGCGAGA TCACTGCTC GCGCAACCC AAGCACTCT GACCTAGCT CTACTCTCG 960

WO 02/102235

PCT/US02/19297

5
 10
 15
 20

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GO3TACATGA  TCTCTCTCCG  CTCTCTCGAG  ACGTTTTTCT  ACGTCAGCTC  GGTTCATCAAC  1020
COCTCCCTCT  ACGAGCTGTC  CTCACACAG  TTTCGGCGCG  TTTCGTGCGA  GGTCTGTGTC  1080
TCCGCTCCTT  CTTCTACACA  CCGACACAC  GACAGACGCT  TCGCTGTACA  TCGCGCTCTC  1140
ACCAACACGA  GCGCCGCGCT  TTGCGACGCG  CGGTCTCTCT  TCGCGTCCCG  GCGCGCTGCC  1200
TCTGCAAGGA  GAACTCGAGAA  GATTTCTCTA  AGCACTTTTC  AGAGCGAGGC  GAGGCCCGAC  1260
TCTAAGTCCC  ACGTCATTGG  TCTCGAGTCA  CTAGAGCCCA  ACTCAGCGCG  GAACGACGCG  1320
AATTCTCTGT  CAGAGMATCG  TTTTCTCGAG  CATGAGTTT  GA

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Seq ID NO: 40 Protein sequence
 Nucleic Acid Accession #: NP_001499.1

1 11 21 31 41 51

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MASPSLPGSD  CSQIDHSHV  PEFVATWIK  ITLLIVLYLI  FVNLHGNV  TIRTVQLIK  60
KQYLQKENVTD  EHVSLACSDI  LVELIGMPHE  FYSIINWPLI  TSSVTLSCGL  HTPLFACST  120
ATLLAVLITLS  FERYIAI  CHP  FRITKAVSGHC  QVLLKILGFW  VTSALVALGL  LFRMHTFPL  180
VYVPSHGSLT  CHRSSTFHH  QSTPMSIII  TALSRRVTF  TAVYLSLVA  TAVYLSLVA  240
MCHNMQVLM  KSGKSLGAG  TEPPLKRSB  SEESTARQQ  TIIFRLIVLV  TLAVCMHQ  300
IERHMAAAR  KHWHTSYFE  AMYLLPFSS  TFFYLSVIN  FLAVTVSSOO  FREVFQVLVC  360
CELSLQJRMH  EKLHVEHRS  TDSARFVQR  PLLFASRRQS  SARITEKIFL  STFGSARFQ  420
SKGSLGLE  LEPNSARFA  NSAAHNGFQ

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Seq ID NO: 41 DNA sequence
 Nucleic Acid Accession #: NM_022358

25 30 35 40 45 50

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GGAGCGCGCG  GTCCGCGCAC  ACGAGCAGAG  TTGGAGACCC  GCGCGGTACC  GCGGCGCGGG  60
TGCATGCGG  AGCCGACGCI  TCGACGCGCG  CGGCTGTGTC  TGTGTACACC  TGTGTACTCT  120
GCTGTGCGGC  CGCTCTCTCT  TCGAGCGGCT  CGAGTCGAGC  GCGSAAAGCG  CGCGCGCGCG  180
ACTCTGTGTC  CAGAGCGCGG  GCGCTCTCGC  GAGGAAAGTTC  GCGCTTCTCG  CCGAGGACTA  240
CCCGAGAGCT  GAGCGCGCTG  CGCTCTCAGC  GAGCGCCGAC  CGCGCGCGGC  GCGAFTGAG  300
GTCGCGCGCG  TCTTCTTACT  TCGGACATAC  GGTCACTACT  ACGATCGGCT  ACGCGCACGC  360
CGCGCGCGCT  ACGTGTGCT  CTGCGCTCT  AAGAGCTTCT  CGGAGCGGCT  TCGGCTCTCT  420
CGCGCGCTG  GCTCTCTTCC  AGAGCGTGGG  CGGAGCGGCT  AAGCGGTGG  TCGCGCGCTCT  480
CGCTGTGCG  GCGAAGTCTC  GCGTGGGCTC  GCGGTGAGCG  TCGGTGTCCA  CCGGAAACTCT  540
GCGTGTGCG  GCGCTGTCTG  GCGTGTGCGC  CAGCCGCGGC  CTGCGGCGCG  TCGCTCTTCT  600
CGACTGTGAG  GCGTGTGCTC  TCTTCTGAG  CTA  CTA  TCT  TCGTGTACA  CCGTGTGAG  660
CGTCTGCTG  GCGGACTTCC  TCGGACTGCA  GAGCGCGGAG  GCGTGTGAGA  GGAAGCTCTCC  720
CTAGTGTGCG  TCGAGCTTCC  TCTCATCTCT  CTGCGGCTC  AGGTCATTG  GCGCTCTCTCT  780
CGAOTGTGTC  GCTGTGCGCT  TCTCTGTGTC  GAGCGCGGAG  TCGCGCGGCG  GCGCTGTGCG  840
CGCGCGCGAG  GCGCGCGGCG  GCGCGCGGCG  GCGCGCGGCG  GCGCTGTGCG  TCGCGCGCG  900
CGCGCGCGAG  AAGCTGTGCT  TTTCGCGCGC  CTGAGCGCGC  GCGGTGTGTC  GTGCGCGGCA  960
GCGTGTGCG  CTGCGCGGCG  GCGGAGGACT  CATCTGAGCA  CGGAGCGGAG  CGCAAGTGTG  1020
AATCTGTGAT  GCGAGGCTCT  GCGTCTGAGT  ATCAGGCGAG  CCGCGCGGCG  GATGTGAGAC  1080
GCGTGTGCG  CCGTGTGCG  GTCTCTGTC  ACAGAGTCT  TCTCATTACT  GTCTGTGCTCT  1140
AAGTCTGCTCT  CCGCTCTTCC  AAAATATAT  TACAGTACA  CAGTAAAAAA  AAAAAAAA  1200
AAAAA  AAAAA  AAAAA

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Seq ID NO: 42 Protein sequence
 Protein Accession #: NP_071753

1 11 21 31 41 51

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MRPSPVRAAG  LVLTCTCLL  VGNVFPDALE  LSAESGRQLR  LVKRGALRR  KPFSSAEDYR  60
KLEHLAQAS  PIRAGAGKHF  KPSFYFAITV  ITTIGYHRA  RGTDSKVFPC  MFYALLGLPL  120
TLVTFYSLGE  RLNAVRELL  LAAKCCGLLR  VTCVSTENLV  VAGLLACAT  LAUGAVAPSH  180
FRONTFRAY  YCFILITLI  GTGDFVALGS  GHALGRKLP  VAFSLYLLIL  GLTVIGAFPL  240
LVVLFVLVAS  ADMFERAAR  PFRPFPAPSE  SRGLALPRP  ARSVGSASVF  CHVHLEICA  300
RNLGFPSPS  SPQVYRQQA  PIRAGAKSI

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Seq ID NO: 43 DNA sequence
 Nucleic Acid Accession #: NM_000869.1

65 70 75 80 85

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GGRAACATGA  TCGAGCTGAA  GGAATGATTC  CAGGAAACT  TCGCACTTCC  CGAAGCTTGG  60
TCCGCAAGT  AGTGTGAGC  TCGAGCTTCA  CGAGGTGTGA  CGAGTGTGTA  CGAGTGTGTA  120
CGCTCGCTGG  AATGAGGCT  GCGAGAGGCG  AGCGAAGCTG  GCGCTGTGTC  GCGCTGTGTC  180
TGAACACTGC  GAGGCACTCC  TAGCTTTGGA  AAGCTCGCTA  TCGTCTGTGT  GTGTCAGGAG  240
GCGTCTGTCT  CTTTACTCT  CGCCACAATC  CTGCGACGAG  GAGGAGCGAG  GAGGAGCGGA  300
AAGCACACGA  TCGCGCGGCT  GCGGAGGCTC  TCGGATATAC  TTTTGACAGA  CTGAGAGAG  360
GCGTGTGCTC  CCGTGAAGGA  CTGAGGAGAG  CGAACACCGC  TATCATATGA  GTCATATGTC  420
TATGCACTCC  TCAACGTGGA  TGAAGAAGAT  CAGGTGTGTA  CGACTACAT  CTGTGACGCG  480
CGATCATGGA  CTGAGAGATT  TCTCTAGTGG  AAGCTCTGAG  ACTTTGACAA  CATCAGCAG  540
TGTGCTATCC  CCGAGGACAG  CAGCTCGGTC  GAGGCGATTC  CGACTGTGTA  GTTGTGTA  600
CTGAGAGATT  CTTCAATAT  CCGCTAGTGT  TATATTGCG  ACTCAGAGCG  ACTTACAGAC  660
TACAGAGCCC  TCTAGGTGCT  GACTGCTGCT  AGCTCTGACA  TCTACACTCT  CCGCTTCTAT  720
CTCCAGACT  GCTGCTGAG  CTTACACCAT  TCGTGTGTA  CGATCGACGA  CATCAGCAG  780
TCTTTGTGCG  GCTTTCGAGA  AAGGTGTGAA  TCGGACAGGA  GTGTCTTCT  GAGGACGAG  840
GAGTGTGAGT  TCGCGCGGCT  CCGTCTGCTC  TTTGCGGAT  TCGAGTATAT  AAGCATATAT  900
TACTAGCGAG  AAGTGAAGT  CTATGTGATC  ATCGCGCGCG  GCGGCTCTCT  CTATGTGATC  960
AGCTGTGCT  TCGCGCGAG  CTTCTCTGAT  GTCATGTACA  TCGTGGCTCT  CTACTGTGCG  1020
CGCAAGAGT  GCGAGAGGCT  CTTCTTCGAG  ATTACACTCC  TCGTGTGTA  CTGTGTCTTC  1080
CGATGTGCT  TCTGTGAGC  CTGCGCGGCG  GAGCTGTGTA  GAGCTGTGTA  GAGTGTGTA  1140
TACTGTGTG  TCGAGTGTG  TCTGTGTGTA  ATAGATTGG  CGGAGACTAT  CTTCTGTGTC  1200

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WO 02/102235

PCT/US02/19297

5	COGCTGGTGC	AAAGCAAGA	CTTCAGCGAG	CCGCTGGCTG	CTTGGCTGGG	TCACCTGGTT	1260
	CTGGAGAGA	TGCGCGGCT	AGCTGGCGAG	AGGAGGCGAT	CACTTCCGA	GTGGCGCCCA	1320
	GCGACCTGCC	AGGCCACCAA	GACTGATGAC	TGCTGACCCA	TGGGAACCA	CTCGGCCAC	1380
	ATGGGAGGAC	CCGAGGACTT	CGAGAAGAGC	CCGAGGAGCA	GATGTATGCC	TCGCCACCA	1440
	CGCTGGGAGG	CCCTGGCTGG	GGTGTGTGGG	CTGCTCGAGG	ACCTGTGCTC	CATCGCGCAA	1500
	TTCTGTGAAA	AGGACAGAGA	GATCCGAGAG	GTGCCCTCAG	CGTGGCGGCG	CGTGGCGGCG	1560
	GTCTGTGAGA	AGCTGTGATT	CCACATTATC	CTGTGAGGCG	TGCTGSGCTA	CACGATCAAC	1620
	CTGGTTATGC	TCGTGTCGAT	CTGGCAGTAC	GCTTGGATGG	GTACAGCCCA	CTGGAGGAGG	1680
	GGGTACAGTC	CTGGTTAGGT	GGGAGACGAG	GATTTCCTCT	TAGCCCCCTC	AGGACCCAGG	1740
10	GATGTCGAGG	GRCATTTTCA	AGACACGAC	AAAGTCCCGT	GGCTGTGTTT	CAATGCGMAT	1800
	TCCTCTGACG	ATACAGACAG	CAAGCTCGGA	ACCTCTCGCG	CAAAAGCTGG	GTGTTCAAGG	1860
	CCCTTACACG	CTTGTGCCAC	CCCGACGACG	TCACATGCGT	TTTAAACACT	GCCTCTTAG	1920
	ATCAGGAGAA	ACTGGGGCAG	TCCTTAAGTC	CACCTCAGTT	GTGAGCTTTT	CCCATATGAC	1980
	CTCCACCTRA	ATAGAGGAGT	TGGAATTTCT	GTCTCTCTTT	CMACACTTGG	CTTTTAGTTG	2040
15	GAAGGTGAAA	CGACGTGCTT	ACTGACAGAG	CCCTGATGCT	CTGTGACGAG	TGAGTGAAG	2100
	CCCTAGTGTG	TTTTTTTCT	TGACTCTACT	TGGGCACTCT	TCCTCGAACA	CTCATCCCC	2160
	ATCAGATGAT	GGGAGTGGGA	AGATATAAAT	CGAGTGAAC	CC		

Seq ID NO: 44 Protein sequence

Protein Accession #: NP_000860.1

20	1	11	21	31	41	51	
	MLPLVQGLL	LLPLFTLAG	QBARSHWTT	FPALLRLSEY	LLMTRKGRV	PTTCMKRFTT	60
	VSDIVYIAL	LVNDEHQVL	TIYIYRQVN	TDFLQWNPPE	DFMTITELSI	PTDSINVEDI	120
25	LINFEVDVQK	SPHIFPVYIR	HQGEVQNYEP	LQVVTACSLD	IYNFEDVQV	CSLFTSKLHI	180
	TIQDINISLN	ELPEKVKSDR	SVPNQGWEH	LLGLVLPYRE	FMSBSNHYA	EMKFTVVRIR	240
	RPLFTVSVSL	LFSPILMVRV	IVGFLYPMH	GBRVFPELT	LLGVSVPLLI	VEDTLFATAL	300
	GTPLVGYVYF	NCHLMLVLSL	ABTFTVRLV	IKGQAGQVYF	AMHLHLYBE	LAMLLCLAE	360
	STSGRFPFAT	QATKTDGCSA	MGRKSHMGQ	QPKFQSPED	RCSPPPPPEH	SLAVLQGLQL	420
30	ELASIRQFLE	KEDEIREVAR	DNLRVGSVLD	KLPHIYLLA	VLAVSPLTVM	LNSINQVYA	

Seq ID NO: 45 DNA sequence

Nucleic Acid Accession #: NM_015507

Coding sequence: 241..1902

35	1	11	21	31	41	51	
	CGAGGAGGA	GCTTCGGCCA	GGCTAGCCGG	GGCGGCCCCA	GGCCCTCCCC	AGGCCCGGAG	60
	CGCCCTGTCC	GGGTGTGCTC	GCTCTCCCTC	CGAGACTGCA	GGGACAGCAC	CGGTACTACT	120
	CAAGTGGAGC	GGAGGACCCG	AGCGCGTCGG	GAGAGAGGAG	GGCGGCGGCT	AGCTGCTACG	180
40	GGGTCCGGCC	GGGCGCCTTC	GGAGGGGGGC	TCGGAGAGAG	GAAGGAGGAC	CGGTGCGGAA	240
	ATGCTCTGCT	CGTGGCTGCT	TCGGTGTCCG	CGTCTGCTGC	AGAGTGTCTC	AGAGTGTCTC	300
	CGAACCGGCG	CCAGGTGCGAG	GCATCACTGG	TTGTTGACAT	CGGCACTCCA	CGCTGGGCTC	360
	TCGTACTATG	GAATCAAACT	GGCTGCTGTC	TACGGCTGGA	GAAGAAAGAG	CAGGAGAGTC	420
45	TTGTGAAGCTA	CATCGCAACC	TGGATGTATG	TTGTGTGGTG	GGTGTGGACC	AAACAAATTC	480
	AGATGCTGCT	CGATGATGCT	CGGGAAGACC	TGCGATCGAG	ATGTGAGATCA	GTGCGAATG	540
	AAACGCCCGCG	CATCGCAACA	CGATATGTGG	AATACACAGC	GAAGGTACAA	GTGCTTTTGC	600
	CTGATGGGCC	ACATGCTCAT	GCCAGATGCT	ACGTGTGTGA	ACTCTAGGAC	ATGTGCCATG	660
	ATAAACGTGC	AGTAAAGCTG	TGAGAGACAA	GAGAGAGGCG	CAAGTGCCTT	GTGTGCTATC	720
	TGACAGCTCC	GCTCGGCCCC	AAATGGAAGA	GACTGCTTGC	ATATGATGAA	ATGTGCTCTT	780
50	GGTAAAGTCA	TCCTGTCCCTA	CAATGGAAGA	TGTGTGAACA	CATTGTGAAG	CTACTACTGC	840
	AAATGTCAAC	TTGGTTTGA	ACTGCATAT	ATCAGTGGAC	GATATGACTG	TATAGATATA	900
	AATGATATGA	CTATGATGAT	CCATCAAGTGC	AGCCACAGAT	CGAATGCTTT	CAATACCGAA	960
	GGGTCTTCTCA	AGTGTAAATG	CAAGCAGGGA	TATTAAGAGC	ATGAGACTGG	GTGTTCTGCT	1020
55	ATCTCGGAAA	ATTCTGTGAA	GGATGCTCTC	AGAGGACCTG	GTACATCATCA	AGACAGATCT	1080
	AGAGATGTGC	TTGCTCACAA	AAACAGCATG	AAAAAGAGG	CAAAATTATA	AAATGTATCC	1140
	CGAGAACCCA	CCAGCACTCC	TACCCCTAAG	GTGACAGAT	AGCCCTTCAA	CTATGAGAGA	1200
	ATATGTTTCCA	GAGCGGGGAA	CTCTCATGGA	GTTAAAGAA	GAATGAGGA	GAAGATGAGG	1260
	GAAGGGGCTG	AGGATGAGCA	TAGGAGAGG	AGAGAGGCGA	AGATGAGAT	AGAGAGGCGA	1320
60	AGCTCTGGAG	GAGATGTGTT	TTTCCCTAAG	GTGATGAGAG	CAAGTGAATT	GGCGCTGATT	1380
	CTGGTCCAAA	GGAAAGCGCT	AACTTCCAAA	CTGGACATA	AGAAATTAAA	TATCTGTGGT	1440
	GACTGCGGCT	TCATCATGAG	GATCTGTGAC	TGGAACAGAG	ATAGAGAGGA	TGATTTTGAC	1500
	TGGAATCTGT	CTGATGATCA	AGTGTGCTAT	GCTCTCATTA	GTGACATGCC	GGCTGTGGTA	1560
	GGTCAACAGA	AGAGCATGCG	CGGATTTGAA	CTTCTCTACT	CTGACCTGCA	ACCCCAAGAC	1620
	AACTCTCTGT	TGCTCTTTGA	TTACCGGCTG	GGCCGAGACA	AACTGGGAAA	ACTTCAGTGG	1680
	TTTGTGAAAA	ACGTGTACCA	TGCCCTTCAA	TGGTGAGAGA	CCMGAGTGA	GGATGGAAG	1740
	TGAGAGGCTG	GGATGAGCA	CTTGTGATCA	CTGACCAAGG	CATCATATTT	CTTGTGATTT	1800
	CGAGCGAGAC	GTGGCAAGGG	CAAAACCGCG	GAATCGCGAG	TGGTGGGCTG	CTTGTCTGTT	1860
	TCAGCGCTTAT	GTCCAGATAG	CCITTATTAT	GTGGATGACT	GAATGTACTT	ATCTTTATAT	1920
	TTGACTTTGT	ATGTGCTTTC	CCGTGGTTTT	TTGATATTGC	ATCATAGAAC	CTCTGGCATT	1980
70	TGAGATTATC	TAGCGTAAAA	ATTGTATGTT	ACACACAGAA	ATATTATGTT	AGAGTGGCTT	2040
	TCCTGTATGA	GTATGAGCAA	TATTTCCTTT	AAATATATCA	TCATCTATCT	TTTCTGTGTA	2100
	TTTCTGAATC	TTTCCACATT	ATATTATAAA	ATATGGAAAT	GTGAGTTTAT	CTCCCTCTCT	2160
	CGATATATCT	GATTTGATATA	AGTAAAGTGA	TGAGCTCTTC	TCACACAACT	CTTCAGAAAA	2220
	TAGAAAARAA	AGACACAGAA	AGGTTTAAAC	TGTTTGATCT	TATGATATCT	TCTGTGAAC	2280
75	TATGACAGA	AGATAGAGCT	TTTGCCGAGG	TGGCTTAGCT	GCTTCTTTCA	TAGCCAAACT	2340
	TGTATATATA	ATTCTTGTGT	ATAATATATA	TCCAAATCAT	CAAAAAMAAA	AAAAAMAAA	

Seq ID NO: 46 Protein sequence

Protein Accession #: NP_056122

80	1	11	21	31	41	51	
	MLPLRLPALP	LLLSNVAGZF	QNAASNRHG	LLASARQCV	QYVOTGLACC	YDRHNSKGV	60
	DEAKTQRCGE	RLNRSNRCG	RLNPOTKAT	CGDNRHNG	RLNPKQRCV	YHRSYKVC	120
	LSHMLMPDA	TCNRSNRCM	INCQYSCDY	EDRQCLCP	SGRLAPWR	GLDIDRCS	180
85	GVKICPVRER	CNRTGSGSYC	KHLIGFELY	ISGRVYCDI	NKCTMSHTC	SHHAFCHTY	240

WO 02/102235

PCT/US02/19297

GSFKCKCKQG YKNGGLRCSA IPENSVKEVL RAGPTIKDR I KLLLAHKHSH KKKAKIRNVT 300
PEPTPTPTPK VHLQPFYHEE IVSRGNSHSI GKCKMESRHK GLEDEKERE KALANDIEER 360
SLKEDVFPFK VYIAGEPQLI LVGRKALTSK LEHEDLHISV DCSFPHGICT WQOREDDPT 420
WYFAIRERAI GTFADPVALA GHKEDIGRL LLLRDLQPSG HPCLLFHYVL ADEKVGKRLV 480
5 FVMSNNLLA WERTTSDEK NKTGKIQIQL GTDATKSIIF RKRKRGKTS GTAVDGVILV 540
SGLCFDSLLS WED

Seq ID NO: 47 DNA sequence
Nucleic Acid Accession #: NM_005046
Coding sequence: 16...777

1	11	21	31	41	51
GGATTTCGCG	GCTCCATGCG	AAGATCCCT	CTCCTGCCCC	TGCAGATCCT	ACTGCTATCC
115	120	125	130	135	140
TTAGCCCTTG	AAATCGCAGG	AGAAGAAGCC	CAGGGTACAC	AGATTATTGA	TGCGCCGCCA
TTTGCAAGAG	GCTCCACACC	ATGGCAGGTC	GCCCTCTCTA	GTGGCAATCA	GTCTCACTGC
145	150	155	160	165	170
GAAGACCTTC	TGGTATACAA	GCGCTGGGTC	CTCATCTCCG	CCGCTCCACA	GATGATAGAG
TACACCTGTC	ACTCGGCGAG	TGATACGCTG	GCGCACGAGA	GAQCTCAGAG	GATCAAGSCC
175	180	185	190	195	200
TGGAAGTCAT	TCCGCAACCC	GGGCTACTCC	AACAGACACC	ATGTATATGA	CTCATGCTCT
GTGGAAGTCA	ATACGACAGC	CAGGCTGTCA	TCCATGCTGA	AGAAAGTCAG	CTCGCCCTCC
205	210	215	220	225	230
CTCTGGAGAC	CCCTGTGACG	CACCTGTACT	GTCTCTGGCT	GGGGACATAC	CACGACGCCA
GATGTGACT	TTCCTCTGGA	CCTCAATGTC	GTGATGTTCA	AGCTCATATC	CCCCACAGAC
235	240	245	250	255	260
TGCAAGAGG	TTTACAGAGA	CTTACTGGAA	AATTCATGCG	TGTGCGCTGG	CATCCCCGAC
TCCAAAGAAA	ACCGCTGCAA	TGGTGACTCA	GCGGACACCT	TGGTGTGACG	AGTATACCTG
265	270	275	280	285	290
CAGAGCTGTG	TGTCCTGGGG	AACTTTCCTT	TGGGGCCAC	CCAAATGACC	AGGATGCTAC
ACTCAAGTGT	CGAAGTTCAC	CAGTGSKLA	ATATGACACA	TGAAAAAGCA	TGCTTACGCT
295	300	305	310	315	320
CACACTGAAT	TAATTAACCT	TGTGCTTCCA	AAGAAATG	CACAGAGGTG	AGAGAGCCGA
TGACCTATGA	AGTCAAATTT	GACTTTAAGT	TTCCTCAAGG	ATATATTTAA	ACCTCAATCC
325	330	335	340	345	350
CTGTGTATA	ACCAATCAAA	TTGTATAAGG	CCTAAACACA	AAACAAATAA	AGAAACACAA
355	360	365	370	375	380
AAACCTCAA					

Seq ID NO: 48 Protein sequence
Protein Accession #: NP_005037

1	11	21	31	41	51
MARSLLPLQ	ILLLSLALET	AGREAAQDKI	IDAPACARGS	HPMVALLSG	NQLKCGGVLV
35	40	45	50	55	60
NERNVLTAAI	CKNEYVTYHL	GSDTLGRRA	KRIKSKSPR	HPGVSTGYH	NDMLVKLAS
QRLSSHYVK	YLLSERCEPP	GTCTTGVSHG	TTSPEDVTF	SDLACVDVSL	LSQCTVYVI
65	70	75	80	85	90
KLLSSSMLC	AKLSDSRKLA	CMSEGSVPLV	CRGTLGLSLV	WTFPCQSPH	HPGVITQVK
95	100	105	110	115	120
FTKINDTAK	KSR				

Seq ID NO: 49 DNA sequence
Nucleic Acid Accession #: NM_003466.1
Coding sequence: 11...1363

1	11	21	31	41	51
GAATTCGGCG	ATGCTCCACA	ACTCCARGAG	ATCTCCCATC	GGAGGGCTTA	ACCACTCGGG
45	50	55	60	65	70
AGGGSCCTTT	GTGAATGGCA	GAACCTCCGC	GAAGTGGTC	CGCAGGCGCA	TGTTAGACTC
GGCCACCAGG	GGTGTAAAGC	CCTGGACATC	CTCTGCGCAG	CTCCGGCTCA	CCCATGTTTG
75	80	85	90	95	100
CTTCAGCAGG	ATCTCTGGCA	GGTACTACGA	CAGTGGCAAG	ATCCGGGCTG	GAATTAATAG
GGCTCCAGAG	CCCAAGGTGG	CGACCCCCCA	GAATGGTGAAG	AGATTGGGG	ACTACAAAG
105	110	115	120	125	130
CCGAGACCTT	ACCATATTTC	CTCCGGAGAT	CCGAGACCGG	CTCTGGCTGT	AGAGGCTCTG
135	140	145	150	155	160
TGACAAATAC	ACTGTGCCCA	GTGTCACTCT	CATTATTAAG	ATCATCCGGA	CCAAAGTGTCA
GCACCAATTC	AACTCCCTCA	TGACACAGTG	CGTGGCCAC	AACTCCCTGA	GTCCCGGACA
165	170	175	180	185	190
CAAGCTGATC	CCAGGCTCAG	CTTAACTCCC	CCCGAGATCA	CCCAATCTGG	ATTCCCTGGG
CTCAACCTAC	TGATCAATCA	GGCTCTGGG	CATGCTCCAG	CTCGAGACGC	ACAGAGAGAA
195	200	205	210	215	220
AATGATGAC	AGTGTACAGG	ATAGCTGGCG	ACTAAGCAT	GAATCAGAGA	CGACGACGAG
225	230	235	240	245	250
CGACACCGGA	AGGACCTCTC	GCACGGATCC	CTTCAAGCCG	CACCACTCTG	AGCCGCTGAG
255	260	265	270	275	280
GTGCGCAATT	GAAGCGAGCG	ACTACCGAGA	GGCTATAGC	TGCCCCAGCC	ACACCAAGAG
CGACAGAGGC	CTGACCCGTC	TCCCTCTGCT	CAACAGCAT	CTGACGAGGC	GGAGAGCCAC
285	290	295	300	305	310
CTGACCCCTC	TCCAGACCGC	CACCTGGGCG	CAACTCTGCG	ACTCAAGAGA	CTCAACCCGT
315	320	325	330	335	340
GGTGCGAGAT	CTCTACATGC	CTTTCGCCAT	AAAGCGAGAA	ACCCCGAGAG	TGTCAGTCTC
345	350	355	360	365	370
TAGCTCCACC	CTCTCTCTCT	TATCAAGCTC	CGCTCTTTTG	GAATCTGACG	AAATCGGCTC
375	380	385	390	395	400
CGGCTCTCCG	CCCTCCAAAG	CTCTTCCGCA	CTGCTGCTGC	AGCTGAGGAC	ATCTCAAGGG
405	410	415	420	425	430
CCAGCCCTCT	CTCTCAGGCG	GAAGATAGTG	GGGCGCCAGC	CTCCCGGATG	ACCAACCCCA
435	440	445	450	455	460
CATCCGCCAC	ACCGGACAGG	CGAGCTATCG	CTCTCTGCCC	ATCCAGGACA	TGGTGGCAGG
465	470	475	480	485	490
AAUTGAATAC	TCGTGCAATG	CTATGAGCCA	CACCCCTCAT	TCCTCTTACA	GGGAGGCTGT
495	500	505	510	515	520
GGCTCTCCCC	AACTCCAGCT	TGCTGAGTTC	CCCATATTAT	TACATCTCA	CATCAAGATC
525	530	535	540	545	550
GAATGACAGG	CCCAACCACT	CCAAGCCCTT	TGACATATG	TAGTTGAGGC	TT

Seq ID NO: 50 Protein sequence
Protein Accession #: NP_003457

1	11	21	31	41	51
MPHSGIRSGH	GGNLQGLGAF	VNGRPLFEVV	RQRIVDLAHQ	GVRPCDLSGQ	LEVSHGCVSK
75	80	85	90	95	100
ILGSHYETGS	IRPGVIGGSK	PKVATPVKEV	KICGVKQSPH	TNFMARIEDR	LLAGRYCNDI
TVFVPSRIRL	LIRFVGGHTL	NPSPESCVAT	GLSGRSHLL	FGSATVPPSL	PGDSRLGCTY
105	110	115	120	125	130
SINGLGLQAG	PGDKRKQND	SDQDCLRLGI	DQSSSSSGPR	KHLIATDAPG	HLHFLBPCFP
135	140	145	150	155	160
GERQYPEAYA	SPSHTKGEQV	LYPLPLMNST	LDGKATILTP	SNTPGLRNLG	THQTPPVVAD
165	170	175	180	185	190
PHSPFAIKG	TPFVSSEST	FGSLSSSAPL	DLQWGSQVFP	PFNAFPAHS	VYQGTQZAL
195	200	205	210	215	220
LSGRNMGVIT	LRPVIPIHPT	SGTSSASRA	IAGNWAGSEY	SNAGHTITY	SYSSEMMFPL
225	230	235	240	245	250
NSSLLESPYI	YSSTSRFAPL	PTTATAPRLH			

Seq ID NO: 51 DNA sequence
Nucleic Acid Accession #: NM_013952
Coding sequence: 161...1357

WO 02/102235

PCT/US02/19297

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1      11      21      31      41      51
TTGAGGAAGA GAGAGAGCAC GCGGCGCGAG GCAACCTCGC GCGCGCGCGG ACCGAAGCAG 60
TGAGGCGCTG CAGCGCGGCC GCGCAGGCGAG GCGCGCGCGC GCGCGCGCGC TACGCGAGGA 120
AGCGCCGAGC CCGCGCGGCG CTGCGAGCGA CTCGCCGCGG ATGCGCTACA ACTCGATCAG 180
ATCTGCGCAT GAGAGGCTGA ACACGCTGGG AGGCGCTCTT GGAATAGGCA GACCTCTCCG 240
GGAATGTCCT GCGCGCGCGA TCGTATAGCT GCGCGA CAG GGTGATAGGG CCGCGCGCTG 300
CTCTCGCGAG CTCCGCGCGA GCAATGCTCT GTCGACGAG ATCTCTGCGA GTGATACATA 360
GACTCGCGAG ATCCGCGCTG GAGTCATAGG GGGCTCCAGG CCGCAAGTGG CTACCGCCAA 420
GGTGGTGGAG AAGATTGGGG ACTCAAAAC CAGAAACCCCT ACCATGTTTG CCGCGGAGAT 480
CGCAGACGCG ATCTGCGCTG AGGCGCTCTT TGCAATATAC ACTGTGCGCA GTGCGAGACT 540
CATTAATAGA ATCTGCGCGA CCGAAGTGGC GCAACCATTC AACCTGCTCT TGGACAGCTG 600
GTCGCGCGCC AAGTGCCTGA GTCCCGGACA CAGGCTGATC CCGACATGCA CTGTAACTCC 660
CCCGGAGTCA CCGCATCGGG ATTCGCTGGG CTCCACTATC TCGATCAATG GCGCTCTGGG 720
CATCGCTCAG CCGCGCGAGG ACAGAGAGAA AATGATATGC AGTATATCAG ATAGCTATCC 780
ACTAAGATCT GACTCAAGA CCGAGAGCGA CCGACCATTC AACCTGCTCT GCGCGAGCTG 840
CTTCAGCGAG CACCATCTGG AGCCGCTCGA GTGCCCATTT GAGCGCGAGC ACTACCGAGA 900
GGGCTATGCC TCCCCAGGCC AACCAAAGG GAGCAGAGGC CTCTACCGCG TGCGCTTGCT 960
CAGCAGACCC CTGAGCGAGG GGAAGGCGAC CCGCAGCCCT TCGCAACAGC CAGCTGGGGG 1020
CAACCTCTCA ACTCAGCGAG CCGTACCCCT GGTGGCGACT CGCCCTCTTT GAGTCTGGAG 1080
CAAGTCCGCT CCGAGGCTGC GCGCTTCAAT GCTTTTCCCG AATGCTGATC CGTGTACGGG 1140
CAGTTCAGGG GCGAGGCGCT CTCTCAGGG CAGAGATATG TGGGCGCCAG GCTGCGCGGA 1200
TACCGAACCC ACATCCCGCC CAGCGCGAGC GCGAGCTATG CCGCTCTCCG CATCGAGCGC 1260
ATGGTGGCAG GAAATGAATA CTCTGCAAT CCGTATGGCG ACACCGCTCA CTCTCTATC 1320
AGCGAGGCT GGGCTCTCC CACCTCGAGG TTCTGAGTT CCGCATATTA TTAGATGTC 1380
ACATCAAGCG CGAGTCACCC GCGCCACACT GCGAGCGGCT TTGACATCT GTAGTTCGA 1440
TGGGACAGT G

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Seq ID NO: 52 Protein sequence
Protein Accession #: NP_039246

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1      11      21      31      41      51
MPEHSHISGR GGLMGLGAG VNRGRLEFV RQRIVDLAHQ GVRPCDLSRG LRVSHGCVSK 60
ILGRYVETGS ITRPVIGGSK PKVATPEVVE RIGDYKQHP TMEANERDR LLAGVGCND 120
TVPSVSSINR IIRTKVQPPF NLPMDSCVAT KSLSPGHTLI PSSAVTPES PQSDSLGSTY 180
SINGLIQTQI PGGSKRKGDD SDDBCKLSI DSGSSSSKGR NKLRTDAPSQ HMLPELCFF 240
BRHYHPEATA SPRTGRTGRT GGLLEHLSH GGLGKATLPF THTPTVPIVA THTPTVPIVA 300
PFTVTCSEA PSFPMFPPF MLPPCTGSSR ARFSSQGERH WQPCFPTH TSPPADRAM 360
PPLPQJAWG EYNTLMPPIA TPTPTPTAR GASPTFAC

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Seq ID NO: 53 DNA sequence
Nucleic Acid Accession #: NM_012427
Coding sequence: 43..524

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1      11      21      31      41      51
CTTGTGGTTC CTCTCTACT GGGGAATCA GGTGCAGCGG CCAATGGTAC AGCAAGACCC 60
CCCTGATGTT GGGTGGCTG TGCTCTGATC ACAGCCTTGC TTCTGGGGT CAGCAGAGAT 120
GTCTCTGCCA ACAATGATGT TTCTCTGAC CACCCCTCTA ACACCTGACC CTCTGGGAGC 180
AACCAAGACC TGGGCGTGGG GCGCGCGGAG GCGCGCGCGT CGGATGACAG CAGCAGACCG 240
ATCTCATATG GATCTCACTG CAAATATGCA ACCACGCGCT GAGAGCGGCC CCGTCTGCTA 300
AGGCGCAAGC AGCTCTACTG GGGGCGGGTG TTGGTGATCT CACAGTGGCT GCTCAAGGCG 360
GCGCCATGCA GGAAGAAATG TTTCAGATCT GGTCTCGGCG ACTACTCCCT GTACCAAGTT 420
TATGATATCT GCGGCGAGAT GTTCCAGGGG GTCAATATCA TCGCCCGACC TGCTACTCTG 480
CACCTTGCGC ACTCTAACGA CCGTATCTCT ATCAACATGA ACAGAGAGAT TGTTCGCACT 540
AAGATATGTA GACCATATCA GGTCTCTCTT CMTTCTCCCT CTGCGAGGAC AAGTCTCTGG 600
GTGTCTGGCT GGGGACACAC CAGAGAGCCC CAGTGCATCT TCGCTAAGGT CCGTCAATGC 660
TTGAATATCA GCGTCTAGAT TCAGAAAGAG CGAGAGGATG CTTACCGAG ACAGATAGAT 720
GAGACCATGT TCGGCGCGGG TGACAAAGCA GTTAAAGACT CCGCCCGAGG TGATTTCTGG 780
GGGCTGATG TCTGCAAGG CTCCCTCGAG GAGCTCTGCT GCGCGCGGCA TCAACTCTGT 840
GCGCGCGGCC ACAGCAAGG TGCTCATACG AACCTCTGCA AGTTACACA GTGATCCAG 900
GAACACATCC AGGCGCAACT CTGAGCTATC CAGGAGCTCA GCACACCGCG ATCCCACTCC 960
CGTCCAGGGA CAGCGCTGAC ACTCTCTTGA GACCTCATAT CTTCCGAGA GATGTTAGAG 1020
ATGTTCTCTC CTGCGCGGCC TGAACCATGT TCTCTCGAGC TCGAGGCTGT CTTCGCGAG 1080
ATTGGCGTGA CGTGTCTCTT CTAGTTGAC CCGGGAACA ATTTCCAAA CTGCTCAGGG 1140
CGGGGCTTGC GTCTCAATCT CCGTGGGACA CTTCTATCT CAGGCTCAGG GCCATCTCT 1200
TCTCTCGAGC TCTGACCCAA ATTTAGTCCC AGAATAAAG TGAGAGATGG AAAAAAAAAA

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Seq ID NO: 54 Protein sequence
Protein Accession #: NP_036559

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1      11      21      31      41      51
NATARPFPWM VLCAITALIT LGVTEIVLAN MYSKDHPSN TVPSSSNQBL CAGAGEDARS 60
DDSSSRING SDMDMTQWV QALLLRFPQ LYCVAVLHP QMLTAARCR KEFVEVRLHG 120
YSLSPVYESG QMPQGVKSI PIPQYSHFH SDMLAKLIKI RIRIPTKDR PINVSHCPB 180
AKTCLVSGK GTTSPQVHF PKVLQCLMS VLGRKCEBA YPRIDIDTFM CAGKAGRGS 240
CGDGGGPRV CNGSLQLVW WSDYPCRFN EKNVYTLCK FTKMIGTQT AHS

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Seq ID NO: 55 DNA sequence
Nucleic Acid Accession #: NM_002214
Coding sequence: 681..2959

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1      11      21      31      41      51
CCGAGACGCG CTTCTCCGCT TTGCTGGCAT CCGGAGCTTC CTCCCTTGCC AGCAGGAGG 60
CAGCGACATC GTCTCTGCCC GTCGCTCCGC AGACGGGCT CCAAGCTCC ACTATATGT 120
GTGGGCTTCC CTCCACACT GGGGAGGCA CTCGCTCAT TTGATGGCCA CAGACTTTT 180

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WO 02/102235

PCT/US02/19297

TCCCTCTGAC CTCGCCGGGG TACCCTCCCA CAGATCGAGC ATCACCCAGT GAATGTACAT 240
 TAGGGTGGTT TCCGCCCCAG CTTCGGAGCT TGTGTGGGTT TGATTGTGTT TGGCTCTTGG 300
 CTAAGCTGAT TTAACGACGA GACCGCCGAC CGGCTGAGGA TGACCTGATG TGGCTTTGCT 360
 TGTCCCGGAG CAGGCTCGCG ACCCTCTGCA GAGCCCTCTC TCCAGTGGCC GCGCGGCCCT 420
 TGGCCCTGGA AGGAGTGCTT TCTCGGAGG ACCGGGSGAG CGCCCTGGCC GAGCCCGGAG 480
 GCGCTTGGGG GCGCTTAGAT GCGGAGGGGT GCGCGGSCCC GCTTACCTGC ACCCGTGTCT 540
 CGAGCCCGCG TGCGCGGCTT CTAGCGGCTT CGGAAAGGCT CCGACGACA CTCCCGCCG 600
 GCGCCCGAGG TGCGCCCGGA GCGCCGAGCT GCGTCCGAAA GCGACCGGAG CGCGCGCGGC 660
 GGGGGCGGCT GTTTTTCCT ATGTGCGGCT CGGCGCTGGC TTTTITTACC GCTGCAATTG 720
 TCTGCCGCGA AAACGACGCG CAGAGTCCCG CTGCTGTGCT CTGGGAGGCC TGAGTGTGTT 780
 CACTGTGCTT TGGCCTGGAG TACGAGGAG TCGTCTGCTT GAGCTGATG TATTTGCTAT 840
 CTTGTGACAG GTGCTGCTT CTGSGTCGAG ATATCGAGAT GTTGCTGCAA GAGGATTTCA 900
 TTTCACTGAG ATCAGAGAGT GACGTTGTGT ATATTGTTTC CAATTTAATA AGCAAAAGCT 960
 GCTCACTGTA TTCAATGAGA TACCATTGCT TGCATGTTAT AATACCCACT GAAATAGAAA 1020
 TTAATACCCA GGTGACACCA GGAAGAGTGT GTATCGAGCT GCGTCCAGGA GCGCAAGCTA 1080
 ATTTTATGCT GAATATGATG CTGTGAGAGA AATATCTGTT GAACTTTTAT TATCTTGTTG 1140
 ATGTCCTGAG ATCAATGACG AATAATATAG AAAAATTAAT TTTCCCTTGA AACCATTTAT 1200
 CTAGAAAAAT GGCATTTTTC TCCCGTGAAT TCTGCTTGG ATTGGCTCA TACGTTGATA 1260
 AATCAAGTTC ACATACATAT AGCATCGAGC CGGAAAGGAT TCATAATCAA TCGCATGACT 1320
 ACATATTGCA CTGATGCTCT CCGCATGAGT ACATCATGTT GCTGTCTTGG ACAGAGAAC 1380
 TCACTGAGTT TGAGAAACCA GTTCAATGAG AGAAGTCTCT TGGAGACATA GATACACGAG 1440
 AAGGAGGTTT TGACGCCATG CTTCAGGAGC CTGTCTGTGA AATCATATCT GAGTGGGAAA 1500
 AAGAGGCTAA AGATATGCTG CTGGTGATGA CAGATCGAGC GTCTCACTCT GCTCTTGATA 1560
 GCAAAATTGG AGGCTAGTGT GTGCCCAATG ACAGGAAGCT TCACTGTGAA AAGAAAGTCT 1620
 AGTCGAATC GACGACGATG GACACCGCTT CACTAGGCCA ACITTGAGAG AATTAATAG 1680
 ACAACACAT TAAATGTGAT TTTGCACTTC AAGGAAACCA ATTTCAATG TATAAGATCT 1740
 TCTCAACCTT CTTCGCGAGC ACCATGCTGT GTGAATAGTA ATCAAAAGCT GCAAACTCTA 1800
 AFAATTGTT AGTGAGAGCC TATCGAGAGC TCAATTCGAG AGTAAAGTGT CAGGTGGAAA 1860
 ACCAGTACA AGGATGAGT TTTAGATTGA CGTCACTCTG TCGAATGAGG TCGGAGAAC 1920
 CAGGCACTGA AGGATCGAGA AAGTGAGCA GAAATGATGA AGTTCTTTTC AATGTACAG 1980
 TTAACATGAA AAAATGTGAT GTCACAAGG GAAJAAACCTA TGCAATATCT AAACTATTG 2040
 GTTTTAATGA AACCGTAAA ATTCATATAC ACAGGAAGCT CAGCTGTGAG TGTGAGACCA 2100
 ACAGAGGAG TAAATGATGT TGTCTGATGA AATCTGTGTA AAGAGTAGAC TTTCTTCTGT 2160
 GTGATGAGTA TAAATGTGAT TTTGATGAG AGATGCTTTT TGTGAGAGT TGCAGTAC 2220
 CAGAGATCA GCTGTTTTCG ATGTGTCGAG GAGTITGTGT TGTGGGAAA TGTTCATCT 2280
 ACAAAATTA GCTGTGAAA GTGTATGAAA AATCTGTGTA AAGAGTAGAC TTTCTTCTGT 2340
 CATGTCACA TGGATGAGT GCTGTGCGC ATGTCAGGCG TGAAGAGGCG AGATGCCAT 2400
 GCTTCAAGTG CTGGAAGAGT GATCATGCC AGTCCGCTTC AGCAGCGGCC CAGCATCTG 2460
 TCAATTCAA GCGCCAGGTT TGCACTGUGA GAGGCAAGTG TGTGTGGA AGGTGTGAT 2520
 CAGACGATCC CAGACGATCT GCGCGCTTCT GTGAGACGCT CGCACCTGTT TATACAGCT 2580
 CCGAGAAA TCGATATGCT ATGCAATGCG CTTCAGCTCA CAATTTGCT CAGCTATAG 2640
 TTTGATGAG CAAACCTCA TGTGCTTCCA TGGACAAACA CAGTATGTC GACCAAGCT 2700
 CAGATGTTT CTCACGCCA AGCTACTTGA GAATATTTT CATCATTTT ATAGTACAT 2760
 TGTGTGAT GTGCTTAA GTCTGATCA TTAGCAGAGT GATACTACA TGGATAGTA 2820
 ATAAATATA GTCTCATCA GATTACAGG GTGCAAGCTC AAAAAGGAT AAGTGTGCT 2880
 TCGAAGGTT GTGTCAGGA GCGTCACTT ACCGAGGTA GAGTCTTCA GATATATAA 2940
 TGGATATGAG CAATTAATAT GCTCATGAAA CTTTCAAGTG CAACTCTAA AAAAAGATT 3000
 TTAACACACT AATGGGAAC TGGATTTGT AATATATGCT CCTAAAGATT ATATTTTA 3060
 AATGTCAGG GAGGACAAA TTGCTCAAG CTATGCAAGT TCTGTGTTGT ACATCGAG 3120
 GAGACGAGC AAGTATGCT ATCATGATG GACTCAATA CTGCTGACT TTTTGGAGA 3180
 AATATGTGCT TTACTACTGT TTGAGATAG TGTGTTGTA GCATTTACT GTATATATA 3240
 ACTTATTTAG ATCAGCATAG AATGTAGATC CTCGAAAGG CACTGATTAC ACTTTACAG 3300
 TAAGTGTAT CCGTAGGCTT CCGACAGAGA ACATATGCT GAGGAGTTT AGCATGTGT 3360
 CACTACAGG GTACATATAT CCGTCACTG GACTGTGAG GAAATATA ATCGCGAG 3420
 TATATCTAA GTTGTGAAA CACTTCAACA GTGTGTGTT GATAGACAA GAKACGTAG 3480
 ATGATATAAT GATTGCTGT TCACTTTTC AAGAGTGGA CAGATACAC CTTAATCTTA 3540
 AAGATTAT CTCTTTTAAA GTGTGTAGT TTATCATGCT GTGTTATAG TGTCTTAT 3600
 TTTGAGAT GATACTAAT GTGCTGATTC TCTCTCTAT GTGTTTGT TGTGTTCT 3660
 TTTTATCG ATAGTATG GTATGATCA GAGCATGGA TTAATATG GTCAATATAC 3720
 TACTGCCATA AAAATCTAAT AATACAATG CACTTATCA GATATAGT TTTAAAGCT 3780
 GATGTGTA

Seq ID NO: 56 Protein sequence
 Protein Accession #: NP_002205
 1 11 21 31 41 51
 | | | | |
 MCGSLAFFT AAVFVCLNQR RPPASFMAWA VVFLSLHLGL QEDKRCASS NAAACAPCLA 60
 LQPCENQCV EDFISQSSB ERCDIVSNLI SKGCSVEGIE YPSVEVLIPT ENGINTQVPT 120
 GVSIFQLRPG AARNFMKLVH PLKKYVVDLY YLVDVSGMHI NHIKJINSVG NDLSEKNAFF 180
 TATRLFGFOS YLTKVSPYI SIHPERIHQ CSDYMDACWP PIGYIVLVL YBNITFEKA 240
 VHEKIGSHTI LQVDFGSEH LGAVGNSHTI GNSKRSKRLI LWDVTSYL ALDSELGAV 300
 YPHDCHILK DNYVYSKTH SIPLSQLQSE KLIDNNHVI FAVGQKQFHV YDPLFLPLG 360
 TIAGEIESKA ANIANLVVVA YQKLISHVK VQENVGQIY FNITAICPDG SELKPMGECR 420
 NVDSNEVLEF RVTVTHKKDG VTGKGYALI KPIQNPBETK IIRHNSCSQJ CENMHPKEQ 480
 CUDTFTLDKQ CFQGDGEMH FDSHQFSSB KSHSDQVPC SIKGSGVQCE CSHKILK 540
 VYGVYKSD FSVYVHSHI CAGHSEAG KCPHSEKSG DKCYQFSAH QCVMSKQW 600
 CGBGTGVCQG RCECTHPST GRHCCEPTC TYACKENWNC MQLHFBNLS QALLQAKCS 660
 CALMEQHYV DQTSCEPSP SYLRIFPIF IVTFVLGLK VLIIRVILQ NNNKIKSSS 720
 DYRVASBKD KLLIGSVCTR AVTYREKPE EIKMISKLAN AHETBCNF

Seq ID NO: 57 DNA sequence
 Nucleic Acid Accession #: NM_001719
 Coding sequence: 123..1418
 1 11 21 31 41 51
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 85

WO 02/102235

PCT/US02/19297

5	GGGCGACGG	GGGCGGCTCT	GGAGCAATGG	ACCGACGACC	GGAGCGGCGG	CTTGCCCGCT	60
	CTTGCACTGG	GGGGTGGTCT	GGCTCCGAGC	CGGAGCGCTG	GGTACGCGGT	AGAGCCGCGG	120
	CGATGACAGT	GGCTCACTGG	CGAGCTCGGG	CGCGCCACAG	CTTCTGGGCG	CTCTGGGCGAC	180
	CCCTGTTTCT	GGTGGGCTCC	GGCTTGGCGG	ACTTCAGCCT	GGACACGAGG	GTCACACTCGA	240
	GCTTCAAGTCA	CGGCGGCTCT	CGACGCGAGG	AGCGCGCGGA	GATCGACGCG	GAGATCTCTT	300
	CGATTTCGCT	CTTCCGCTCG	CGCCCGGCGC	CGGACCTCTG	GGGACGCGAC	AACTCGGCGC	360
	CGCATTTCAAT	CTTGAGGCTCT	TACAAAGCCA	TGGCGGTGGA	GAGGGGGGCG	GGGCGGCGCG	420
	CGAGGGGCTT	CTCTCACTCC	TACAAAGGCC	TCTTTCAGTA	CGAGGGCCCC	CTCTGGGCCA	480
10	CGGCGAGGA	TAGCAATTTG	CTCAACGAGG	CGACAAATGG	CATGAGCTTC	GTCACACTCG	540
	TGGACAGTGA	CAAGGCTGTC	TTCGACGAGC	CTGACGACCA	CTGAGATGTC	CGGTTGATGC	600
	TTTTCAGAGT	CTCCAGAGAGC	GAACTGTGTA	CGCGAGCCGA	ATTCGCGATC	TACAGAGACT	660
	ACATCGCGGA	AGCGTTGCGA	AATGAGACCT	TCCGATCGAG	CTTTATTCA	GTCCTTCAGG	720
	AGCACTTGGG	CAAGGAATCG	GATGCTTTCC	TGCTCGACGG	CGGTACCCTC	TGGGGCTCGG	780
15	AGCAAGGCTG	CTGATGTTGT	GGAGTCAAGG	CGACCGACAT	CGGATCGGTG	GTCATCTGCT	840
	GGCAAGCTCT	GGGAGTCTAG	CTCTCGTTGG	AGGACTCTGA	TGGGCAAGCG	ATCGACACTTA	900
	AGTTTGGGCG	CGTGAATGGG	GGGCAAGGCG	CGCGAGAACG	GACGCGCTTC	ATGTTGGCTT	960
	CTTTCAAGCG	CGACAGGCTC	CAGTTCGCGA	GGAATCGGTC	CAGCGGAGCG	AAAGACGCGA	1020
	GGCAAGACCG	CTCTAGAGCG	CGGAGAACCC	AGGAAGCCCT	CGGATGTCCT	AGACGCGGCA	1080
	AGACACGCG	CAGCGACCGG	AGCGAGGCTC	GTGAGAGAGA	CGAGCTTTTA	GTGCTCTTCC	1140
20	GAGCACTGGG	CTGGGCGGAC	TGGATCATCG	CGCTCGAGAG	CTACCGCGCC	TACTACTGTG	1200
	AGGGGGAATG	TGGCTTCCTC	CTGAATCTCT	ACATGAAGCC	CACCAACGAC	GGCATGTGCG	1260
	AGACGCTGGT	CGACTTCATC	AAAGCGGAAA	CGTTGCCGAA	CGGCTCTGCT	GGGCCACGAC	1320
	AGCTCAATCG	GATCTCGCTC	CGACATCTG	ATGACGAGTC	GACGCTCATC	CTGAGAGATT	1380
	ACGAAJACAT	CGTGGTCCGG	GCTCTGGGCT	GGCACTAGCT	CTCTCGAGAA	CTCGAGACCT	1440
25	TTGGGGCCAA	GTTTTTCGTG	ATCTCCATCT	CGTCCGCTTG	CGCAGGAAAC	AGCAGACCAA	1500
	CTGCGCTTTG	TGAGCACTCT	CGCTCCCAT	CGCCACATTT	AAAGTGTGTA	GAGTATTAGG	1560
	GACATGACAC	AGGATGATCA	TGTTGATGAG	CTTTCGATGG	CGACATCCGA	ATGAAACAGA	1620
	CTCTCAAGCG	TGTGAGAGCA	AAACTCATGA	CGAAJAAJAA	ACAACGCAT	AGAAJAAATG	1680
	CGCGGCGCAG	CTCATTTGGT	GGGAAGTCTC	AGCAATGCAC	GAGCTCGTTT	CGAGAAGTAA	1740
30	TTATGAGGCG	CTACAGCGCA	GGCCACCGAG	CGTTGGAGAG	AGGGGGGCGT	GGCAAAGGGT	1800
	GGGCACTGCT	GTGTCGTGAC	GAAGAAGAAA	TTGACCGGGA	AGTTCTGTGA	ATAAAGTGTA	1860
	CGTAAAGAGC	AATGATGT					1920
35	Seq ID NO: 58 Protein sequence						
	Protein Accession #: NP_061710						
	1	11	21	31	41	51	
	MHVRSLRAAA	PHSFVALNAP	LFLRLSALAD	FSLDNBHVHS	FHRRRLRSQE	RRRQRRRLS	60
40	ILGLRHRPP	HLGRKSNRAP	MMNLQLYNAM	AVRSGGGGPG	GGSTVPYKAR	FSTQPPPLAS	120
	LGRSHRPAAT	GGTGRFPFIR	THRRRPFPLD	SLRRPGRGAT	RRRRRLRRLD	RRRRRLRRLD	180
	IRRRFRRRT	RISVTVQLGR	HLRRSLDLFL	LDRLRLWASS	RRRRRLRRLD	RRRRRLRRLD	240
	IRRLGLQLSVE	TLGGGSLNPK	LAGLIRRHDP	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	300
	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	360
45	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	420
	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	480
	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	540
	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	600
	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	660
	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	720
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	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	1140
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	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	1320
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	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	RRRRRLRRLD	1440
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WO 02/102235

PCT/US02/19297

TCCTGGAGCCC GACCAAGCTG GGAACCAAGA TCACACTCTT CCGAATATGC TCCTCGGTGA 2100
 TCCTATGAGT GGCCTCCGAG GACTCAGGCC GACTACACTGT CATTCGAGGC AACACGCTCA 2160
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 AGGCGCCCTGG GAGCCCTCCC CCGTCAAGA TGTACGAGAC CATGSGTGTG TGGTGGGGTG 2280
 CCGCTGTGGC CTACATCATT GCGGTGCTGG GCTCATGTTT CTACTCGAAG AAGCCTCTCA 2340
 AAGCCACAGG GCTCGAGAGG CAGCCCGAGG GCGAGGAGCC AGGATAGAGA TGCCTCAAGC 2400
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 GAGAGTGA CAGCTCAGC GTGTCTCGGC TCGTGGGCTT GTCCCGGAGG GCTGAGCCCT 2760
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 GCTGATGTCT CCGCCAGGCC ATCTCGGAGG GTGACTTCTC TACCAAGTCT CATGTCTGGG 3120
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 CTCTCTCTCT ATACAGGCA GGTGTGGTGC CAGAGGTAC CCGAATTTCT GCGCTCTAC 3660
 CTCTCTCTCT AGCTCTGCGT AACTCTGCTA CTGCTGCGC ACCTTCTCT GGGAGAGGCT 3720
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 TCGACCTGG GCTGTGGTGG AGGGGTGGGC CTTGGAAGT AGGAGGGTGG 4080
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 TGTTTTGT TTTCACCTG CTGCTCTCAA TAAATAGCC TTTTITA

Seq ID NO: 60 Protein sequence

Protein Accession #: NP_002812

40 1 11 21 31 41 51
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 NGARSGSPAR PRRLPLSLV LLLPLGGTGT AIVFKQPSR CDALQRRAL LRCEVASGPG 60
 VHYVLLDGA EVQCTERRFA QSSSLFAAV DRDQSGTFF CVARSDVTE EARSANASFM 120
 IKWIRAGPVV LKRPASEABI QPQTQVTLAC IIDGHERPTT QMFDRTPLS DQSHHTVSS 180
 45 KRNULTRPA OPRBSGLNSC CAGAGAGGAC SSGNFTLTA DSRPARVYLA PQDVVYATE 240
 EMHFQGPFA OPRBSGLNLF EDPFTTMS RPYELARATY FANELLRLO VSRPMAGIYR 300
 CTGQGQRPFF IILEATLLLA EIEDMLPFLF RPYTAGSEER VTCLPPKGLP PPSVEMVYAG 360
 VRLPFGHRYV QKGELVLVAN IASSDAGVYT CHANLAQOR RODNVITAT VPWLLKPGPD 420
 50 SGLBEKRPY LDCLTQAPLE PTVVYVYHNM LISEDSEFEV FNSGLTILS VEDTDTMYR 480
 CWSPTPAGSI BAPAYVQILE KLETPFPFG QCGHEFELK TYPICAPRE EPTFKMERAD 540
 GSSLPHNVID NAGTLHFARV TDDGAGHYTC IASNGPQGI RAHVLTIVAV FITFKVEPER 600
 TTVYQHTAL LQCEAGQDPK PLIQWKKGR ILDPYTLGPR MHIPQNGSLV IHDVAPEDSG 660
 RYTCIAGNSC HIGHTEARLY VDKFVPBES DPGSRPFYFY NIQTIGLSG AAVALIIDL 720
 55 GHPYCKSC KAKLKAQPE GEPSEKELN GGLPAGQPG ALGEPVALT SLOGPANTV 780
 KRSTSDKSGI FRSSLOVIT TLQSEPFQEV FLAKAGLES GVATLVLAK SLOTEBDOO 840
 LDFFREELMG KRLNINNVRL LGLCLRAEP HYHVLVVDL GDLAQFLAIS KSEDKLESQ 900
 FLSTKQKVAL CTQVALSHEN LBNHRPVKD LAARNCVLSA QRQVYSALQ LSKDYINSEY 960
 YHFAKQVWL RMRSPALLS GDFSTKSEW AFVULMHQVY THGNHFGQD ADEVLADLG 1020
 AGHARLQPE GCPHSLMLA CRNALSPFD RPFSEIASA LGSTVDSKP

Seq ID NO: 61 DNA sequence

Nucleic Acid Accession #: NM_006103

Coding sequence: 29..406

65 1 11 21 31 41 51
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 GAGACAGTGG GGTGCGCCCG AGCTCCAGGC TGACCAAGAC TCACAGCAG AGTGCTGTCTC 180
 GAGCAGCGAA TGGCGGACA ACCTCAGATC CCGGACGCC GCGTCTGCCA CTTCTCGACT 240
 70 TCTCTGCCCA AATGATAGAG AGGTTTCTCT CCGCCAGGTG ACATTAATCT TTCCGAGACT 300
 GCGCTCTCTG GCGAGAGGCG GCGAGAGAGA CCGTCAAGTGT CTGAGCAGA TGAATATCT 360
 CCGAGATGCG TGTGGAAGG TGTCTGTGT CACTCCCAAT TTCTGAGTCT CAGCCACAGC 420
 CAGCTCTUAC AGTGAAGAGA GAAAGTTTCT GCGTGGCCT CAGTCTGTT CAGAGCCACC 480
 75 TGCCCTCCCC TTTTCGGGA CTCGTATATC CTTCTGGGC TGACACAGC TTTCCTCTT 540
 CCGACCAAT AAGTAAACCA CTTTCAGAGA AAAAAAANA AATA

Seq ID NO: 62 Protein sequence

Protein Accession #: NP_006094

80 1 11 21 31 41 51
 | | | | |
 MPRAGPLGA RALLLSLLF GFTLVSGTGA RKTGVCPBLQ ADQNTQRCV SDGBCADNLK 60
 CCSAGATFC LILCPNDKSS CPQVNTNFPQ LGLCRDQCV DSGCPQMKC CRNGCGKVC 120
 VTFHF

85 Seq ID NO: 63 DNA sequence

PCT/US02/19297

1 11 21

Seq ID NO: 65	DNA sequence	11	31	41	51	
	Nucleic Acid Accession #: NM_006475.1					
	Coding sequence: 26..2538					
55	11 31 41 51					
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	TGTGCTGTA GTTGTAAACC TATAAAGCC ATTCATCTG CTGCTGCTG	180	200	220	240	
	ACCAAAAGAG AATATCTACG CAGCTGTATG AGCTGTATGA AATAGTCAT	240	260	280	300	
	AACAGACTG TTTTATATAT TGTATGCGCT GACTGATGTA GAATGAAGAC	300	320	340	360	
65	TGCTCCAGAG TTTTGGCCAT TGACATCTAT TATGCGAGTC TGACATCTAT	360	380	400	420	
	ACCAAGAGC TGTGACAGAG TGTACAGCTG TGCGACAGTC TGATATCTG	420	440	460	480	
	TTCACTACTC TGTCCAGCGA TGTACAGCTG TGCGACAGTC TGATATCTG	480	500	520	540	
	GTTTTCGACA GTCAGCTGGA TGTGTAATTA TCGATATCTG TACATCATTA	540	560	580	600	
	AGAGATATAT TGTGCTGGA TCTTAAGAAAT GCGATGATTA TCTTCTCAT	600	620	640	660	
70	TTCTCTCTTT TGTGCTCTAT TCTTAAGAAAT GCGATGATTA TCTTCTCAT	660	680	700	720	
	ATCCATGGGA ACCAGATCTG CAAAGATGCT GTATCTCATG TCTTCAAGCG	720	740	760	780	
	CAATATGAT CCTCAATATG AGCATCTTCT GATGACAGAG ATGA CATTCT	780	800	820	840	
	GCGATCGGTA TGTCTCTGGA CATTTATGAG CCGCTTGACA TCTTCTCTA	840	860	880	900	
	CGCTCCGCGA TGTCTCTGGA CATTTATGAG CCGCTTGACA TCTTCTCTA	900	920	940	960	
	GNGACAAAG TGCCTCTGCT AGCTATCTGA AGTACACAGA TCTTAAATAC	960	980	1000	1020	
75	TCTTGATCTA TGTCTCTGAT AGCATCTTCT GAGACAGCTG AGGAAATATA	1020	1040	1060	1080	
	TGTGCTGCGG GTGATCTGAT AGCATCTTCT GAGACAGCTG AGGAAATATA	1080	1100	1120	1140	
	ATGATATCTG ATGATATCTG AGCATCTTCT GAGACAGCTG AGGAAATATA	1140	1160	1180	1200	
	CAATTTATCT AGCTCCGCGT AAACACAGTA ACGCATCTCT CGGATCTCTA	1200	1220	1240	1260	
80	GCTCTTGCAT TCTCTCTGAG GGCATCATGA GATACACTCT TGTCTCCAGC	1260	1280	1300	1320	
	ATGATATCTG ATGATATCTG AGCATCTTCT GAGACAGCTG AGGAAATATA	1320	1340	1360	1380	
	CACATATCTG CAAATTAAGT TGGCTCTTAT GAGCTTATATG AGCGCAAGAT	1380	1400	1420	1440	
	ATCGAGAGCA AACAGCTAGC AGTCTCTGTA TTTCTATCAG CTGTCTCGAT	1440	1460	1480	1500	
	TGCTGTGAGC TGTGCTGAGC GCAGAGAGAG AACCTGTGCA TTCTACATAT	1500	1520	1540	1560	
	CCATGACGAG CAGAGATAGC TGTGCTGAGC TGTGCTGAGC TGTGCTGAGC	1560	1580	1600	1620	
85	TCTGTGAGC TACTGAGAGC TGTGCTGAGC TGTGCTGAGC TGTGCTGAGC	1620	1640	1660	1680	

WO 02/102235

PCT/US02/19297

ACATTATTGG TGCACCAACA TGATGCTTTT AAGCGAATGA CTAGTGAGAA AAGAAGAAAT 1680
CTGATACGGG ACAAAAATGC TCTTCAAAAC ATCATCTTTT ATCACTGAC ACCGAGATT 1740
TTCCTGGA AGAGGTTTGA ACCTGCTGTT ACTACATT TTAAAGCAAC ACAGAGAAC 1800
AAAATCTTTC TGAAAGAAAT AAGTGAATGA CTTCTGGTGA ATGAATTGAA ATCAAGAGA 1860
TCTGACATCA TGACAAACAA TGTGTGTAAT CATGTTGTAG ATAACTCCT CTATOCAGA 1920
GACACACCTG TTGGAATATGA TCAATCTCTG GAATACTATA ATAAATTAAT CAATATACAT 1980
CAATTAAGT TTGTTGTGTA TGACACCTTC AAGCAAACTC CCGTACGCT CTATACACT 2040
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ATTATCAAAA CTGAAGGAGC ACACATAACA AAGTCAAAA TTGAAGGTGA ACCTGAATCT 2160
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GACGAATA TTAACGCTGT TGAATATGAA TACATAGTGA TTCTATCTGG ACCTGAGAA 2340
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ACAGAGAGC AATCATCAAA TAATTCGAAA CACAATTTTA ATATTTTTT TCTGAATGA 2700
GAAACATGAG GGAATTTTGT GAGTGAAGCT CCGTGGTGA AGGAATTTGA GAAATATATA 2760
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CCATTGAAA GACCGAGCT TGTATGTATG TTATGATACA ATAAATGCA CCGAAGCCT 2940
TATCTTCCA TGGAGAGCTA AGTTATATAA ATAGTGCTCT GGTGTACAAA ACTTTTATA 3000
TCGAAGGCT TTGCATTTT CATATATGAT GGTATTCTG GAAATATATG TTATTTTATA 3060
25 TCTCAAGCT TTGATCTGA GAATTTTGT GATATCTCT TTGCAATGA TATTTTATA 3120
TCTCAAGCT TTGATATAA CCAATTTTCA GATATAAGA GAATTACTTC AATTTAGTA 3180
ATTCAGAAA ACTCAGATT TAAGTTAAAA AGTGTTTG AGTTGGAA

Seq ID NO: 66 protein sequence
Protein Accession #: NP_06466.1
1 11 21 31 41 51
NIPPLNPLS LLLLLNPLN ANNNYKILA NSRIRGRDQ PNVCAQLIL OTKEKYPSTC 60
KWKYKSGIC QKTVLYECC PYGNRMBGK CQFVALDIR VYGLGIVGA TTTORYSAS 120
35 KLRESIBGK SPTYPAPNSE ANDNLSDIR RGLSHNVBE LNALNSHMI NKRNLTKDLK 180
NOMLIPMYN NGLTYLNNP NQVTVNVAR IIRNQIKTN GVNVIDRVL TQCTPSIDPL 240
IEADDELSE RAATLTGDI DALRGRCHP KALPDLRFE NGKVSASAL 300
MYHLLATLG CSHNWSVAN FTLESGTIE TCGDSDSTV NQIMNVNIG IVNNNGVHL 360
IDQVLLPDS QVSLILAGQ QTPPTDLVA LGLSALRDP GEYLLAPVN NAFSDTILN 420
40 VQRLLKLIL NLLKLVKVL NBLNNGQLE TIOGKQLRV VRTAVCIEN SOWKSGKQ 480
RQGLNIFRE IIRAPERSL SRLNQDKRF TPLSLLEAD LKELLRQED WLPFLPQ 540
FGQTSRERE LIRPDLGLI NLLVLLRPG VPLSGDEPC VTNLLCTQG SKFLKQVND 600
TLLWNLKSK BSMITNTGV INNVKLLYP ADTPVNDQL LEILANKLY IQIKFVRSI 660
FKELPVTYT TKIITKVPE KKVLEBSLQ PIINTGPTL TKVILBOEP FLIKESBTI 720
45 TELVHQBFI KRYTKIDG PVSEIKETR BBNITGPEI KYRITGGG SIBETLKLK 780
QSEVTKVTF IEGDGHLLF DEEIKRLGG DTPVRKIQAR KRVQSRRL RBRGQ

Seq ID NO: 67 DNA sequence
Nucleic Acid Accession #: B05 sequence
Coding sequence: 1-927
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55 TCTCTCTCT CCGCGCTCC CCGAGCTCC CCGCTCTCT CCGAGCTCC CCGAGCTCC 180
CATGCTCCG CCGCTCTCGA GTGCTCCGAG CAGCGAGCA CAGTCAAGT GTTAAAGCC 240
AATCATACG AATGCCCCC GAGCTCTCCG CCGTCAATG CCAACTCTT CTTACAGGC 300
AAGCAGCTG CCGCAGCA CTCTCTTAC CTGCGCTCA ATGTCTCCG CCGAGCTCC 360
60 AGCTCTGCC ACATCTAGA AAGCTCCAC CTGAGAGCA ATGCGCTCA GCGTCTTAC 420
CAAGTCAACC TCGCTGATT CCAAGTCTA CCGCAATTA GGGTTTCTC GACACATA 480
CCCTGATCT GCACTCCCA CATGCGAGC APTGTGACT GCTCAGGA AACAGAGTA 540
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TTGCACTCA ACAGTCTGA CTTGAGTGT GACCGATTC TTCCGCAAT CCGTCAACC 660
70 TCTTATGCT TCTTGGATAT TGTTTAGCC CTGATAGCC CATTTTCTC CCGTGTGTT 720
TATTTTAACT CCGAGGGAT AAAAAATGG ATGATATCA TCAGATATG CCGTGGAGT 780
CAGATGAGG GGTGATATGA CATATATGA ATCATATG ACCCGATT AACCAAGCT 840
AGTTCAACT CCGATGCTC GAGTGA

Seq ID NO: 68 Protein sequence
Protein Accession #: B05 sequence
1 11 21 31 41 51
MPGCGRSPA AGDGRRLAR LAILVLLGWS SSSPTSSAS PSSAPFLAS AVSAQPLPD 60
75 QCRACCESE AATVRCVNR NUTEVFDLP ATVRMLPLG NQLASRFLY LERKYLALQ 120
ELRHLRSHN SVLSVGTFT RHLTHRESLI LERDALVLI NQLASRFLY PRFTVPLNN 180
PNVCDGNAD MYVNLKREY VQGRDLTCA YFENHNRVL LRLNSADLC DPLDPSLQT 240
SVFLAIVLA LIGATFLLV YLARGIEKLN NENIRDAED HMGVYLYKE INADPLNTLN 300
SSNSDVL

Seq ID NO: 69 DNA sequence
Nucleic Acid Accession #: NM_000095.1
Coding sequence: 26..2299
85 1 11 21 31 41 51

WO 02/102235

PCT/US02/19297

CAGCACCCGAG CTCCTCCGCGCA CCGCATGTGT CCCCACACAC GCTTGCTTTC TTCTGCTCAC
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 GCGCGACGAG CTCGACGGAG TCGATTCTCT GAAAAACACG GTATGTGAGT GTGACCGCTG 240
 CGGATATGAG CAGTCAATAC GCACCGGGCT ACCGAGGGTG CGGCGCCGTC TCACATGCGC 300
 CGCCGGCTTC TGCTTCCGAG CCGTGGCTGT CATCCAGAGG GAGAGCGGGG CGCCCTTGCG 360
 CGCGTGGCCG CCGCTCTCTA CCGGACAGGG CTCTCCATCG ACCGACGTGA ACGATGCGAA 420
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 GCGTTCGCGG CCGGCTTACA CGGCCCCCAC CCACAGGGCG GTGGGGCTGG CTTCGCCAA 540
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 CCGCAATCTC CAGTGTGCTA CCGGACGGAG CTCTTCGCGG CAGTGTGAGT CAGGAGCGG 660
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 CTGCGCCGAC GATGTCCAGG AGCATGCGAG CTGGTCTCTA GAGCGGATG GCTGCGGCTC 780
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 GAGCCGAGC CAGCGCAACA CCGACGAGGA CAGTGGGGCG GATGCTGGG ACAACTGGCG 1080
 GTCCGCGAG AGCGAGGACC AAGAGGAGC AGACCGAGCG GCGCGGGGG ATGTGTGTGA 1140
 CCGACGATCT GAGCGGACG GATGCGGAA CCGAGCGGAC AACTGCTCTA GGTGACCGA 1200
 CTGAGACAG AAGGACAGTG ATGGGATGG TATAGGGGAT GCGTGTGACA ACTGTCCCCA 1260
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 CAGTCAAGC CAGAGTGAG AGCGAGATCA GAGACTCTCG GAGAACTGTC CCGGCTGGC 1380
 TGACTGCCC CAGAGGAGCT CAGACACCTA TGCCGATGAT GCGCTGTGGG ACGAGCGAG 1440
 CAGCATGAC GAGCTCCCTG ACGTCCGGA CAGCTCCGCG CTGTGTGCTA ACCCGGCGCA 1500
 CGAGAGCGG CAGACGGAGG CCGTGGGCGA CGTGTGCCAG GAGCACTTGG ATCGAGACA 1560
 GCGGTAGAC AGATGTGAG TGTGTGCGA GAGCTCGTGA GTACGCTCA CCGACTCTAT 1620
 GCGCTTCAG ACGATGGGCG TGACAGCGGA GAGTGTGCGG CAGATGTGCT CAGACTGAT 1680
 GGTGTACAC CAGAGGAGT AGATGTGGA GAGCATGAG AGGCCGCGG CCGTGGCTGT 1740
 GCGTACACT GCGTTCAGAT CCGTGGACTT CGAGGCGAGG TTCCATGTGA ACAAGTCTAC 1800
 GCGTAGAGC TATGCGGGCT TCACTTTGGT CTACGAGGAC AGCTCCAGCT TCTACGTGGT 1860
 CAGTGTGAG CAGATGAGAG AAGCTTATG CAGAGCGAAC CCGTTCGCGT CTGTGGCGCA 1920
 CCGTGTGCT CAGTACGAG CAGTGTGCT GTCCGAGCT CCGCGGAG ACTGTGCGA 1980
 CCGTCTGGG CAGTACGAG CAGAGAGTCT CCGAGTGGCG CTGTGTGGA CTGAGCGCG 2040
 35 AAGCTGGT TGGAGAGCA AGAGGCTCTA TCGTGTGCTC CTGCGCACCC GCGCCGAGT 2100
 GCGCTATCT AGGTTGGAT TCTATGAGG CCGTAGGCTG GTGGCGGACA GCGAGTGGT 2160
 CCGTGTGCT CAGTACGAG CAGTGTGCT GTCCGAGCT CCGCGGAG ACTGTGCGA 2220
 CAGTCTGGC AAGCTGGT ACCGCTGCA TCGACACTC CAGAGGACT ATGAGACCA 2280
 TCAAGCTGG CAGAGCTAG GAGCCGGGTG AGGACCGGCG GAGTAGAGC CAGCTTACC 2340
 40 CGCGCTGAT GCGGCTCTG CACCGAGGCC AAGGGGTGGC GTTCTGAGG GGGAGTGG 2400
 AAGGGCTAG AGAGGACAA ATAAAGTGT TGTGAGGG

Seq ID NO: 70 Protein sequence

Protein Accession #: NP_000865.1

45 1 11 21 31 41 51
 | | | | |
 MYPDTACVLL LTLAALGSG QGSPFGSLD PQMLRELQS THAALQVDRD WLGQVREIT 60
 FLKNTVMEDC ACGQGVSRV GLPSVRPLAE CARGCPFGV ACIGTESGR CCRCPAGFTG 120
 HSGHCTQVBE CBNPFCFVR RCMTPFPEE CAGCFPGDS PTHGQGLAF AGAFRQVCTD 180
 INRGTQVIB CVNPFVCTI RSPGCGQPG PDPVQDQAG QRRAGPLCP DSRPREEMH 240
 ADCVLERDGS RSCVQVQHA GNGILLGRD DLDGPFDEK RCPFPCKRD KCTVTHPSGO 300
 EDVDRDGI AGCDPADDGD VPHEKHICFL VRNPQRNTD ESKKQDACM CSQIHEDQK 360
 DTGQDGRGA CDDIDIGRI RQAGNDPFR PHSQDQSDG DGIQADRCR PQSHFDGAD 420
 VSDPFDGAC DDCQDQDDQ HGRDRICPT VPSHQSQSD HDQDQACD DQDNDVPSG 480
 55 RDRCLVPSH QGDADSDQV GVCQDQFDEA DKVDDIDVC PENAFVLTLD FRAFTVFLD 540
 PEGDAIDPM VVVLQREIS VQTHNSDFGL AVQYTFNWF DFTGTFRHT VTDDYAGFI 600
 FOYQDSSEFY VNMHQEQT YWQNFPRAY RSPQILQAV KSTGQGEQL RHALMETDT 660
 EQVLLHLD PRVQHEDEK STYNFLQHRP QVYVIRFRY RSPFLVADSN VVLDTMRGG 720
 RLQVFCPSG NITRAKLRYE CMTTIPSEYE THQLQA

Seq ID NO: 71 DNA sequence

Nucleic Acid Accession #: NM_024626

Coding sequence: 71..91

65 1 11 21 31 41 51
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 TCTCCACAC ATGCTCTCT TGGGCGGCTT CAGTCTGTG AGCATATTA GCATCATCAT 120
 TATCTTGCGT GAGACCAATG CACTCATCAT TGGCTTTGAT ATTTCAGGGA GACACTCCAT 180
 CAGACTCACT ACTGTGCGCT CAGCTGGGAA CATTCGGAGG TAGCGATATC TGAGCTGCAC 240
 70 TTTTAGAATC GACATCAATC TTTCTGATAT CCGTATACAA GGTCTGAGG AAGGTGTTTT 300
 AGACTTTCCT CAGTATCTT AGTACAGGAA AGATGAGTCT TCGGAGATCG ATATACATG 360
 CAGAGCGCGG ACACGACTGT TTGCTGATCA ATGTATAGTT GCGAATGCTT CTTCGCGCT 420
 GAAAAACGTG CAACTCAGC ATGCTGSCAC CTCACAAATG TATATATCTA CTTCATAAGG 480
 CAAAGGGGAT OCTAACTTGT AGTATAAACC TGGAGCGCTTC AGCTGCGGAG AAGTGAATGT 540
 75 GAGTATATAT CCGACCTGCA AGACTCTTGG CAGTGTGAGT CCGGAGAGCT TCCCGAGGCG 600
 CAGATGTGCT TGGGCTCTT AGTGTATCAT GGGAGCCAC TTCTCGAGAG TCTCCATCAT 660
 CAGCTTTGAG CCGAAGCTCT AGATGTGAC CATTAGGTT GTGTCTGTGC TCTACAAATGT 720
 TACATCAAC ACACACTACT CCGTATATAT TGAATATGAC ATTGCCAAAG CAACAGCGGA 780
 TATCAAGTGT CAGCATGTCT AGATCAAAAG CGCGGTCTAC CTACGCTGCT TAACTCAGA 840
 80 GAGTCTCTCT CAGTCTCTT CAGTCTCTTC CAGTCTCTG GAGTCTCTG CTTCAGCTG 900
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 CAGAGGATCT ACAGAACTAT TCCACACCA GATATGAACT AGTTTATAT TTCTGCGAGG 1020
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 CAGAGAGCA AGCTCATCT AGTACAGAG TAAAGCTGA TATGAGAGT 1140
 85 TGGGAATAA ATTCATGTA ACTAGATGTA ACTGTGTGAG GCGTAGAGAA CCTGGTTTT 1200

WO 02/102235

PCT/US02/19297

GAOTAGAAA GGGCTGGAA AGAGGGGAGC CAACAATCT GCTGCTTCC TCACATAGT 1260
CAITGGGAAA TAAGCATCT GCTCTTTGG CTGCTGGCTC AGACAGAGA GCTAGAGCTC 1320
TAITGGGAGC GAGATTAACA TCTCTCACTG AACGAGAGTG ACAGAGGCTA TGGGAATG 1380
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CAGCGCAAT TCTGTAGAGG AATGCGCTGA GTTCACTCT AGCTTTTCT ACTCTGAAT 1500
TAGATCTCCA GAGCTCTGCT GCGCAAGATT CAATTAAGG CACAAACAT ATACCTTCCA 1560
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AATGAGCTT TGAAGAGAAA GATATCTTTT TTCTGAGC CTCTCCACG CTCTCAAT 1680
GTAACCACT GCGCTCTGCG ACTGTGAGC CAGCTGACT GTATTACAT TGTATAGA 1740
AAACTGATT TAGATCTCTG ACTGTCAG AGATGACTA AATACATTT TCCTAAAAA 1800
AAAAAATAA A

Seq ID NO: 72 Protein sequence
Protein Accession #: NP_078902
1 11 21 31 41 51
| | | | | |
MASLQGLFW SIISIIILIA GAIALIIFG IGRHSITVT TVASAGNIGE DGLSCTFEP 60
DIKLSDIVIQ NLREVLGLV HEPEKDELD SEQEMFRGR TAVFADQIV GNASLRKLV 120
QLDAGATYK VIITSGKGN AHLEVTGAF SMPDEVVDYV ASSETLRCHA PRWFPGQTVV 180
NASVVDGIAN FBSVSTFSE LASSBNVMKV VSVLIVTTH HTSCHEKD IAKATGDYKV 240
TESHKKRSH IQLLNLKSL CVSEPTAEN ALLELSPYLA LK

Seq ID NO: 73 DNA sequence
Nucleic Acid Accession #: XM_057014
Coding sequence: 143..474
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CGCGGGGAGC CGAGCGCTGT ACGAGCTTCC TCTCTCGAT CTCTCTCCGC TCGAGCTCCG 180
CGCTCGGCGC CAGCGGGGAG CCATGCGAAC CAGCGCGCCC GCGCGCTCCC CGCGCGGCGT 240
CGCGCGGCGC CTGCTGCTCC TCGTCTGCTGA CCGTCCCGCG CGCTCGAGCG CCTCTGAGAT 280
CGCGAGGAGG AAGCAAAAGC CGACACTCGC CGAGAGGAGT GTGGTGAGCC TGTATATAGG 300
CAATGCTCTTA CAGTGTGAGC TGTGTGAGAC GTGTGAGAC GCGAGAGTCC GCGAGATG 360
CATCTCGGCT ACACCTGGGA TCGCCAGTCG GATGTGAGCT AAGAGAGAAA AGCGAGATG 420
CTGAGGGAAA AGCTTGTAGG ATCTCTGAGC ACCCAACTAC AGGCACTGTT CATGAGATTC 480
ATTGAAATAT GCGCATGATC TTGGGAAAT TTGGGAGTGT ACATTACAAA AGATGCTCTC 540
AAATGAGTCT CTAGAGTATT TTGTGATGCG CTGACTTCGG CTAAGAGTGA AAGATGATG 600
CTGCAAGT TGTGTGAGC CATTCATGAG AGCTGAGTGT TCGAGAGCTT TCCCATATGA 660
AGCTATGATT TATTGTGAGC AAGGAAAGCC TGAATGAAT TCACAAATTA ATATTGCTAT 720
CACTCTCTCT GTGAGAGGAC TTGTGAGAGG AATTGTGCT GTATTAGTGG ATATTGCTAT 780
CTGAGTGGAG ACTGTGTGAG ATTAACCAAA AAGAGATGCT TCTATGAGAT GGAATTCAGT 840
TCTGCGATC ATTATGAGAG AACTAGAGAA ATAAAGTCT GTATTGAGT TCTCTACTCT 900
TTTTTTTATT ATGCGTTGGA ATGTGCTCAT TAAATGACAT TTAAATGAAG TTATATGATA 960
CATCTGAATG AAGAGCAAGC CTAATATGT TTACAGACAA AAGTGTGATT TCACACTGTT 1020
TTTAATCTTA GCAATATCTA TTGTGCTCA ATGAGAAATG GTTTCATAT TTTTATTAGT 1080
TGTATGAT ACTGTCTTCA TGTGACAT CTCTGAGCT ATATATGGA ATATTGTGT 1140
GCTCTTTGT TTTTCTCTT AGATAGCAT TTTTAAAAA ATATATAAGC TACAACTCT 1200
GTACATGTT GTAAATGTTA AGAATTTTT TTATATCTG TAATAAAAA TTATTCTCA 1260
CAACCTTAAA AAAAAAATAA AAAA

Seq ID NO: 74 Protein sequence
Protein Accession #: XP_057014
1 11 21 31 41 51
| | | | | |
MRPGQPAAP QLRGLLLLL LLQLPAPSA SEIPEKQKFA QLRQREVVDL YNKLQGPDA 60
GVPRQDPSG ANGIPTPGI PQRDGFQKEK GBLCESEPE SWTHYKQCS NSSLAYIDLL 120
GKIAECTFK MRNSALRLV FSSSLKLCR HACOQRYFT FPGACSEPL FIEALITYLD 180
GSPENNTIN IHTSSVQL CQGIAGLAD VAINVGTCSB YPKGASTGM NWSRIILIE 240
LPK

Seq ID NO: 75 DNA sequence
Nucleic Acid Accession #: BC010423
Coding sequence: 248..1780
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| | | | | |
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GATGAGAGCT GGTGTGTAG AGAGGGGAGC GAGCTGGTCT TGGCTCCCT AGTGAGAGC 120
CAGAGGAGAG GAGAGAGAAC TCTGAGAGCT CCGCTCTTCT GGTGAGTCT CTATATCAAG 180
TCTGAGGCGC GTCGCAAGAG AGATCTGGT GGAACCTCAG AAAGCTGGG CAGTCTGCT 240
TTGACCATG CCGCTTCCC TGGGAGCGGA GATGTGGGG CCGGAGGCT GCTCTGCTCT 300
GCTCTACTG CTGGAGCAT TTACAGCGCG GTGCGCGGCG GTGAGGCTGT AGCATCTAGA 360
GCTCTACTAT GGTGTGTAGT GCGAGAGGCG AAGACGCGCT TCTCTTAC GAGGAGACT 420
CGCGAGGAAA GTGGGGGAG TGCATAGCG TGGGTGTGAG CGCGCGGAG GCGCCACAGA 480
ACTAGGCTTA CTGACCTCA AATACGGCT TCAITGAGC CCGCTTAGG AGGCCCGCT 540
GAGAGCGGAG GAGCGCGGCG GAGCGCGCT GAGAGGCTCA GTGCTCTGCG CAGACCGAGT 600
GAGAGCGGAG ACGAGAGAGT ACGAGAGTCT GTGAGAGCT TCTCTGCG GAGCTCTCA 660
GCGCGGGGCG CGGTCGCGG TCGTGTGCG TCGCTGCGC TCGCTGCGC CTGCTGCGC 720
ACTAGAGAG GCGCAGGCG TGAACCTGCG AGCTCTCTG ACAGCTGAG GCGAGCGAG 780
CGCCAGGCTG ACTGTGAGCA GAGAGTCAA AGGCACAGC TCGAGCGT CTCTGAGCA 840
GCTCCGCTCT GGTGTGTAGT CTAAGAGATT CAGCTCTGCG CTGCGAGCA GAGAGAGCA 900
CGCGGAGCTG ACTGTGCTG TCGCTGCGC TGGCTCTCT CAGGAGCAAAA GATACACCA 960
CATCTCTGCG GTCTCTCTC TTGCTGAGC CTCTGTGAG GCGCTTGAAG ACCAAATCT 1020
GTGCGACAT GTGAGAGAG GAGCTATGCT AGTGAAGCG AGTGAAGCG AGCCCGCTCT 1080
CTCATACAG TGACACGAGC TCGATGAGCT TCGCCGAGT GGGGTACAG TGGTGTGGA 1140
CACTTGTGCG TTGCGCGGCG TGACACAGTA GCGACGCGC ATCTACTCT GCGATGTG 1200

WO 02/02235

PCT/US02/19297

	CAMTAGGTC	TCTCTAGGG	ATTCTCAGGT	CACCTGGAT	GTCTCTGAC	CCGACGAGA	1260
	CTCTGGGAG	CAGGTGAGC	TAGTGTGAC	CTGGGTGAT	GTGGTGGGT	TGATGCCGC	1320
	ACTCTGTTT	TGCTCTGGA	TGGTGTGGT	GTCTGTGAT	TCCGATACC	ATGGACGCA	1380
5	GGCCGCGAC	ATCACCGCA	ATATATAGG	GGAGCTGAC	GTGACCGAG	AGAATCGAT	1440
	CCGGAGGCT	CATTCGCAT	ACACGGACC	CAGAGCCAG	CCGGAGGAG	GTGTAGGGT	1500
	GAGACCGAG	GGCCACCTG	ATATGCTCA	GGACACAGT	AGCTGCTCT	TGATGAGTA	1560
	AGAGCCCGG	GGCCGCACT	ACTCCACCT	GGACCGGTT	AGGAGATAG	AAACACAGC	1620
	TGATCTGCT	TCTCTGAGT	CTGGGCGGC	CGAGGAGC	GAGATCGAG	GTAGAGCGT	1680
10	GAACAGGCC	ATGACCAAT	TGTTTCAGG	GAATGGGAC	CTACGGGCA	AGCCGACGG	1740
	CAATGGCAT	TACATCAAT	GGCGGGGAC	CTGCTCTGA	CCAGGCGCT	CCTCCTCTC	1800
	CTAGCGCTG	CTCTCTCTG	TGATGAGG	GATTTTACG	CATCTTGAG	GCTCTCTTA	1860
	ACGACCGAT	CTCTCTGGA	AGATGTCTC	CACTCCACT	ACTCTTGAC	CTTCTACTC	1920
	AACCCCTCG	TTCATCGGA	GGGCTCCAC	ATTGAGTCT	CTCCACACAT	CAGATCGAGT	1980
	CACCTGTCT	GTGCATGTT	GCCTCTGTG	GTGTGACTG	ACTGTGTGT	TGTGGAGGG	2040
15	TGACTGTCT	TGAGGGGTT	ACTGTGTCT	TGTTGTGAT	TATGTGTCT	TATCAGAGT	2100
	AATGTACAT	TGCTGTGAT	GGCGGGGAT	TGTGTGTTT	CGTTGGGCA	CACTCTGAG	2160
	CTTTGAGCT	TGCTGTGAT	GGCTGTGTT	GACCTCTGC	TGAAAGAGC	GTTATTTCT	2220
	CAGACCCCG	AGCATATTA	ATGATCGAG	GTTTGAGGA	GAGAGTGGG	GACTGTGCT	2280
	CAGACCCAG	TGTGCGGCA	TAGCTGGAC	TGAGATCTC	CTCGGTGTG	AGGAGACGT	2340
20	TCTCTTACA	CTCTGAGAC	ATGTGCGCA	GTGTGAGC	GCAATCTCT	GGTTCAGCA	2400
	GAGGCTTGA	CGTTTACAG	AGCCCTTTC	CCTCTGGGT	CCTCTGGGC	TGCTGATCT	2460
	ACATATTTT	TGTAAATATA	CATGCGCGG	AGCTTCTTG	CAGAGATAT	GCTCCGATC	2520
	ACTTTTAAT	TTTTTCTTT	TTTTTCTTG	CCCTTTCAT	TAGTGTGAT	TTTTATTAT	2580
25	TTTTTATTT	ATTTTTTTT	AGATTTTGA	TCCGCTGCT	ACGATATAC	CAGACCTGT	2640
	CTGTAAAAA	ACCAAAACC	AAAAAAAAA	AAAAAAAAA			

Seq ID NO: 76 Protein sequence

Protein Accession #: AAM10423

	11	21	31	41	51		
30	NPLSLGAMH	GPEAWLLLL	LLASFTGRC	AGELESTEDV	TVVLOGDAKL	PCFYRGDSGE	60
	QVGVANAR	DAGEAQELA	LHSEKYLAV	SPAYBQWVE	PPFPHPLDG	SVLLANAGLA	120
	DESEYCNVS	TFTTETGRT	LVPLVPLP	CTGGLTAAAS	CTADSGES	CTADSGAPAS	180
	VTMDIEKRG	TSRSFDEIR	SAVTSFPL	VPSRSHWQCF	LCTCVHSPGL	LQDRITHTL	240
	KVSLFLAREH	RGLEDSGLWR	IGSGGNMLK	LSBGPPFPY	NWRLGLPLP	SGVRVDIAAL	300
	GFPLLTETIS	GIIVGCHNS	FSRBDQVTV	DVLDPQDSG	KQVLDVASV	VYVGVIAHL	360
	FLCLVYVVL	HRRIKRLG	CHGKREEL	TLITENSIRL	LASHITPOS	QPSREVGALA	420
	BSHPLGLEN	SSCVMSPT	SEBSYTLT	VRBIETQEL	LSFPGHASE	SEDDQDIHQ	480
	AMNIFVQENG	TLRAKPTGQ	LIYNGRLV				
40							

Seq ID NO: 77 DNA sequence

Nucleic Acid Accession #: NM_003474.2

Coding sequence: 37..3036

	11	21	31	41	51		
45	CACATAAGCT	CTTCTAGTC	CCCGGCGCCA	CTCGGACAT	TTCCTCATTT	ATTGCAACGG	60
	TCAAGGCTGG	CTTGTCGAG	ACAGCGCGCC	GGCGGACCA	CCACACACA	CGGGGGGAGA	120
	CTTTTTTAA	AATGAAAGC	TAGAAGAGCT	ACGCGCGGC	GGGGCGGCTG	CCGAGGGCT	180
50	CGGAGCTGA	CTCGCGAG	CGGAGATCT	CTCGGCTCC	GACCGCGGCG	CGCGCTGGC	240
	GGCGCGGG	GATGTGAG	GCTGCGCC	GGGGCGGAG	AGCTGTGCA	CTGAGCGC	300
	GGACGATGG	CAGCGCGCC	GCTGCGCGG	TCCCGCGCC	GGCGCTCTCT	GCTCGCGCT	360
	GGCGGTGCT	TGCTCGGCG	CTCGGAGGC	CGAGGGTGA	CGTTATGAA	CGAGGAGAA	420
	GCTGATGAG	TGTCGATGC	CTCTGTGG	AGTGGGAC	CTCGATCCC	AGTAAAGAC	480
55	TTCGACTCA	AGATGATCC	AGAATGCT	ATAATTGAC	TACGACGGA	AGGAGAGAA	540
	TATCTGCAAG	ACGTACTGA	TGTCCTCCCT	GCTCGAATTT	ACGCGGTAT	TCTGGGTGAC	600
	TGTTACTAC	ATGGACATCT	ACGGGATAT	TCTGATGCT	CAGTCAGTCT	CAGCATGTT	660
	TGTGTCTCA	GGGAGCTAT	TGTTTTCGA	AATGAAAGCT	ATCTCTTGA	ACCATATAT	720
60	ATGTGACAA	CGGATGACA	ACTCTTCCA	CGGAGAGC	TAAAGAGCT	CGCGGATCA	780
	TGTGGATCA	ATACCAACAC	ACCAACCTCT	GCTCGAAGA	ATGTGTCTTC	ACCACTCTCT	840
	CAGACATGG	CAGAGAGCA	TAAAGAGAG	ACCTTCAGG	CAACTAAAT	TGTGAGCTG	900
	GTGATCTGG	CGAGCAACG	AGAGTTTGG	AGCGAAGAA	AGATCTGSA	AAATGTTAG	960
	CGAGATPA	TAGAGATCC	TATGATCTT	GTGATCTCT	AGAGACTCT	GAATCTGCT	1020
65	ATCTGTGTC	TAGGCTTGA	ATGTGGATAT	GACATGACA	AATGCTCTCT	ATGTGAGAC	1080
	CAATGACA	GCTCCATGA	ATTCTTGAC	TGGAGAGA	TGAGCTTCT	ACCTCGGAA	1140
	TCCCATGCA	ATGGCGAGT	TGTCAATGG	GTATTTTTC	AGAGACACC	CTTGGGATG	1200
	CGGACATCA	TAGAGATCC	CATCTCGGG	GAATGTGAT	GGACATCTA	GGACATCTA	1260
	CAGACTCCC	TGTGTGCG	GCTGACCTG	GCATCTGAG	TGGCCACAA	TTCGGGATG	1320
	AATCATGAC	CTATGAGAG	GGGCTGTGAC	TGTCAAATG	CGGTGAGAA	AGGAGAGCTG	1380
70	ATCATGAC	CTTCCACGG	GTACCATTT	CCGATGTGT	TGACGATTT	CAGCAGGAG	1440
	GATCTGGAG	CGAGCTGGA	GAGAGGAT	GTGATGTTT	TTTATTAAT	GGCCGATCT	1500
	AGGATGCTT	CTCTGAGCA	GATGTGCT	ATGACATTT	TGAGAGAGG	AGAGGATCT	1560
	CAGCTGTGG	AGCGAGAGA	ATCTATGAT	CCTCTGTCA	ATGCCACAC	CTGTACCTCT	1620
75	AGCGGAGAC	CTGTGTCGC	ACATGGGCT	TGCTGTGAG	ACTGCCACT	GAGGCTTCA	1680
	GGAGCAGCT	CGAGGACTC	CAGCATCTC	TGTGACTCT	CAGGTTCTG	CGAGGGGCT	1740
	AGCGTGTAC	CGGACGCA	CGTGTACT	CGAGAGGCT	ACTGTATCA	GGATGTGAC	1800
	GCTATGCTC	ACATGTCAT	CTCGGACAT	CGAGGAGC	AGTGTGTAC	ACTCTGGGA	1860
	CCAGTGTCTA	AACTTCCCC	TGGGATCTG	TTTGAGAG	TCAATCTCG	AGGTATCTC	1920
	TATGGCACT	GTGGCAAGT	CTCGAGAGT	TGCTTTGCA	AATGGGATG	GAGAGATCT	1980
80	AAATGTGGA	ATCGAGAGC	TCAAGAGAT	CGGACCGC	CACTATGCT	TACCAATCC	2040
	GTTCACAT	AAACACAAAT	CCCCCTGAG	CAGAGAGCC	GGATCTCTG	CCGGGGAGC	2100
	CACGTGTACT	TGGGCAATG	ATCACGGAG	CCAGGGCTTG	TGCTTGAGG	CAGAAAGTT	2160
	CGAGATGAA	AAATCTGCC	GATGTGCAA	TGTCAAAAT	TGATGTCTT	TGGGTCTAC	2220
	GATGTGTGCA	TGCATGTCC	CTCGAGGGG	ATGTGTGCA	ACGAGAGAT	CTGACCTCG	2280
85	CAGGCCCAT	GGGACCTCC	CTTCTGTGAC	TGATTTGGCT	TGTGAGAG	CAGAGACAC	2340

WO 02/102235

PCT/US02/19297

GCGCCCATCC GCGACGAGA TAACCAAGGT TTAACCATAG GAATCTCGGT GACCATCTCTG 2460
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 TTTCAGAMTA AGAGACGAG CTCTGAAATA CTAGAGTGTG TGCCCTCTTC CGGCGACAT 2580
 CTGGCTCTCC AACCTGTGCA GCGTCAACTC GCGCACTCTG GAAAGGCGCT GATGAGGAG 2640
 CCGCAGGATT CCTACCCACC GAAGGACAAAT CCGAGAGGAT TCGTCAGTGT TCGAGATGTT 2700
 5 CCGCTCAGTA GACCCCTAGC CGGCTGGAAT GTCCCTCMAG CCGATGTCAAC TCCMGAGTGT 2760
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 AAGCTCTGAC TTAGCGACGA CCGAGGCGACC TGTAAAGCCA ACCGCCCTCA GAGCGCTCTG 2880
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 10 CAAATGGAGA CTGGAGCTCG CTTGGAGACC CTGAGACACC CTGAGACGTC CTCACAAATA TCCATACAAA 3000
 GCGCGCGATG TCGTCAAGAG CTCTATATAT TCGTCAAGTC CGACAGAGCT TTTTCAGATA 3060
 TGGAGACAGA AGTTTGAACAT ATCTTTCAGC TCCAGCTGGA GTTTTGTGTA CCACCTTTTA 3120
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 15 GAGATATGTT GATTAACHTG CAGTGGCGTG TAGTAGGCAAT TTTTACACAT ACAGATGTT 3300
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 25 CAGTAGGTTT ATTTAGCTTG GGAAGGCTGG TTTTCTGTA AGAACCTAC TGCCCGAGCA 3900
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 30 AACTGATG ACCTTTGTA CTGGGAAJAA CTACAGGCA TCGATATGGA TGTCTATGG 4140
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 35 CTCTGATC CTGCAATGCG TGAATAGGGA GCGATGTTTC CAAGGCTTT TAAAGTACT 4440
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 40 TGACACAGA ATCTGTGTT GCGTTCGAGA AAACAAACT CGATTTCAT TCCCGGTGT 4680
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 ACCAAAAAAA AAAAAAAAAA AA

Seq ID NO: 78 Protein sequence
Protein Accession #: NP_003465

1 11 21 31 41 51
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 50 SGRHPEVLNI ELQRESKELI INLEBNBGLI ASSPTETHYL QGTDVSLAR NYTVILGHY 120
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 SHHTPHLAA NVVFPPEQST WARHRESEL KATRVLEVLT VADREFPQKQ GDELEFVQR 240
 55 LLEIANRUVK FXPFLNLRIV LVGVVEVNDM DECVSQDFP TSLHEFLNR HKLLKPKSH 300
 DNGLVSVGY PQDTTGMAP IISMCTADQM GYIVMEIDRN PGLAAVTLAH ELGRHFGNNH 360
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 60 AKCRSHSGD LFEFCTGASP HCEANVLYLD GHSCQVDGY CNGIICOTHE QGVTLMGRO 540
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 IETNPLQQQ GRLLCRGTHV YLGDMDPEPG IVLATGTCAD GKICLARGCQ NISVGVHBC 660
 AMQCHGRVNC NNRKNCICBA HAPFPFCDKP QFGSDTDSGP LRGRKALUT IGILITLCL 720
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 65 DSYFPKIDNR RLKQCNQVDI SRFPLNGLVF QPQSTRVLP FLIRAPRAPS VFAPRLPAKP 840
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Seq ID NO: 79 DNA sequence
Nucleic Acid Accession #: NM_003714
Coding sequence: 135..1043

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 TGGTACACTT TACCCCGGCG CCGGCGGACC ACCGCCACCA CCGCACCGAG GTGCTCCAGC 240
 ACAGGAGCTC CCGAGCGAAA GCGCCGCTGTG CCGTGCGTGA TACGCGGAG ATGACGACCT 300
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WO 02/102235

PCT/US02/19297

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Seq ID NO: 80 Protein sequence
Protein Accession #: NP_003705

1 11 21 31 41 51
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 ISERKFAIRE MYSGLQRECT LKHLDCAAQ ENTRIVEME HFKDLLEHF VDL/VNLLLT 180
 CGEVRKEALT HSQVQCRQI WGSLSILEF CTSALQKPT APFERPQVD RTELBRANHG 240
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Seq ID NO: 81 DNA sequence
Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
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 GCATCTGGA CAGAGAGAG ACATCTCCG CCAACAACC CTTCCTCCG AATGTGAGT 300
 50 GAGTGTGCG TCAACTGTA AGGATGAGT ACCTCTCAT TTGCTTTGT GGTGCTCTG 360
 AGCATGTGA GGGACAGCC TCAATGCA GAGACTTGC CTTCAGATT TGAAGTGGG 420
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 TTTTGACTC GGCATGTGT TGGAGCTCC ATCAAGATA CGTAGGCTC TCTTTACTG 540
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 CAGAGAGAA TTGTAACAT TCCCTCTTC ACANATTT TGAATGAT AALAGATAG 660
 55 CCTTAACTT TATGCTCTC TCCGCTCTG CCACTCGGG GCCCAAAAT TTTCAAGAT 720
 AAGAACTCG TGGATCTCT TAATGTGAT TGGAAAGAG ATTAGAGTG ACATATCTA 780
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Seq ID NO: 82 DNA sequence
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 CAGATCGAT GTAGAGAGT AGACTCTGG AGCCTTGCTG TTTCTTCTA TGAATTTTA 240
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 ATTTCAAGTG CAGACAAAT GATATGTGCG TGGCTCGAG TGACATCAT GTTCTTATG 360
 GATGAGTGA TGTATGCTA GTTGGAGAG GATGAGGAG CTGAGGACT TCCCATGCG 420
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 80 GGCCTCTCA CACACTCTG CAGTCTGCG ATCTCTTCA GCGCCAGCC AGCTGAGAG 900
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WO 02/102235

PCT/US02/19297

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 GGTGTATTCG TGAATGCGCC CCGAGGCGAC ATGCGTCCCG TCGAGAGGCG CAGAGCGGCT 2340
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Seq ID NO: 83 Protein sequence

Protein Accession #: XP_061091.1

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 DQSNVSGVGS FESSESLTPT VCGGLSTPTF RYSPGARGFS STPLREPLFD PGTQAGSEVKA 180
 RIKRMVFKGG RTYTEILAKY LMRGLFGGR NASVQILILI VTGSGQGVQD ALFSQLEKAR 240
 GVTIVFANGVR FPMLELIAL ASEPGHVLV LABQVIEDTH GLFTLSBSHA ICSSATPTAGS 300
 PELVFERMLR GILGLGPDGS QPGQNCSTCV PELGLQGCL CLARAGDIAN CALLESLEAC 360
 VDLILLDSBG AGLGATLDDA AVDPSVFR FVLSRGLGAG TCTGAGAACG CAGCTGCTCT 420
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 APGLTDEPR ANGLTGLDGA PLGAGVGSAG TALLIYDITG MYVQAGVTSR VRGAVVLTG 660
 GSGALNANVP AQGLKNDIIS VLVVGVGPLV GDLRLRAGF RDELILVAVY ADLRYVQVQL 720
 IEMLGGEAKQ PVHLCKPSPK MNEGSCV/LN GSYRCKCRDG WEGHCHNRE NSSCIVCVSQ 780
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Seq ID NO: 84 DNA sequence

Nucleic Acid Accession #: Bos sequence

Coding sequence: 1..2424

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WO 02/102235

PCT/US02/19297

GTATCCCTCC CCGAGCACTA CAGAGAAGGC CTGGGCACTG AATATGTGCC TACTTCTGG 2400
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Seq ID NO: 85 Protein sequence
Protein Accession #: Bos sequence
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10 MPFFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SIOMMCSAAV DIMFLDGSN 60
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10 NVFPGGRTET ELAKLYLHHR GLRGGHNASV PQILLIVTDG KSGQDVALPS KQLSERGVTV 180
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15 KAKVVFVGRV RAWLSBSRSA RVGVATYSSE LMAVAVPGRY QVVDLWMSL DGIFFRGAPT 420
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20 QNBSQVLYQ NSVPTKCRQ GHSPHICRER EMSSGSCVGS QWILELTPLR UNKPVQSSS 780
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Seq ID NO: 86 DNA sequence
Nucleic Acid Accession #: Bos sequence
coding sequence: 89..2356
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35 AGCAGAGAGT AAGGCAAGAA TCALAGGAGT GOTTITTCAA GAGAGGCGCA CGGAGACCGA 480
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Seq ID NO: 87 Protein sequence
Protein Accession #: Bos sequence
1 11 21 31 41 51
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80 MPFFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SIOMMCSAAV DIMFLDGSN 60
SVKGSFERS KHAFAITVCDG LDISPERRRV GAFQSPSTPH LEFLPDSFT QQRVKARIKR 120
10 NVFPGGRTET ELAKLYLHHR GLRGGHNASV PQILLIVTDG KSGQDVALPS KQLSERGVTV 180
FAVQVPTFPM HELANLASEP KQHVLLARQ VRDANTWGLFS TLSSAICSSS ATQCVKFAH 240
PCBRTLELVW REFACAFARQ RGSRTLAFL AAKCPFSYMK RVFLTHPATC YHTTCGBCD 300
85 SQPCQNGSTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEK RVDLFLDLS SAGTLDGFL 360

WO 02/102235

PCT/US02/19297

RAKVVYFEFV RAVLSSEDSRA RVGVATYSRR LLVAVPVGVEY QDVPELVNSEL DGIFPRGGPT 420
 LKGSALARAQA ERGPGSATPT GQDRPRKPVV LATESHSEKDI VAGPARKHARA KEILLALGVGS 440
 ENVAIRALEII TQSGDLPWII SPKQDLPWII PELQKQKSTQ QPQPCPTQAL DLVPMPLATSA 460
 SVGPNFAGM QSPFVPSCLQD FEYVYDPTVQ GLVYVYQSVQY TAPGLDTKPT RAMKLARISQ 600
 APYLAGVGSYA GTALLHIYDK VMTVORGARP GVPEKVVVLT GGRGASDAAY PAQLKRNHNI 660
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Seq ID NO: 88 DNA sequence
 Nucleic Acid Accession #: NM_019894
 Coding sequence: 1..1314

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 CTSGAGCTCC GGTGATGAGT CATGPGSEGT GCTCTACATA AGGACCTQAL GATATATATSA 180
 TACTCTCTCT GCGGACAGCC TCTCCATCTC ATCCCAAGGA AGCAGCTGTG TGACAGAGAG 240
 CTGAGCTGTC CTTGAGGGHA GGACAGAGAG CACTGTGTCA AGAGCTTCCC GGAAGGGCCT 300
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 20 AAGCAGATGG GCTACAGAGC CAACCCCACT TCCAGAGCTG TGGAGATGG CCGACAGCCAG 480
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 GGGCCCTGTC TCTCAGGCTC CCTGCTCTCC CTGACACTGC TTCCCTGTGG GAGAGAGACT 600
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 25 AGACTCCAGT ACACCAJAJCA GCACTCTCTG GAGGAGAGCA TCTTGACCC CCACTTGGTC 720
 CTCACGCGAG CCACTGCTCT CAGGAAACAT AGCAGATGTT TCAACTGGAA GGTCCCGGCA 780
 GCTCAGAGCA AACTGGGCGA TCTCCCATCC CTGGCTGTGG CAGAGATCAT CATCATCTGA 840
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Seq ID NO: 89 Protein sequence
 Protein Accession #: NP_063947.1

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 QMFWPSAFEN FTBALAETAC RQMOYSKPT FEAVETIQDQ DLQVVEITEN SQSLMFNNS 180
 GPCLSLSLVS LELCALOKSL KTRPVVGBE ASDVDQHWQV SIQYDQHWQV GSSILDRHW 240
 45 LTAMCFRKH TDYPRNKRVA GDEKLGSFPS LAVAKIILIE FHFVPRKDD IALMLQPL 300
 TFSFTVPTIC LPTFIRELIT ATPLMLIQQG FTGKSGSRS DILLQNSVQV IESTICNAID 360
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Seq ID NO: 90 DNA sequence
 Nucleic Acid Accession #: NM_002776.1
 Coding sequence: 82..912

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 GCGTCTCTCT CCGAAACGCT GACGCTGTCT GACGCGAG CTTATGAGCG CCGTCTGCG 240
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 TCTCTGCTCT GTTCAAACT CTGCGGCTCT CCGACCTCTT AAACATCTCT CTTCTTCACT 1080
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 AAAAAAAAAA AAAA

Seq ID NO: 91 Protein sequence
 Protein Accession #: NP_002767.1

1 11 21 31 41 51
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 85 MPAPHELSA ASGARALAKI LPLIMAGLMA AKAAIIPQND TRIQPEAYGA PCARGSPWQC 60

WO 02/102235

PCT/US02/19297

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YKQSGGFLP RTTDEHLEL LELAPVPVPO FVRLALQLPY RQAGQDQX VACMUTTAAR 180
RVKYHSLGTZ SSITLSPKE CEVFPQVVT NMKICAGLDR QDDPCQSDGQ GPLVCDFTLQ 240
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Seq ID NO: 92 DNA sequence
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Coding sequence: 182-658
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GCTAAATCTG CTATATTATT CAGAGGAGAA ACCTAGACAA CTAGAGATCA TAAGGCGCTC 780
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CACTCAACTC CTGCTTGTTT TTCTCTTGCC CATAGGAAGG TTACCAAGTA GAATCTCTGC 1140
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Seq ID NO: 93 Protein sequence
Protein Accession #: KP_114433.1
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35
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YGNHHLASI LSLKEASTIA EYISGYGRSO PIWGLHDPQ KRQMQHIDG AMYLYRSHS 120
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Seq ID NO: 94 DNA sequence
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Coding sequence: 1..4086
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AATATGAGGA CAACACCTC CTGACGCTTG GATTTAGACA CCGTGGAGT TTTTAACTG 1080
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WO 02/102235

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Seq ID NO: 95 Protein sequence
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WO 02/102235

PCT/US02/19297

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 GTEAKHMOO LQVQYTHPE LAQDVDEKGG YDPFTYDEL SHHTFSECV TVIHSNGLLI 600
 KVVVYHSLG HCFPTEDGPE SRNTHOCLG LLVKSOTLLP SDRDSKMKCM ITEDSYPGYI 660
 PEPDQCNAY VHYIDPKSGT HILNCAAGS ESKESERELV HVPFGSVCM YSPQSEIPI 720
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 VYDVSSEYPT SYLSDSDHVL VHPDSDHVP DWRGACSCD TACHTTQATK TSHLEKHELI 1020
 HUPFSLHVL EALHSTYTH QQQPVYTLG KGTTHHWCZ ABELALMLV RFWMSDHLV 1080
 GLCYPROTFP SILSDVHRL LKQTSKTOV VRTLQMDRVE QSYPRSHRY WDEDSGLALF 1140
 LKXQNDREK FAFCSMOCE RIKIKALIFP HAVGSDCTAT AYPKETERAV VDVPHPKPLF 1200
 GSOIATXHF LVVWSSSGK RPHHLMDFA TIVEDVQYF SEEDGIVVV IDQNGKRVVS 1260
 HTSFRRILQ GIPWGLIVV ATTFDHTVL HASKGRYRV GHWTRVLEKL GADRLKELK 1320
 QWAFVGRKS FRFVNTLTD ESKAKIFPV VPFPVVKKK L

Seq ID NO: 96 DNA sequence
 Nucleic Acid Accession: 1: NM_020436 and AK001666
 Coding sequence: 63-324

25
 30
 35
 40
 45
 50
 55
 60
 65
 70
 75
 80
 85

1 11 21 31 41 51
 CAGAAATTTG TGGCGAGAG GGCATAAAC TGGCGCTCTC CGGAGCGCCC GATCTCCCA 60
 CCAATGTCAG GCGCAGACG GCGAAACCCC AGCAGATCAA CTCGAGAGG GACCAAGGCG 120
 AGCAGGACCC GAGCGACGAC ACCCCGGAGT TTGACAGTC GCGCCAGCG CGCCGCCCG 180
 CGGCGGAGCT GGTGTCTCTG GTGACCCAC CAGGAGATGA CCAAGCTGCG AGTGAAGAT 240
 AAGCCAGCAT AAAGCGCTCT GTTCGAGAG AGACAGCTCT CTGTAGAAA TCTGTGCGCG 300
 AGTTTCTGAG CATTCTGAG TCTCTGAGC ATGACAAJAA TCTCTCAAT TCTCTCAAT 360
 TCTCTCAAT GAACTGACG GAGGCGCTCG TGGTCTCAG AGACTCTCC GAGCTCTAC 420
 TGAGCCACCA GCCACAGAGT CCGCGACGTA AGGACTGTCA CAGGAGAAAT GCGCGCACT 480
 CAGAGGACAT CAGGAGGAG CCGGATCGCG AGCTGTGCTG GTACTTAAG ACGAGAGCA 540
 CCGTCCGAC CAGCTATAGCT ATTAGCACA AGGCAAGATG GCGACAGAT GCGACAGCT 600
 ATGTGACTT CAGGAGCTA CCGGACACA AGTGGCGSTG GATCCAGCG AGCGCGATG 660
 CACTCCCTGC CCGCTGCTCT GGTGCGACA GAGTCCCGTG GGTCTCGAG CAGATCTGT 720
 GTCTCGACCA CAGGAGCTA CAGCAGATCC AGCTCGTGGC CGAGATCCGC ATCGAGCTGA 780
 AACTGTGCT CTCCTGCTCG CTCGACGTA CCGCGCGAG GCGCCACAT CTGAAGCTCT 840
 TGGCACCA CAGTGTCTCG CAGTGTCTCG CAGCTGTGGC TTGTCTCAG CAGGAAGCT 900
 GAGCGCAAG TCTGTCTCTG GATGCTTGA AAGCAAGCAA GCTACTCAC GCCAACATCC 960
 CTTCTGCAAC CAGCTCTCTG TCCCAGGCG TGGACCTCT CACTCTGAAG CAGCGTGG 1020
 CGCGGCTCT CCGAGACTCT ATGTCCCGCC TCCCGAGCG TTGTCTCTCT CAGCGCTGG 1080
 GCTCTGTCT CTCGACGCT CTTCTCTCA CTTCTGCTCT AGACACTCT AAGAAAGGGA 1140
 AGGGGAGCC ACCGACATCT TCCCGGTGCG ATGTCAAAC CAAAGACGAG GCGCGCTCT 1200
 ACGAGCACA GTGTANGTAC TGTAGCAAG TTTTGGAC TGTATGCTCC TTGACATCT 1260
 ACCCTCCGTC CACACTGAG GAGAGACCTT TGTGTGCTC TGTCTGCTT CAGTCTCTA 1320
 CACGCAAGG CACTCTGAG GTGACCTTC ACCGACCTC CCGGTGAG GCAAACTCC 1380
 AGCTGTTCG CAGGTTCG CAGAAAGTGG CCGCGGACA TGGCATCCCC TATGCACTCT 1440
 CTGTACCTGA CCCATAGAT GAACGAGTC TTTCTTGA CAGCAACTCT GTCTCTGTA 1500
 CAGCTCTGT AGGCGTACT CAGATCTTT GTTGTGGAC TAATCCAGG GACCTCAAG 1560
 GTGTCTCTT GCGGTGTGAC GTGAGCTGT GCGCTCTCT AAGAAAGTGG GTTGACCA 1620
 CACTCCCTGG GTTGGGACCA AACTATAAT CCCCAGAGCC TGTGTCTC CAGGAGGAT 1680
 GGACCCCTGA GCCAGCTGGA GAGCCCTGGA AATTGACGA GTTGTGGAG AACATGCA 1740
 AGCAGCACG GATGTCCAC GAAATGTCTA TTTCACAG AGTCCTAAG TGTGAGAGCT 1800
 CACTCAAGT GATGTCTGAC GATGACCG GAGGAGAC GAGTCTGT ABAATCTCT 1860
 GCGGAGCTT TTTACAGAA GATGACCTGA AGACACACT TGGGTCTC CAGACACCA 1920
 CATCATTA GAACGAGCAT TGTGTGCCCA TCTGCGAGA GAAATGTACT AATGTCTGA 1980
 TGTGTGACCA ACATATTGCG ATGCAGTGG CCGGTGAGT TCCCAACAG CCGCTGCA 2040
 ABAATCTG TAACTTTAG GTTCTGTGAC CATGAGCTT GGGGAGAC GCGGACCG 2100
 GCGTCTGT CCGTACGA GTTCTGCAA CATGACCT AGACCTGAGT AGTCTCCAG 2160
 AGCTCTCAG CAGCTCTCC AGGTGCCCA CCGCTCTCC CAGCATCAC TGGGATCAC 2220
 CCGAGCTAG GTTGTGCGAT ATGCTCTCT TAGATGCC CAGGAAAGTG GTCTCTGCC 2280
 CTTTAACTT GCGAGCGCC GCGAGCGAG AAGAGCTTC GTTGGAGCC GATCTCTGA 2340
 CAGAGCTCT ATGCTGTGAC GTGAGGAC AGGATTTCT GAGCGAGCC CAGATCTCT 2400
 GAGAACAC CACTCTCTG CACTCTCTCC CGGCAATAG TCAAGCGGA AGCATCAAT 2460
 CAAAGCTCC CAGTCTGCG AGCAAGTGG AGAGCTCGGA GAACAGCCCG ACTGAGATG 2520
 AAGCTGGAG CAGTCTCTCT TCCAGTTTA TGGAGGCC CCGCATCAT GTCAAGATG 2580
 AAGTCTGCG CAGTCTCTG ATGCGCGGA CAGTCTCTC CAGTCTCTC CTTTGTCT 2640
 CAGCCGAC CAGCCGACCG GCGAAGCAC ATGTCTCAC ACCTGTGCG AAGACTCT 2700
 GCTCTCTAG CCGCTCTCAG ATCCAGAGC GACTCTCAC TGGAGGAG CTTTGTCT 2760
 GCAACATGT TGGCGAGCT TTTACACCA AAGCAGCTT AAGGTTCAC TACATGAC 2820
 CAGCTGCGA CAGTACTCT CCGGCGCTGT GCGCATCTG AGCTCTGAG AACCTGCG 2880
 CTTCTCTAG TACGAGCA AAGAGGCTT CTTCAAGGA CAGTCTCTC CTTCAAGCT 2940
 CTTCTCTGA TGTGAGCT GTTGTGTGA ACCAGTAC CAGTCTCTC AATGCGGCT 3000
 TGGCTGGA GAGCATAG ATCTCTGTA TCCAGATGG GCGGTCTCT ACCTGCGCT 3060
 TTTCTTGGG GCGCTCTGT GTGTGAAT CAGCCAGCT CTCAAGTGT GATCTCTCT 3120
 ATGCGGCT CAGTCTCTG GTGGAAGAC CAGTCTCTC TGGAGCTCT CTTCAAGCT 3180
 AGTCTCTCA CTTCTCTGA GAAGAACAGA TTGCTGAG CTAAGGAGCA ACTCTCTG 3240
 AAGAGCAAT CCGACACAG TGAATCTCT AGAATCTCT TTTTCTGA AGACTCATC 3300
 TCTCTCTCT TCTTCTCTCT TACTGATG CAATGATG TACTACTCT GTTGTGAGC 3360
 ACGACTCG GCAATGCTA CATCTGAT TGTCTCTG CTTCTCTGA AAGATGT

WO 02/102235

PCT/US02/19297

Seq ID NO: 97 Protein sequence:
Protein Accession #: NP_065169.1

	1	11	21	31	41	51	
5	NSRRKQAKPK	HINSEEDQGE	QOPOQOTPEF	ADAAAPAAPA	GELGAPVHPE	ONDEVASEDE	60
	ATVKRLRRRE	THVCKRCCKAR	FFSTSEFLER	KENCTKINPVV	LINMDSRGTV	PSRDFSGAVL	120
	SNQPTFSQSK	CHRMEDQDGE	EMHREHREDA	SVPELKEETA	LEPPQGLIIV	LAKCEVAMTH	180
	VTGLGALQTK	WAKGSDASA	LPAFVPGANS	IPWVLRLCLC	LQOOOLQOTC	LTEQIRICVN	240
	NWASHALHSS	GAGATDLETL	GSMSQQVSA	AVALLSQKAC	SQGLSLDALC	QAKLPHAKTP	300
10	SATSLSLFQL	APPTLKPODT	RVLNPMMSRL	PSALLPQAPG	SVLPGSPSFT	VALDTSEKKG	360
	GKPFILISVD	VEFDKDAALY	KHKCYKCSKV	FUTDSISLIR	IASRSTSEKRP	VCISVGRHPT	420
	TKCNLKRPH	RIHQVKAQD	-FAEFDQKTA	NKMTIPVALS	VPQFIDPSLS	SLQSEPIVLT	480
	TSVGLPNQLS	SGTNFKDLTG	GLSPDQLQEG	PSFESBQDPT	LPFGVGHYNS	PRAGPQSGS	540
	TPEFGSETLK	LQGLVENIDK	ATTDNIECLI	CHRVLSQGS	LMHYRTHNG	ERPFQCKIKG	600
	RAFSFTGNLK	THLQVHERNT	SIKTHSCPI	QCKEPTNAVV	LQKHSIMNKS	QDTWPTPLPE	660
15	HFCLTFQSEF	HTVCEKQDQ	ALCKDDYVSS	IVDEVBKQSR	APSSSSRVPT	PLYSIHSAEP	720
	TLOFAMQSL	DASFQVGPAP	PHLQGOGRRE	HGVSVEDGLT	NDSSLSMGDQ	EYSGRSPDIL	780
	ETTSFQALSP	INSQAESIKS	KSPADGSKAR	SSNSRSTEME	GRSSLSTFI	RAFFTVEVEA	840
	VQTFVFGSPT	LSPTCHPLLA	AQPRRQAKGH	QCTRCGRNFS	SASLQIHER	THTRKSPFVC	900
20	HICQARCTTK	KLHYVRYTH	GNMRSKSRAG	RMLALISYMA	LLOTDGKIVS	EITPFSILAP	960
	SUNVDVVMG	QTSKSLKGL	AVKTNESVI	QSGVPTLPE	SIGATSVNM	ATYSKMDGSG	1020
	SGISADVERP	SATQCVPIQG	PFPHLEENKI	AVS			

Seq ID NO: 98 DNA sequence

Nucleic Acid Accession #: NM_006612.2

Coding sequence: 553..1095

	1	11	21	31	41	51	
25	TTCTCCCGCA	ACCTTCCCTT	CGCTCCCTCC	GGTCCCCCCC	TGCTCTAGC	CTCCGACTCC	60
30	CTCCGCCCTC	CACGCCCGGC	CTCTGCGCTT	GGCGGACCTA	AAGTGAGTAA	ATTACAGCCT	120
	TTCTGTTTCT	CTCGGCTGTC	TTCTTCCGCG	CTGTGCGAAT	GGCCGCTCTC	CGCTGTCTCT	180
	TGTCGCCCTC	GGCCCTCTCT	GGGCCCCCCC	CTTTCAGGTT	CACCTGTGTC	CTCCGACTAT	240
	CTCTGCCCTC	CTCTATGATC	CTCTGCGGAT	CTGACACTCT	CTTTCGCCCT	CTTTCGCCCT	300
	CCGAAAGATA	CACACTGATC	CCGCGCGGAC	CCCGAAGACA	GGCCCTCTCT	CCTGACAAAT	360
35	CAGACGAATT	CTCCCCCCCC	CCCCAAJAAA	AAAAGCCATC	CCCCCGCTCT	GGCCGCTGCG	420
	ACATCTGGCC	CGCCGACATC	GGCGCGAGGG	GGCTCTGGAC	AGGATGTGTC	CGCAGAGAGG	480
	ACAGGCCGCT	CTCCGCGACG	CCGCGCGGAC	GGCGCGGAGC	CGTCCCGGAG	CGTCCCGGAG	540
	TTCCGACAGC	CAATGGGAAT	CCCAATGGGG	AAGTGGATCG	TGGTGTCTCT	CACCTCTCTG	600
	CGCTTGCGCT	CGTCTGCAAT	TGCTGCTTAC	GGCCCGAGTG	AGACGCTGTG	CGGCGGGGAG	660
40	CTGCTGCGCA	CGCTCGAATT	GGTCTGGGG	GAGCGGGGCT	CTACTCTCMG	CAGCGCCCGA	720
	ACGAGCTGTA	CGCTCGGAGG	CGTGGGCACT	GTGAGGGAAT	CGTCTTCCCG	CACCTGTGAC	780
	CTGCTCTCTC	TGGAGACTCA	CTGCTCTACT	CTTCTCAAGT	CGAGAGGGAT	CGTGTGACAC	840
	CGTCCGACCG	TGCTTCGGGA	CAACTTCCCC	AGATACCCCG	TGGGCAAGTT	CTTCAAAATAT	900
	GACACCTGGA	AGCATGCCAC	CCAGCGGCTG	CCAGAGGGCC	TGCTCGCCCT	CGTGGTGGCC	960
45	CGCGGGGCTC	ACGTCTCTCG	CAGAGGCTCT	GAGGGGTCTA	GGAGAGCCAA	ACGTCACTCG	1020
	CGCTGATGTC	CTGACCGGCA	CAAGAGCCCG	GGCGCGGGGG	GGCCGCTCTC	AGAGATGCGC	1080
	AGGAATCGGA	AGTGAAGCAA	ACTCGGCGAA	GTCTCGACCG	GGCGCGCACC	ACTCTCGAGC	1140
	CTCTCTCTGA	CCAGCGACGT	TTCCATCAAG	TTCCATCCCG	AAATCTCTCT	GGTTCACAGT	1200
	CGCCCTGGGG	CTTCTCTGGA	CCGATCCGCG	GTGCGGCGCG	TCCCGGAAAC	AGGTGACTCT	1260
50	CGTCCGCGCC	CTGCGCGG	CTGAGGAGAC	ACAGGAGAGT	CTTCAAGACT	GTACAAATCT	1320
	GATTCGCTTT	AAACACCTCT	CAACATACCT	CCCCCC			

Seq ID NO: 99 Protein sequence

Protein Accession #: NP_006663.1

	1	11	21	31	41	51	
55	WGIPMKRML	VLTATLAFAS	CCIAAYRPSB	TLCGGELVDT	LQPVCGDRGF	YFSRPASRVS	60
	RRSNQVIBEC	CFRSCDLLAL	ETVCAIPAKS	RRVSTPPTV	LPDFRFRITP	GFQDFDTRNK	120
60	QGTQLRML	PALLRARKH	VLAKLEAPR	SAUSKRELLA	LPTQDFPMGDS	NPFEVAGRW	

Seq ID NO: 100 DNA sequence

Nucleic Acid Accession #: NM_064217.1

Coding sequence: 55..1092

	1	11	21	31	41	51	
65	GGCCGCGAGA	GTAGCAATGC	CTTGGACCCC	AGCTCTCTCT	CGCCTTCTCT	TCTAAGGATG	60
	AGCCGAGACG	AGAGACTCTA	TAGCCGCCAG	AGACGCCCTC	ACTCGGCTCT	ACTCGGCTCT	120
	AGCACCTCGC	CCGAGCGAGT	CGTCCGGAJA	GAGCCTGTCA	CGCCATCTGC	ACTCTGCTCT	180
	ATGACCGCGT	CCAAATGTCCA	GGCCACAGCT	CGCTCCGGCC	AGAAAGTGAAT	GGAAATAGAC	240
70	ATGTGGACAC	CCGACGACTC	AACCGAGCAT	TTACAAATTA	ATGACTTTGA	GATTGGGGCT	300
	ACTCTGAGGA	AGCTTCAGAA	GGAGTACGTA	TACTCTGCTC	GGAGAGAGAA	AAAGCAATTC	360
	ATCTCTGGCG	TGAGAGTCTT	CTTCAAGTCC	CGATGAGAGA	AGAGGGGCGT	GGAGCATCAG	420
	CTGCGCGAGG	AGATCTCAAT	CCAGGCGCCAC	CTGACCATC	CTCAACATCT	GGTCTCTTAC	480
	AACTATTATT	ATGACCGGAG	GAGGATCTAT	TGATCTCTAG	AGTATGGCCC	CGCGGGGGAG	540
75	CTCTCAAGAG	AGCTTCAGAA	GAGGTGACCA	TTTGACIMAG	AGCGAAGACG	CAGCATCAGT	600
	GAGCATCTGC	CGATCTCTCT	AATTTATCTC	CATSSAGAGA	AGTTATATCA	CAGACATATA	660
	AAAGCAGAAA	ATCTCTCTCT	AGGCTCTCAG	GGAGAGCATGA	AGATTCTGGA	CTCTGGCTGG	720
	TGCTGTGATG	CGCCCTCTCT	GAGGAGGAGG	ACAAATGATG	GCACCCCTGGA	CTACCTGGCC	780
	CCAGAGATGA	TGAGGAGGCG	CTGACACAT	GAGAGAGATG	ATCTGTGGTG	GATTGGATGT	840
80	CTTCTGTGAT	AGGATGAGCA	CTTCTGAGC	CTGACATGCA	CGAGACATCA	CAGACAGATC	900
	TATCTCCGCA	CTCTCAAGGT	GGACATTAAG	TTCCGCCCTT	CTGTGCCCAT	GGAGGCCGAG	960
	GAGCTCATCT	CCAAATCTCT	GAGCATATAC	CGCTCGGAAC	GGCTGCGCCT	GGCCGAGTTC	1020
	TGACCCACAT	CTGAGTCTCG	GGCCAACTCC	CGAGAGGGTC	TGCTCCCTCT	TGCCCTTCTA	1080
	TGCTGTGCTC	GATGTCGCTC	CGCATCTACT	CGGATCTACT	TGTTTGTATG	TGCTGTGATG	1140
85	TATAGSGGAA	AGAGAGGATC	CTTCAATCTT	CGCTTATCTG	TTTCTTACTC	CGCTCTTGTG	1200

WO 02/102235

PCT/US02/19297

TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 101 Protein sequence

Protein Accession #: NP_004208

5
1 11 21 31 41 51
HAQKINQYFW FFKQTAPSG LGLTLPQVLR KEVTPPSALV LMSKRNQST AAPQKQVHE 60
SSGTPDLTR HPTIDPEIG RPLGRKPKFN VYLAREKKSE FIVALEVLFK SQIEKKRVEH 120
QURREIEQA HAHPHNLR LNYFFYDRRI YLLYLRAPRG RYKSLGKST TFKGRTAT 180
MEELADALNY CHOKVVIHR IKPHNLALGL KGLSLIADRG HLYKAPSLHR KTMCTLODYL 240
PFHEIRERKH NKKVDLWICG VILCTELLVAN FPFESASINE THRIRKVDL KFPASVPTGA 300
QDLISKLLRH NFSEBPLPLQ VSMAPWVAN SRKVLPPSLV QSYA

Seq ID NO: 102 DNA sequence

Nucleic Acid Accession #: AK025790

Coding sequence: 56..1662

15
1 11 21 31 41 51
AGTATCCGAG GAGGAGCAAG TGGCACGTCT TGGGACCTAG GCTGCCCGCT CCGTCATGTC 60
GGAGGCGMTC CTTCTCCGCG CAGGCGGCTT CCGTCTCCGA GACAGATGTC TACTTCTCTC 120
CATGCTTGAAG TCCAGCAGCTG CAGATTGGGG GTCTGTGGTA GCGAGAACCC TCGTATCAGA 180
CTGCTCTGTC GTCTCTACCT CCGTAGAGGA CAGACGAGCG GTTCCATCTG AGGACAGTAT 240
GGAGAGAGTG AAGATATACT TGAAGGTTAG GCGCTTGTTA CTTTCAGAGT TGGAAACAGA 300
GGAGATGATG GGTGTGTCCT GTATTCAGAA HGTGAGGACC CTGTGCTAC AACGACCCA 360
GACCTCTTT GCGTGAAGA GGAATGAGG GGPATTTGGC CAGCTCCACG ACGGTTCCAC 420
CTTTTCCGAG ATCTTTGGGC CAGAAGTGGG ACAGCGATCC TTCTTCACCC TAACGTGTGA 480
GGAGATGTTA AAGATGATAC TCAGAGGGCA GAACTGGCTC ATCTATACAT ATGAGATCCG 540
TAACTCAGGG AAGACCCACA CAGTTCAGAG TACATCTMAG GATGGAGGGA TTCTCCCGCC 600
GGCTCTGGCG CTGATCTCTA AGGCGACCTT CATCCACACG CTGATCTGAA CAGTCACTG 660
GCGCTCTGCT TCGCATGAGG TAACTTGCGT AGACAGCAAG CAGATCCGAC AGGAGAAAT 720
GAGAGAGCTG TCCCTGCTAA ATGAGGCGCT CCGAGAGGAG GAGCTGTCCA CTTCCTTGAA 780
GGAGAGTGTC TACATCGAAA GTGCGATGAG TACAGACACC AGCTTCGACA GTGCGATCTC 840
TGCGCTCTCT TCTATCGCAT AGTATACGCG CAGTCCAGCA CTGATAGAAA CAGTCACTG 900
ATGCGACAGC CCGAGACGCT CCGCCATACC TGTCCCGGCA AACATTCGCT TCTCCATCTG 960
GATCTCTGCT TTTGAGCTCT ACAACGAACT GCTTTATGAC CTATTAGAAC GCGCTAGCCA 1020
ACCGACCAAG AAGCAGAGCT TCGCGGTATG GAGGATGCAA AATCGCAATC CTTATGTGAA 1080
AGATGATGAC TGAATGATGC CAGAGATGTC TGGAGAGCTC TAAATATGCG 1140
TGTAAAGAAC CAGAGCTTGG CCGAGCAOCCA CTTCAACCGC AACTCCAGCG GCGATCCAG 1200
CATCTCTCTA ATCAGGATCC TACACCTTCA GGGGGAAGGA GATATGTCCT CCAAGATCAG 1260
CGACACTGTCA CTCTGTGATC TGGCTCCGCT AGAGCGCTCG AAGATCAGA AAGATGTGTA 1320
ACGTTGTGAG GAGACAGAAA ACACTAACAC CTCTCTACAC ACCCTGGGCC GCGTATATGC 1380
TGCTCTCTGT CAAGATCTCT AGACCTGGCT CAGACGAGAC CTCTCTCTCT TCTGTTCAG 1440
CAGTGTGACT CAGAGTGTCC AAGGTTCTCT CACAGCGCCA GCGGCTTCTT CAGATATTTG 1500
CATGTGTGAT CCGTGTGCAT CTACCTATGA TGAAACTCTT CATGTGGCCA AGTTCTCAG 1560
CATTGTGAGC CAGGTGATCT GTGCATGCC CACTATATCA ACTGGATTC CCACTCCGCG 1620
ACTGTGTC CAGAGAACAT AGTTCTCAGG TATCTCCGCG AGGCTTGAAG GCGCTTGAAG 1680
CAGACACAGG CCGTAGATAT GATATTGAAA ATGAACTGTA CATCTCAATG TATGCGAAG 1740
AGAGGCTCCT ACAAGTTGTG GAAOCCATGA AGACACTGCT TTTGAGGAA GAGACAGAAA 1800
AGACTACGCT GAGATGTCAT CTCGAGATG AAMTTTGAAA TGAGATGCTA GACACATGTC 1860
ACACGCGGGA ACGTGGGCTC AGTGAACAT TGGACACCA AAGAGACTA TTGCGGAA 1920
TGATGAGGA AAACTAAAT ATCTCTCAGG AGTCACTGAC AAGTTTATC CAGAGAGAA 1980
TTGAGGAGCG GGAATGAAAG ATTGAAGAGC TAGAAGCTCT CTTCGAGAA OCCAGACAA 2040
AGTCAGTGGC CCACTAGCAA TCAAGGCTCG AATTGGCCCT AGGCGGCTCA CAAAGTGTG 2100
CAACTCTGCT CTGACCGGCG CAGCTCTCAG AGTTTAAAG TAAATACAG CAGTGCAGAG 2160
CAGACCTAAA CTCTACGACT GAGAGTCTCT ATGATATCA GAAATATGA GAACCACTG 2220
CCTCAGCAG ACGCTTCCAC ATTAGTGTGG ACAGAAAGTT AAGAGAGGGC CAGAGAATA 2280
TAAGCTGTT GCGACAGAG CTTCAAGAAC TTGTGTGATC TCTCAATCA CGAGAGAGAG 2340
CTTGTGACCA CAGACTCTGG CAGAGAAAC TTCTCTAAGC CTGACACTG TGTATGATA 2400
CTTATACCA ACGAGCGGCT ACTCTGCGCT ACCTCAGAAA CAGCTATGGT CTATGATAG 2460
TGAGCTCTCG GAGAGAGCA GCAATGTATG CTAGCAGATA TCACTATGTG TTGAACCTCC 2520
AAGCGCAAGT TCTGCGAAA AAGCGCGCTG GTACACACCA GGAATAACAG CAACCACTAG 2580
ARACACACC AGGAGAGAAA CAGTCTCTTC GAATTTTACT TCCCGAACA CCAACTCGCC 2640
AAAGCTCAC AAGATGCGCT CCGTATGCGCT CTGAGAGGCT TCCCTCTTAC 2700
TCAAACTGG GCGCTTTGCG ARAAGTACT AACGCTGTGG GGAAGAGAA GAGCGATCAT 2760
GGCGCTGAGG TGGGTCAGCT ACTCTCTCCA AGMATAAGT CTCTTTATG CTTTACATA 2820
TATCACGAT TATATCCAG AGTCAGACT CAGACATGAT CTTTTCTCT ACTTTTGAT 2880
TATACACAC TATATCTGTAT TATATCTGTAT LCTGAGNFW YGGLAHVPT DASEKMLLE 2940
CAGACAAAA ACACTATAT TAAGCATATT ATTGTTCACA TTTTATATG AATTCQAAAT 3000
GTAGCAAAAT CATTAAAAA AATTAAAAA GGGACAGAAA AA

Seq ID NO: 103 Protein sequence

Protein Accession #: NP_005724.1

75
1 11 21 31 41 51
MSQGLLEPPA GLEEDDDVVV SPHESTAAD LGSVVRNML SDCHVYVSL EDGQVPSFD 60
SHEVTVVYLR VFLLPRLR RQKQCVRI ENVEYVLAQ PDSFALKEB SRIHQATHR 120
FTFGPIGFBE VQAGSFFRLT VKENYKDVLL QGNHLYTYG VTNSEKTHI QTTIKDGLL 180
PRSLALIFNS LQQLAHTPD LKPLLSNEVI MDSKQIRQE ENKGLSIAG GLOBEELST 240
LSENVIEER IGZTFSRDS IAGLSLIGC TSSSQLETS HRNQPTDPA LPVYANRFS 300
NIHFFETIN ELIYLLPFL SQPKRQYLA LCHGKNWFY YGLAHVPTD DASEKMLLE 360
VGRKNSPAS THLANSERS HSIFSRILH LQEDGIVPK ISELSLADLA GSERCKDQS 420
GERLKAGNI NTSLETLGRC IAAALNQCN RSKQLVWPF DSKLTVFQG PFTGRGSCN 480
TVNPNCAST YDETLHVAKP SAIASQVTC APTYATGPI PALVHQGT

Seq ID NO: 104 DNA sequence

WO 02/102235

PCT/US02/19297

Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11..793

1 11 21 31 41 51
5 AATCCCGGACAT ATGGCGAAG ACACTCAAC TGTTCGTTC TCCAGGGCC TGTGATTTT 60
TGGAAATGTG ATTATGTTCT GTTGGCCCAT TGCCCTGACT GCGAGATGCA TCTCTCTGT 120
ATCTGACACA CACAGCTCTT ACCAGCTGCT TGAGGCCACC GACACAGATG ACATCTATGG 180
GGCTTCCTCG ATGCGATAT TTTGGGGTCT TGCCCTCTTC TGGCTCTCT TCTTAGGZAT 240
TGTAGGCATC ATGAGATCCA CAGGAGAAAT TCTCTCGGCG TATTTCACT TGAATGTTAT 300
AGTATATGCC TTTGAAGTGG CATCTTGTA ATCACAGCA ACACACGAG ACTTTTCCAC 360
ACCAACCTCT TCTCTGAGAC AGATGCTAGA GAGGTACCA AMCAACGCC CTCACAACAA 420
TGTATGCGAG TGGAAAJACA ATGATGTGAC CAATACCGG CAGAGCCCTA TGCTGTACGA 480
CAATGTCTGT GCGGTAAATG GTCCATCAGA CTCCCAAAA TACACATCTG CTTCTCGZAC 540
AGAAATAAT GATGCTGACT ATCCCTGGCC TGCTCAATG TGTGTTATGA ACATCTTAA 600
TGAACCTCTC AACCTGAGAG CTGTATAACT AGGCGTCCCT GGTTTTATC ACATACAGGG 660
CTCTATGAA CTGATCTCTG GTCCATGAA CCGACATGCC TGGGGGGTTC CTTGTATGAG 720
ATTGSCAT CTCTCTGGA CTTTTTGGGT TCTCTGSGT ACTGATTTCT ACTGGGAG 780
AATTGATAT TAAAGA

Seq ID NO: 105 Protein sequence
Protein Accession #: NP_008863.1
1 11 21 31 41 51
25 MARNSIVRC PQELLIFNV IIQCCSIAT ARCTFFVSDG HSHVPLEAT DNDIDYDAM 60
IGIPVIGLFL CLGFGIVCI HSSRGKLLA VFLMLTVA FVVAICTLAA PQDPTFTNL 120
FLKMLERVY KNSPFPNDD WKNNGVTKM DRLMLQDKC GWPGSDWCK YTEAFRTNN 180
DADYFPWQC CVNNLEKFL NLEACKLGVF GFYRNGQCYE LIGSPNIRHA MVAMFGFAI 240
LCHTFWVLG THFYHRIEY

Seq ID NO: 106 DNA sequence
Nucleic Acid Accession #: NM_002740.1
Coding sequence: 178..1968

1 11 21 31 41 51
35 CCGGGSTTCC GCTCTCTCG GCGAGCGGAC CTTTGGGTGC GCGCTCGGGG CAGGTTGGCC 60
AGTAGGTGAG GCGAGCGGCC GCGCTTCTCC GCGAAGGCCA GCGCGGGGAG TCGCCCAAG 120
CCGCGGAGAC GCGCCCGGCA CCGCCCGCAT CCGAGCTTGA GCGCGGGGAG TTAGAGATG 180
CGACCGGAGA GCGAGAGCTC CACGCTCTCT CAGCGCGGCG CAGCGGGAG 240
CACTTCCGAC AGGTCGCGGT GAAAGCTTGC TACCCCGGGG ATATCATGAT AACACATTT 300
GAACCTTCCA TCTCTTTAGA GGGCTTTGAC AATAGGCTTC GAGCATGTG TCTTTTGAT 360
ACCAAGACAG TCTTCCGCTT GAAATGGATA GATAGGAGAG GAGACCGTGG TACAGTATCA 420
TCTCAGTTGG AGCTTTTAGA AGCTTTTAGA CTTTAGGAG TCTCTGACT 480
TTGATTCATG TGTTCCTCTG TGTACAGAA CCGTCTCGGA TGCCCTGTCC AGAGAGAGAT 540
AAATCATCTT ACCGTAGAG TGCACCGCC TCGAGAAAGC TTTATGTGC CANTGCCACC 600
ACTTTCCAGC CCAAGCTGTT CACAGCGGCT GCTCATCTGG CCACTCTGAC AGACCAATTA 660
TGGGCACTTG GAGCCGAGG ATATAAGTGC ATCACTGCTA AACTCTTGCT TCATAGAGAG 720
TGCATAAAC TCGTCAAT TGAATGSSG CGCATCTTCT TCGCCAGAGA ACCAGGATG 780
CCATCGATCT AGTCACTCAT GCATTCTGAC CATGACAGCA CAGTAAATCC ATATATCTCT 840
TCAAGTCAAT AGAGTTTGA TCAAGTTGAT GAGAGAAAG AGGCATGAA CACCAAGGAA 900
50 ATTTGGCAAG CTTCATCCAG TCAAGTCTT CAGGATTTTG ATTTCCTGCD GGTATATAGA 960
AGAGAGAT TTGCAAGAT AGCTTTGCTT CAGTTTAAAA AAGCATGCD TATTTATCA 1020
ATGAAGTTG TGA AAAAGA GCCTTTTAA ATGATGTAG ATATTGATT TGTACAGACA 1080
GAGAAGCATG TTTTGAACA GGCATCCAT CATCTTTCC TTGTTGGCT CCAATTCTGC 1140
TTTCAGACAG AAGCAGATT GTTCTTTGTT ATAGATGTG TAAATGGAG AGACCTATCA 1200
55 TTTCATATCG AGCAAGAG AATAGCTGCT GAGAGACAT CCAATTTTA CTCGACAGA 1260
ATCGCTCAG CATTAATAA TCTTATGAG CAGAGGATA TTTATAGAA TTTGAACCTG 1320
GACATATGAT TACTGCACT TGAAGCCAC ATTAACACTA CTGATACGG CATGTGTAG 1380
GAAGATTAAC GCGCAGAGA TACACACAG ACTTTCTGT GTACTCTTA TTACATGCT 1440
CTGATATTT TAAAGAGAA AGATATGCT TCAAGATGCT ACTCTGGC TCTTGGAGTG 1500
60 CTGATCTTGT AGATGATG CAGCAAGCTT CCAATTGATA TTTGTTGGAG CTCGACAGT 1560
CTGACACGA ACACAGAGA ATATCTCTTC CAGTTATT TGGAAJACA AATTCGATA 1620
CCAGCTCTCT TACTGTAAA AGTCTCAAGT GTTCTGAGA GTTTCTTAA TATTCAGACT 1680
AAGAGAGAT TGGTGTCTA TCTCAACCA GCAATTTGCT ATATTCAAG ACACCTTTA 1740
65 TCGGAGAGA TTTATGGA TCTGATGAG CAAAGAGAG TGTACTCTCT CTTTAAJACA 1800
AATATTTCTG GGAATTTGG TTTGACAC CTTTGTATCT AGTTTACTAA TGAACCTGTC 1860
CAGCTCATCT CAGATGAGGA TGAATTTGT AGGAAGATG ATCATGCTGA ATTTGAAGGT 1920
TTTGAATATA TCACTCTCT TTTTGTCTT CAGAGAGAT GTTCTGACT CCAATTTTCT 1980
AAGCTGAT TCACTCTCT TTTGACATTA ATGCTGATAT AGATTTGCT CAGCTGAG 2040
TACATTAAC CATTTTATAT TTGCACTTA CAAAJAACA CCGTATATCT TCTCTGTAG 2100
70 ACTATAGAA TCAATATATA CATCTGTTT ACTATGAAA AAAAATTAAT ACTACTAGCT 2160
TCCAGCAAT CATGTCAAAA TTTAGTTGAA CTGTTTCTT AGTTTAAA AGGCTACAG 2220
ATGATTAAG AAGTTACCT TTTTGTAAA AAAAAAAGA G

Seq ID NO: 107 Protein sequence
Protein Accession #: NP_002731.1
1 11 21 31 41 51
75 MSHTVAGGGS GHSHQVRVK AYRGDIMIT HFEPISFPG LCNREVDMCS FMSQLFTMK 60
WIDEDDPCT VSSQLELEBA FRLLYLNDS ELLIHFPCV FEPNPGMPCG EDKGYRGA 120
80 RWRRLTCAN GHPTQAKPK FRANKICTD RIGLGRGTY KICMKLLVH KCKHLYRGA 180
CRSHSLQEP VMSRSGHST SDNGTTPY NPSHSLD WELKDMWT BEHRAESI 240
GLQDPDLLE IGSGTAYKL VLRKLEKTR IYAMVYKSL WNEDEDHW QTEKIVFQA 300
SHHFVLGLH SCPTSERLF FVIEYVND LNPIMQRKQ LBEHAFYS REISLALNYL 360
HERGIYREL KLVNLDSE GHKLTDYD CSHLRLPQT TSTFCUPHY IAPSLKRG 420
85 YGSDVHRL OLVLFENAG RSPEDVGS INFQNTSEY LQVILEROI RIFRLSKA 480

WO 02/102235

PCT/US02/19297

ASVLKSPFLNK DPFEKRLGCHP QTCFADIQKH PFPRNVDMHM MEKQKVVPFF KPNISGHEPL 540
DFDFQSFTRF FQVLITDDDD IYRKIDQSRF BQFEYINPLL MSABECV

Seq ID NO: 108 DNA sequence
Nucleic Acid Accession #: NM_000349.1
Coding sequence: 127..984

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10	G	G	G	G	G	G	
	G	G	G	G	G	G	
	A	A	A	A	A	A	
	G	G	G	G	G	G	
	T	T	T	T	T	T	
15	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
20	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
25	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
30	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
35	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	

Seq ID NO: 109 Protein sequence
Protein Accession #: NP_000340.1

	1	11	21	31	41	51	
40	L	L	L	L	L	L	
	L	L	L	L	L	L	
	L	L	L	L	L	L	
	L	L	L	L	L	L	
	L	L	L	L	L	L	
	L	L	L	L	L	L	
45	L	L	L	L	L	L	
	L	L	L	L	L	L	
	L	L	L	L	L	L	
	L	L	L	L	L	L	
	L	L	L	L	L	L	
	L	L	L	L	L	L	

Seq ID NO: 110 DNA sequence
Nucleic Acid Accession #: B08 sequence
Coding sequence: 131..682

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50	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
55	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
60	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
65	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
70	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	
	G	G	G	G	G	G	

Seq ID NO: 111 Protein sequence
Protein Accession #: A020968.1

	1	11	21	31	41	51	
75	M	L	K	S	D	R	
	M	L	K	S	D	R	
	M	L	K	S	D	R	
	M	L	K	S	D	R	
	M	L	K	S	D	R	
	M	L	K	S	D	R	
80	M	L	K	S	D	R	
	M	L	K	S	D	R	
	M	L	K	S	D	R	
	M	L	K	S	D	R	
	M	L	K	S	D	R	
	M	L	K	S	D	R	

Seq ID NO: 112 DNA sequence
Nucleic Acid Accession #: B08 sequence
Coding sequence: 228..884

	1	11	21	31	41	51	
85	M	L	K	S	D	R	
	M	L	K	S	D	R	
	M	L	K	S	D	R	
	M	L	K	S	D	R	
	M	L	K	S	D	R	
	M	L	K	S	D	R	

WO 02/102235

PCT/US02/19297

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1      11      21      31      41      51
|      |      |      |      |      |
CGCGGCGCGG CGCGAGCGCG GTGCGCTGGG AGCCTGCGCC GGGAGCGCGG TGAGGGCGCC 60
GAGAGGCTCG GTGGCGCGCG GCGCGGAGGA CTCCTCGGGA GAGGAGCTTC AGAGTGTGTT 120
5      TTTTAGCTGT GCTTTTAAAG TGATTTGAAG AGAGCGGCTT TGAAGATATG CCACACTCTC 180
GCTCGTGTGT GCGCAACGCTT CTGCGCTGTG CTGCTCTTGT TAATGCACTG GATGTGTGCT 240
ATTACTCTGA GTGCAAACTT TTTCACGTGT CGAGAGAGGA GCTTCAACAG CACATCTCTC 300
10     TTTCTAGGTT GTGCGTCTTA TCGCGGAGCG TGCCAGATA TAAGAGTGTG GACCCGCCCG 360
CACAGAGGTT GCGATGCTGT CTCCTCTGTC AGGCTCTGCG TATAGCTGTT GTCCAGATCG 420
TTATCTCTTC AGAAAGCGTG GCAITTTGCA AGAACATCTA CTCTTATPAT GTAGGCGCTC 480
CTCTCGAGCC TAGACGCTTT CCAATAGCTT TCGATGCTCT TACTGTGAAA AACCGAGCG 540
15     ATATATTATA TCGCATCTGA TGGCGAGAG ACAATATGTG TCCCAAAAT ACACAGTACT 600
GTTTGACAGT TCATCACTTC ACCAGCGACG GAGAGAGCAC ATTCATACCC AAAAAGTGTG 660
CTCTCGAAGG TGAATGTGAT TTTGTGGTGT GCGACGACAG CGGAGATTTCT GACATATGCG 720
ATGTATGCTG TGTGCAACTT GGAATATGCT CGATGTGAGT ATTCACACG AATGACATA 780
20     ATGCGATGTT TGCGCTTAAT GACGCTCAGA GAACATCTGG CAGCATGCCC CCCACACTCT 840
ACCTACAGGT GCTTGCCTCG GTCTTTGGGC TCCCATTGCT GTGATGCCAC CATCTCTAGG 900
AGAGGCGCAG ACCAGGCTCT AAAGCGACAG CCAAAAAGTG TGGAGACGTT GACTTTGCG 960
GTGAGATGCA ATCTTGCAGT TGGTGAAGAG TGACAGCTGG ACCTGAGAGC GAAAGCGAGT 1020
30     GATTGTGCTG GAGCAAACTG TCCGCACTGA GCGCCAGAGA CTGAGGATGG GAATTTGCGA 1080
GGGCGCTAGA AGATGTGCTG ACTTCCAGGC TTCTCTGTCA AAGAGAGCTA GTTTGGGCGA 1140
GTCTCTGAGA GAGATGCTGT GCAACTGATC CCACTGACTC AGGCGCTTAG CTGAAGAGAT 1200
TTCTGTAGCT CTTGAGCTGC CTCGAGAGCT GCCAGGTGCA ACCCTCTGTT TTAATGTATT 1260
25     AGCTCAGAG ATCTGTGGA AATCTAGCCG TCCCTCGTGT GAGAGAGAGG TTTTCCCGAC 1320
CAACGACATA GTCAATGAGA AAGGCAACTG TACGAGAAH ACTTCCAGTG GAACATATAT 1380
GAATCTATT TGCAATTAT TGCGGGAAT AAAGCTTTTA AATTATRAA

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Seq ID NO: 113 Protein sequence
Protein Accession #: Bos sequence

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30     1      11      21      31      41      51
|      |      |      |      |      |
NOYADYSECK PFGSRESEP VMLLLKVMK LLRLTKYKS SRPANKVSM LICHILALIA 60
VQIVIFPSES WAFAGINIFY NVKPLDPTG PFSFCEFTC SHAGNYNOC BHAEDEKCPQ 120
NTQYLCTVHF FTSRHSSTSI TKKCASSBEC HFVCGHSRSD SEHTCRSCC BGMICNVRLP 180
35     TSHNIAVFAV MHAQTSGSS APTLYLPVLA VVFLVPLL

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Seq ID NO: 114 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 402-1025

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40     1      11      21      31      41      51
|      |      |      |      |      |
ACTTCTTGAG CGCGGCTGCG TGCGTGGGAA CAGGCTCCTT GCGCGCTGCC CAGCGCTGCG 60
CACTACACGA CTCGCGCGCC CTCGCGCCTC CTTCACACTC CTGTGTGGAG CCGTGGGCTT 120
10     TCCCAACGGA GCGCGGCGCG GCGCTGACTC CTCGCGGCGG AGGCTCACTC GTCCCGCGCC 180
GCGCCCTCTG CGCGCCCGCA GTGTTTGAGA GCGAGGAGCG GCGCGCGCGC GCGCGCGCGC 240
30     GTAGCGGCA ACGCGCGCCC CAGCGCGGTT CCGTGGAGAG CTGCGGCGCG AGCGCGGCTA 300
GGGCGCGGAG AGGCTCGGTC GCGCGCGGCG GCGAGATATG CCACTACTCT GCGCTGTGTT 360
GCGCAACGCT CTCGACTAGT CTGCTCTTGT TAATCACTAG GATGTGTGCT ATTACTCTGA 420
40     GTCCAAACTT GTCTCACTTT CCGAGAGAGG GCGTGGAGAG CAGATCTCTC TTCTCAGAT 480
ATAGAGGTTC GAGCGCGCCA CCGACAGAGT TCGACATCTC CTCTCTCTGT CAGACTCTG 540
50     CTATAGCTGT TGTCCAGAT GTTATCTTCT CAGAAAGCTG GGCAATTGCC AAGAATATCA 600
ACTCTATATA TGTGAGGCTC CCGCTCGAGC CTCACCACTT TCGAAATAGC TCGAAGTGT 660
TACTTTTGA AAACCGAGG GATAATATTA ACTCGAATCG ATGCGGAGAA GACMAATGAT 720
60     GTCCCAAAA TAGCAAGTAT TGTTTGAGC TTCTTCTCT CACGACCCAC GGAAGAGGA 780
CATCATCAC CAAAAGTGT GCGTCCAGAA GTGAATGTCA TTTTGTGGT TCGCACAGCA 840
CGCGAGATTC TGAACATAG GAGTGTAGGT CTCTGTGTGA AGGAATGATC TGCAATGTAG 900
AATTATCCAC CATACACTC TATCGTAAAT GCGCGCTGAG AGAACATCTG 960
70     GCGAGGTC CCGCACACT TACTACAGG TCTCTGCTG GGTCTCTTGT CTGCAATGCG 1020
TGTGATGCGA CCAATCTTAG GAGAGGAGCA GACCGGCTC TAAGACAGAA GCCAATAACT 1080
GTGTGAAGGG TGAACTTGG AGTGAAGATC AATCTTGAC TGTGTGAAGA GTGCACATG 1140
80     GACTCTAAGG CGAAGGCGAG TGCTTTGCTT GATATAAATG TTCCGCGATG AGGCCACAGG 1200
ACTGAGAGTG GGAATTTGG AGGCGCTGAG AAGATGCTCT GACTCTCAGG CTCTCTGCT 1260
AAGAGAGGTT AGTTTGGGC AGTCTGCGAG AGAGATCTC GGCACATGAT CCGACTCTAC 1320
90     TAGCGCTTTA GCTCAAAAGH TTTCTTGAAG TCTTGAAGCT CCGCAGAGGCG TGCGAGTCA 1380
AAGCCTCTTG TTTATGTGAT TAGCTCAGAG CATCTCTATG AATCTTAACC CTTCGCCCTCA 1440
100    TGAAGAGGCA GTTTTCCCGA CCAACAGCAT AGTCAATGAG AAGGCACT CTTCGAGAGA 1500
AGCTCTAGT GGAATATATA TGAATCTATT TTSCAAATTA TGSSGGGAAA TAAATCTTTT 1560
AATTATACA ATGT

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Seq ID NO: 115 Protein sequence
Protein Accession #: Bos sequence

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70     1      11      21      31      41      51
|      |      |      |      |      |
MLLITLSAML FTVFERSLTT TSPSRYKSS DRAHKKVSM LICHILALIV VQIVIFBSW 60
AFANVIFSEK VFAAGINIFY PFSFCEFTC SHAGNYNOC BHAEDEKCPQ TQYLCTVHF 120
75     TSHRSTHSIT KKCASSBEC FVCGHSRSD SEHTCRSCC BGMICNVRLP RHNIAVFAV 180
HQAQTSBSSA PTLVLPVLA VVFLP

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Seq ID NO: 116 DNA sequence
Nucleic Acid Accession #: Bos sequence
Coding sequence: 1-1059

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80     1      11      21      31      41      51
|      |      |      |      |      |
ATGCTATGGC AGCAAGATTA TCGAACCAGG AGAGAGGACC ATGCGTCCCG TCGTGAATTC 60
TGCGGTGTAT CTCGACGGTG CCGCTTGCCTA AGCCCGCTGA CCGCTTTGGT TATAGTTTCC 120

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WO 02/102235

PCT/US02/19297

5
 10
 15
 20
 25

TCAATCTGCTG AGAGAGGTGA GGAAGCTGCA GMAAGAGACT TTGMAACTAG CAGAGGTGGG 180
 TGTCTGAGGA TGAAGAGAGG AAGCAATGCG CATACACTAA AAGTGCAGG TGAAGCGGGA 240
 GTCTCTGATG AGAGAGTATC AGAGAGTATC CCGAGAGATC TACGTATAGT CATGTATGAA 300
 GATGTGAAAG GCATCTGACA GAGAGAGATG AGAATCACAG TAAACCAAC AAAGGAATG 360
 CAGAGAGAT ATTTTCACGT GAATATGGA AATGTAATG GCCACAGCTT GGATGAGATG 420
 ATATCTGACG TCGACAGCTG GGAATATGCT ATCTCTTCGG ACCAGATGCG AGGTCTGSCG 480
 CTTACACAGC AGGTAGAGTG TGGATATAT TTGGTAATG GAGCTTCCA AACGAGACG 540
 ATGACCAAC CCACTGATGT AAAATATAA GAAGCTGAC CAGTGTGCTT TTTCACCTTA 600
 GATATAGAG TCGGAGAGCG CCGAGACACA AGAATAAAC AAGAACTCTC CATATCTCT 660
 TGTACTGCA CATTTCCAAA TAGCTTCAG TGGTTCAGT GTGAAACCG AGGGATATAT 720
 TATACAGCA ATGACAGCA AGAGAGACAA TGGTGTGAC AACCAACA GTACTCTCTT 780
 ACAAGTCTAT ACTTCACAG CCAAGAGAGA AGCACAATCA TACCAAAA GTGTGCTTCC 840
 AGAAGTGAAT GTCATTTGT CGGTTGCCAC CACAGCGGAG ATTCTGAACA TACGAGTGT 900
 AGGTCTGCTG GTGAGAGAAAT GATCTGCAAT GTAGAAATAC CCACCAATCA CACTATGCA 960
 TGTCTGGCG TAACTGCGCG TCGAGAGACA TCGGCGACGA GCGGCCCGAC ACTCTACTCA 1020
 CCACTGTCTG CCGTCTCTTA TGTCTCTTA TCTCTCTTA GCGCTCTTA CAGAGAGAG 1080
 CGAGACAGC CTTCTAAGC ACAAGCAA AACTGTGTA AGGTTGACT TTGAGTGAA 1140
 GATCACTTCT GCACTTGTG AAGAGTGAC ATTGAGCTC AAGCGGAGAG CAGTGTGTTT 1200
 GCTTGATATA AATGTTGCG CATAGGCCA CAGAGCTGAG GATGGAAT TTGCGAAGGCG 1260
 TGAAGAGATG GTCTGACTC CGGCTTCTC GTGCAAGAG AACTGAGTTT GCGCTGTCT 1320
 CGAGAGAGGA TCGTGCAAC TAGTCCACG TGACTAGGCC TTTAGTGAA AGGATTTCT 1380
 GACCTCTCTG ACTGCGTCA AGGCTGCCAG CTGATAGGCT CTGTTTATG TGATTAGCT 1440
 AGAGACCTTC TATGAATCT AACCTTCTC CTAATGAGA AGGATTTTC CCACCAACA 1500
 GCTATGTA TGAAGAGGC AACTGTACA AGAAAGCTC CAGTGAAT TATATGAAT 1560
 CTATTGCAAA ATTAATGAGG GAATAAAGC TTTTAAATA TACAATGTA A

Seq ID NO: 117 Protein sequence
 Protein Accession #: B05 sequence
 1 11 21 31 41 51

30
 35

MVHQGYQYTR REHQORLEP CRVSAQCPL SPULSVIVS SSABGEEAA EEFETSRGG 60
 FRMRHEBRIA ENHYQSEVE GADSEAAASD PELALAKIDE DYKIVQGNM RIFYNAGN 120
 GTFPLFLEIG IVPLTQEDH IIPACFVEH LKMGATRT 180
 KHKFDVKKK ETEFVCLFT DIRVTAQHT RIKQKVST S MATFFNFSK CFTCCAKEM 240
 YNCRHAEKDC WCFQRTYCL TVRHIFTSHR STSTKKCAS RSECHVVOCH HSRDEHETEC 300
 RSCCEMICIN VELPRTHTA VFVHGAQRT SOSSAPLTLY FLVLANVFLP LL

Seq ID NO: 118 DNA sequence
 Nucleic Acid Accession #: XM_038659.6
 Coding sequence: 528-1688
 1 11 21 31 41 51

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 85

AGTAGGGAGG TGGGGGAGG CCACTGATGA CGGAATGGCA ATCACTATTG ACCTCTGATC 120
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 CTTCTGCTCT GACCTCGGAG GATGAGCTGT GATGAGCTGT CAGTCTGCTC 300
 GAATCTCGG GCTGGAGAGG ACTCCAACAT CTGGGGGCGG CCGGGGAGG CAGCTTAGT 360
 GTCTCTCTCG TGATGCAAT CCTAGGTGCT GAGTCTCCG CCGCGAGAGG GCGGCTCTCG 420
 AATCGAGCCC GCGAGGTGTA CTGCGCGGCG CTGCGGAC TGCCCGAGT CTGCTTGACG 480
 CCGAGACGCG GCTCTGAGG CCGAGAGCG GTCTCAAGG CAGAGGCTA GACACTTGG 540
 GATCTGCCCT CGCTGCACT CGAGCTTCC TCGTGCGCA CGAGACATG AAGATATGA 600
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 TTAAGGCTAA AGACCTATA GTCAACAGG CATACCTTTT AAAGGAAJAA CAGAGGCCA 720
 ATATCTGCT TTGTGACAT GTGTCTCAGG ATCATATCT GAGCTGAGG TGCTCTCTG 780
 AGTTTGATG GAGAAACCT CATATCAGC CTCTCAGAA CCTGTCAATG CAGCTTCTG 840
 CATGACCTTT GCATCTGTA GTGGAAATAT TGAAGAACTT GAAGCATTT CGAGAGATG 900
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 TGAAGGACG TGTCTGAGG TTGACAGAG AGAGACTCTT AGAGATCTT CAGACATCT 1020
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 CATTCATGG AACTGAGCT TCTCTTGAG TCAAGAGCG TACCAAGGCC CTGCTCTTG 1140
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 TCTCTCAGG AGTGAACAG GGTGTGCTC TGAGCTGAG AATCAATG GGTATATTA 1500
 AGGTGACGA GATGACTCT ACCTATGAGT CAGTCTGAG CAGCTTGG GAGACACG 1560
 TGAAGAGAT GTTGTGCTCT GTATCAAGCT GTGTGTGTT GCGAGTTCT GATATACG 1620
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 GAGACAGCT GTTCATTTA AATGTGATA GATTTCTTG TCTAACCTG CATATATAG 1800
 TTTTATGAT CAATGTGTA CAGAGATGAT TGTCTCTA TCGCAAGAA AATGATCTG 1860
 AATCACTAA TGTGTTTCA TACTTGATA GTAGTACTT ACTTACTT ACTGAGAAA 1920
 ACTTAAATG AAGCCATATA AAGTGAGAT TTCTCAAGT ATTTTATGCT CTCTCTT 1980
 ACTTACTTA GATATATAT AGTATATAT TCTTATAT AATTTAGT CTTCTCTTA 2040
 ACAAATGCA ATTTTATG TGTGTGGA AGCTATTTG AGAAAAATC ATAGTTTCA 2100
 TTTCTGAG CCAATCTTA CAGAGATGAT GTTTTCTA TTTTAAAT CAGATCTT 2160
 AAACTGAT TTTCTCCAT CAGTCTTTT TGAAGTCTT CAGATCTT GTTAAAGTA 2220
 ATATCTGAT GATATGAT CAGACAGCT GAGTACTCT TGTCTATG GAGATGAT 2280
 GTGATTTTC CACTATGCT TCTTCAACT TGTCTGTAG CTGCTGAGT GTGAGGAG 2340
 TACAAGTCT AGGTGTCTT GGTCTATAGA TCTTGTATC CCCCAGTCT GATATATAG 2400
 AGGTACTAGT TAAATGTTT TATAAGAT CAGTGAAC TTTCTCTTA TGAAGTTGA 2460
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 GATATAGAT ACTTATAT GTCTTATTT TCGTAGACT ACTAATCAT TAGATATAT 2580

WO 02/102235

PCT/US02/19297

CTGAAGGATA GTTAGTTTAG GAAATCACTT CATATTGATT GTATTAGANT TATCTTGAAA 2640
 TTAGAGKAT ATGCTCTAAG GAGG93ACCC CACGCCCCAG GCATATGACC ACACAGAGAG 2760
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 GAGCAACAAT CCAATTTGTA ACTCTGCAAT GACGAGATCT AGGCTATGGC CTCTCTATGA 2880
 GAATCTAATG CTCTGATGAC TGGAGGTGAA CMGTTTCATC CTGAAACACC CTCTACCCCT 2940
 GCAATCTCTG GAAATATCT GTTCTACAAA ACCTGCTCCCT GTTCTCAAAA ATGTTGGGGA 3000
 CCACTCTCTC AGAGAGATGG CATGATATCA TACCAACCAA ATGGAATAGA CAATGTCTTT 3060
 ATGTCAAGTG TTAATTTGTA AAGATAATCT TTTTTTTTTT TTTTGGTAG AAAACAAGA 3120
 GGCATATCTT GATTTTATTA CTTGCTTTTT GAGGTGATCT TTTCTTTTGA ATGAGATATT 3180
 GAGAGACAG TGGTGGAGCA CCGAGGAGAG CACTATGCGT TGAATCTTGA TCTCTTAGG 3240
 AGCTGTGAGT TAAATTTGTA TCCTTTGTGG TTTATCTAAG GAAAGTCANA TCTTGACAGA 3300
 AAACATTTTT CTTGGAGAGG TCACTCTCA GACATTGTAT TTTGGTTTTCC CTAAGTCTTC 3360
 ATATCTTCTT TCTTCTGAGA CATATTTTAT TCTCTTTTCA GAGAAGAGAA ATAAANAAGA 3420
 TTTTAAAGT TCTTGCACTT GGAAMAATTT CCTTGAGAGA TCTTAGACCA AGTAAAGAA 3480
 GGCCTTAACT TCTTTTCCAA ACCTTTTAAAC CATAGCTCTC TTTATAGACA GGAATAGATA 3540
 AATGAMAATT GAGAATATTA AGATGAAAG GATGATAAAT AATATCTTT AGGGGGCTTT 3600
 TAAATGTGTA TCTGAAATCT TGGGAGAGAG TGTCTTTTTC AGGCTGAGAG TGCTCTTGAC 3660
 TGTGCGCTGC GACGTGTGTA CCCCAGAGA CATCTTAAGG GTTGTCTTTC GCCTTGCTTA 3720
 ACTCCTTTGA CCTATCTTCT CATATAGTAG TCTGAGAAA AGTGTCAAGT AATTAAACT 3780
 GTCTAGTGT ACAATGTAA CTAATTTCTA TTCTATGAG AATGAGAMT TATTATTGT 3840
 CCACTCAGCA ATTTTATACT TTGCATCTCC AATTTATTGT TGGGAGACTT TGTCTATTGT 3900
 GAAAGTTAGA GACATTTATG TTTGTATCAT TCTTTTATA AAACCTCAG AGCATTTTGA 3960
 AGCCTTTTCT ATCAGACCA GTGAANACTA AGATTAAGT TTTTAAACT GGGGTCTTCC 4020
 TGAAGAGAG AACCAATCC ACCATTTGTA TTTAGTAT ATAGACAGGA ATTGACCTTG 4080
 AGCCTTTCT GTTAAATAGA TTTAACAAGA ACATCTGCA ACTCTTTTCT CTTGTGCAT 4140
 ATTTGTTTAA TGGAGTGA TTAATACAGC AAGATGACCA CATTAATACT AGCAGTAT 4200
 CCACTTTTCA AGCATTAAGT TTTAGACAGC TTTTAGGCTT ATAGAGCT CTGAGAGCT 4260
 ACGATAGA ACGTGTGCA CTAATCTGCT CAAGAACTCC AACAATTTA TATTTCTCT 4320
 GATATTGCA TAAITGGCTG CAATTACTTA ATGTTTAAT TGGTGTATCA AATGAGATT 4380
 AGCAATCAC AAGTGCACTA ATATAAGCA AACCTGTGGC ACTTAAAGT ATAAATGATTA 4440
 ACTTATATT CAGTTCTTCT TCTTTTCACT TTTTTCAGT TCTACATTC AGACAGCACT 4500
 TGTCACTT TTTGAAGA CACCATGAGA AAGCATGAG TTAATATGA GTGTCAAGTA 4560
 AAGGCAAAA CTTGAGCTG TCCATAAAG ATTTGCTGT GAAATTTTC TTTGTGAG 4620
 TCAATTACTA AGATTCAAC TGTGATATA CCAAAAGAG AGTGTACTTC AGAGATGTT 4680
 TCGATGCTCT CTAGACAGAG AATGATAAA TATATAAC CCGCTTTAGC GTTCTTTTTC 4740
 AAGAGAGA AGAAGAGAG AAGGAGAGG GACTGAGAG TCTTTTGTAG 4800
 GATCAGGTT TTTTCACT GGTAAACATT CTAATTCTCT TCTCAAGAG ATTGCTGTA 4860
 GAAAAATGT AAGAC

Seq ID NO: 119 Protein sequence

Protein Accession #: XP_038659.2

1 11 21 31 41 51
 MEDCSNGCA ECTGGSGSIE VYGTWKLH IYTPATLIE IYFPMNLFG TTFTHMLV 60
 SWSEPFMEK PHIKPLQNL LHPOSSALHY AVELFSLKA FQVIMIKRL FQPMHNDIM 120
 YRGAIRATLP VFKSELLLEC IQLVLKLDG WVPYTESAL YIAPTIGTE PELGVKKPK 180
 ALLFVLLSPV SPYFSSTGFN PVLIAHPKY VRWKGOTGD CMKNGYGSB LPAQCEAVN 240
 CGQVLMLHG EDQITTSVET HMLHLWLNE DSEELATFP LQIILPQVT RKLCLDIARQ 300
 YEFYFVRY LQDLDLAL EDIRVEMHFG STACVCFVF SDILVKGST HPTNEMGPK 360
 LSRILXELT DIQVREESD WTVLVS

Seq ID NO: 120 DNA sequence

Nucleic Acid Accession #: XM_005377

Coding sequence: 121..1194

1 11 21 31 41 51
 TCAAGAGGCG GTCTGCGGCG TCTGTGGGCG TGTGCGGCT GTGTGGAGTG CCGTCTGCCC 60
 CCGAGCTGGA GGGAACTAG TCTGCTCCAG GTGGCAGCTG GGTGAGCAAA GCGAGCCOAC 120
 ATGAGACCGG ACTGTACCCA TCACTATTTC TAAGCATATG ACAGCGGGGA GGATTTCTAC 180
 CGCTACAGCA CCGCCAGGGA GAGATCTGAG AAGAATTTGG AGTTGTGGCC GCGCCCGCTG 240
 ACTTGGGTCC GAGTCCGAGA ACCACCACTT CAGCTTTGAT CTTCTGGAGC CCGGACGGTA 300
 GGGTCCGCTG GCGAGCGAGC GGAATCCCGG GACTCTGAGA AAGCTGTGGA GCGGACATAC 360
 GCGTCCCTCA TCGCCCGTGA TGCATGTGG AGCGGCTCT CCAACAGAGA CGCGCTGGAG 420
 AAGAGGTGTA GTGACTGCTG TGCCTTGGC GCGCCCTGG GATACCTGCC CAGAAGTCT 480
 GCGACCCCGC ACTACATCTC CCAACTCGAA CGCCGCAACC TAGCCCGCAT TCTCCCTCT 540
 TTTTGTGGCG ACTCAAGTCC CGGCGCTGAG TCGAGTCTGT AGAGCCGAGG GCGATCCGG 600
 GGTGAAGAAA TCGACTGAGC AGTAAAGAG AGGCACTCT TGAATACAGG GAGCGCGATC 660
 ATCATCGGCG TGGTGTGAGA CTTTCTGAT TCCCGATAGA ATCTCTTCCA CATCTCCATC 720
 CACCGACAC AGCCACAATC TGTGCTCCCT TTCTCCGAG AAGCTGCTCT CCAGAGAGAG 780
 CTTCAAGAGA CTTACTAGCT CCGAGAGAGC AAGCTCTAGG GGGAAAGAT 840
 GATAGGAG ATGAGAGAT TGTAGGCTCT CCACTGTAG AAGGTAGAGC TGCCCATGCC 900
 TGGCAGGCCA AACCATCCA TTAATGATCT GGAATTTGGA CCAAGAGAA GTACACACAG 960
 TACCTGAGCG CACAGAGAGC GAATGATGCA CGTTTGGGCT TCTTGGCTCT GAGGAGACAG 1020
 TACCGCCGCT ACTCATGCT CTCTAGGGTT TCCAAGTAAA TATCTCTAGC GAGGCGAGC 1080
 GATACTTAC ACTGAGAGCT GAGAGCTCAG GAGAGCTATG CTAGAGAGCA AAGCGCTGCT 1140
 GAATGCGAGC GAGCGCAATT CGAGAAGAA ATTAGACTAC TCGATAGCTA CTGACCAAAA 1200
 AGCGTGACCA TCTGTCTTAA AAGAGACAA ATTTTCTTT TGAATCTCC TCTCCCTCT 1260
 AGTAACCTAT ACTCTTTTCT TACAGCGAGA CACCTCGGAC AGTAAATGCT AGAATGAT 1320
 CGACGACAGT ACTTATGCT ATTAAGCTTT CTAATCTTGG AAGCTTCTGA ACCGCTCT 1380
 CTCTCTCTCC TGAATATGAG GAGTGGCTTT TGTCTTCTG CACCTTTGGC TCTCTAGAG 1440
 CGACCTGACT GAGGAGATCT GGGTGTCTTC TGGTCACTA TCTCCAGAA AAGCGTACG 1500
 AAGATGATG ACTCAGGTGG TGGATTTGTT TGGGGCTCC AGCTGGAGCG AAATCTTACA 1560
 CTCACTGA ACTTGAAGCT AGGAAGAAG GTCTCTGGG TATACAGAG ACATCTGAT 1620
 GTGAGAGCT TCTCTGCT CATTCTTTT CAGAGAGACA CAAAGCTGC CTTGGTGA 1680

WO 02/102235

PCT/US02/19297

AMCAGCTCA	GAGACTTGAT	CAAQGTGAC	CTTACACTCA	CTGTGCAGCA	CTACACATG	1740
CTGTGAGGT	GGAAGCTGTA	TATATATGA	TATATATGA	TATATATGA	TATATATGA	1800
TATATATGA	TGATATATGA	TATATATGA	TATATATGA	TATATATGA	TATATATGA	1860
TATATATGA	TATATATGA	TATATATGA	TATATATGA	TATATATGA	TATATATGA	1920
5	CCCLATCTCA	ATGCTGTGAC	TACAGACATT	TAMAGAGACT	TGCTCTGTAA	1980
	TAAAGGCT	CTGAGCTCT	TCTCTGTGAT	GAGGAGACT	TCTCTCTCA	2040
	TGCTCTCATC	TGCTCTCTGT	ATGCAATGAG	TCTCTACAGA	CCCTTTCCCG	2100
	ATATTTCCTT	AAGCAACAGG	GAAATGGGTC	TTAGCTTGGS	GCTTGAGGAA	2160
	CCCTGAGCTA	TGAACTCAAT	CCCTGACCAT	GTGTTTCTTG	AGGAGCCCTT	2220
10	TTTTCTTCAT	AGGACTTATG	GCTCTCTTGA	AGGAGACACT	GTAACACTTT	2280
	CTCTCTCTCA	ATCTCAATCT	TTCATCTGAT	ATTTTGAGT	TCTCTACAGA	2340
	TGTGCTCTTT	CTGTCAGCTA	CAAGGAGCTT	CTGTGCTCTG	CAGCAACCTC	2400
	CACCAACCTG	CAATGATCA	GATCTCTCTC	ACAGAACTCT	GCTCTCTCTG	2460
	GAGAGCTGT	GGAACCTCTC	CAGCTCTGAC	TGCTCTGTGAT	TGCTCTCTCT	2520
15	AAGATATCT	CTGAGCTCT	CTCTACATAG	GAAATTTTCT	TTTTTTTCTT	2580
	GAGAGCTGAT	CTCAACTCTT	GTCCGCCAGG	CGAGAGCTTA	ATGCGATCTA	2640
	TGCAACCTCT	GCTCTCCGGG	TTCAGCGAT	TCTCTGCTCT	GAGCTTCCCG	2700
	ATCGGAGGG	CTCGGACACA	GCGCTAGCTA	ATTCTCTGAT	TTTTAGTAGA	2760
	CACCAATCT	CGCAAGCTG	TCTTCACTCT	CTGACTAGG	TGATCTACTG	2820
20	AGATTTTGCC	ACGACGTGAC	CTCTGAGCTC	CACTGTGAAT	CAGAGTGCTT	2880
	TGGGAAGTC	ACCAACCTCC	AGCTTTGCTAT	GTGGGTGAT	TCTGAACCTC	2940

Seq ID NO: 121 Protein sequence

Protein Accession #: NP_005368

1	11	21	31	41	51	
MURSEHYHY	TGCTGCGGFT	RCTTPEEDIM	KKFLNPPFH	TVSRSEPSF	QMSQCTMPV	60
OCAGDETSPE	DYKNDANST	ASLIREDDM	GFSTSEPLE	RAVSDLLAV	ADSYSPKEF	120
ATPDYTPLE	AQNLAPFPC	LLGEPKIQAC	SRSSSPDESD	GBEIDTVKK	RQSLSTRKPV	180
11AIVRADLL	FMNLFH31	HQQQENYAAP	FPFSECFQSG	APKPMFKEA	LEREAPGKD	240
DKEDIEIVSL	FPVSEFAMGS	CQPKPIHYET	SNWTKRKH3	YLERKRNQD	RERFLARLDE	300
VPALACSRV	SKVMVWKAT	ETLHELAESE	SRMATEKQGL	ECRRGQLGR	IEYLAST	

Seq ID NO: 122 DNA sequence

Nucleic Acid Accession #: AB006625.2

Coding sequence: 356..4750

	1	11	21	31	41	51	
40	GAGGTTTGGG	AGGCGGCGGA	GATGTCCACC	CTGGGCTGGT	GCGCGCGCGC	GCGCGCGCGC	60
	GCCTATGCTT	TGCTCTCTCT	GCTCTTCTCT	CCGCGAGCTC	CGGCACTACT	GAGGAGTACT	120
	TGCTCTCTCT	GATCTCTCTT	CCCTCTTGGA	GAGCACTGCG	GAGAGGAGGA	GCGATAGTGT	180
	CCAAAGCGTA	GTGGGCTGGG	TCCGCGCGGA	GACCGCGACT	AGGAGGAGGA	TGATCGAGCT	240
	CTTGCTCTCT	GAGCACTGAC	TGACACTCAT	CCCTGAAAGC	CTCAAGCCTT	GGGTGCGAGC	300
45	AAAAAAGCGG	AGGAGCTGGA	AGAGCTCTCT	GAGGATCTGA	AGGAGAGTGA	AGGAGAGTGA	360
	CCACACGGA	GCGGACGAC	ACAGTACACT	CCGCGCGGCA	CGCCGAGGAC		420
	AGAGGAGCTC	TCCACACTCT	ACTCAGTCCA	TCTTTCAGCT	GGTCAACGGG	ACTGGGACCG	480
	GAGGCGCAGA	AGCAGAGACA	TGGAGCCAGC	AGGCCGCTGG	TGCCACACCA	GGAACCCGAG	540
	AAGCAGCTAG	CCCTCGCGGG	ATCTTTTCTT	TCTCTTGSGT	GCGAAAGACA	GCTTTGAAAT	600
	GCGACGAGAG	GAGCAACGGG	ATCCGAGGCG	TTATGAGTCC	CGATCTCMGG	ATGCTGATTC	660
50	ATACCAAAAT	GTGGTGGAC	TGCTGAGGA	CAGGAAACTC	CACACACRA	TCCAGGACCA	720
	CATGCGAAAC	TACAGGAAC	TGCTCTCTCT	CGGATGCGAG	CTTGCTGAAG	AGCATGGCCA	780
	TGCCACATGA	AAAGCTGGGC	ACTCATGAG	ATCCAGAGGA	AGTGGCTACG	CAGACGACCG	840
	TGATGCTGTA	AAATCTGGA	CTGAGGCCA	AAATCAACC	CACCGCGGGA	CACCGTGTGA	900
	AGATGATCTC	TCCACGCTAG	GATATATGGA	AAATCTCATC	AAAGATGTGT	CAGCAGTTC	960
55	CAAATCGGGA	AGGACAGGGG	AGTCACAGGA	CCGCTCACAG	AGATTCCCCA	GATGTCTGGA	1020
	TGATATAGTG	AGGACACTTT	CATTGACCAA	GAGGAGTCTA	GTGATCCAGC	AGCGGTTTGA	1080
	TAAGAGGAT	GCTGATGAG	GTGATCTTGA	ACCTCTTTCT	CCGAGAAAGG		1140
	AGTTCTTGAA	AGGAAAGGCG	GCTACTCTTT	TGACAGAGCT	GCGAGAGGAT	CGATTTCAGG	1200
	TCAAAGAGGC	TGTCACAGGA	AGAGGCCCTT	TGAATGTGGT	AGTGAGATGA	GAAAGCCCAT	1260
60	GAGCGTGAGC	AGGCTGAGCA	GCTCTAGCTC	CCCTCTCTTT	ACCGATCTAC	AGCCATTGGA	1320
	TTTTTGCGCA	ATGCGATATG	TATGTGATGA	GTGTGGAGGG	TGCTTCAGTG	TGCTTCTGGA	1380
	CTATCTTGAG	CAGCAGTGA	AGATCTATAG	AGGAGACTCT	TATGTGTATG	GTGAGTCTCT	1440
	TATCCACAGT	GTGGGCTCTCA	GTGAGTTCTA	GAAAGGTCAG	GTGGGAGGGA	AGCTTTTGTG	1500
65	ATGTAGGAGC	TGTGAGAGGA	CTTCTACATG	GAGTGGCGCC	TGCGCTGAAC	ATGCGAAGAT	1560
	TGCTCTGAGA	GTTTATCTTG	TGGATATGTA	GATTCAGAGA	TGTGAGAGAG	CTTCTATGCC	1620
	TGACCCGACC	CTGAGGAGCA	AAATGAGAA	ATATGCGTGA	CCAGTCTGGA	ACAGTCTGGA	1680
	GGTGTGATAG	GAAAGCTTCT	TTCATAGTTC	TGCCCTGATG	GAGCAACAGA	AAATCCACTT	1740
	TGGGAGTGAC	AAAGATAATG	AGCTTGAGCA	TGAACGTGAA	CTGTGAACGT	AGGCCGCGGA	1800
	AGAACTTAGG	CCGACGAGGC	CCCTTATATG	GTCTCCAGAA	ATGTTATGTA	AGGAGAAAT	1860
70	GTGCGAATGAG	AGGAGGAGCT	AGATCTGAGT	CTCTCTCTCT	TGCTTCCGGA	AGGACAGGTA	1920
	GAACATCCAT	ACTAGAGGCG	ACCCATTGGA	AGAAAGGCTT	AAAGTGTGTG	AGGAAACCTT	1980
	TATTTCTGGT	CAGTCCCTTA	AAAGGCGCTCA	GAAACTTTAC	ATAAGAGGGA	AGCTCTGTGA	2040
	CTTTACAGAT	GSCCGGGATG	CCCTTACATG	AAAGCTCAGG	CTCAGTGAGC	ATCAGAAATG	2100
75	TGATCTCTGA	AGGACACTCT	TGAGAGGAGC	AGGCTGTGAG	AAATCTGTCT	TTCATGTGAT	2160
	CCCTTATCTG	GATCTCTCAT	AGATCTATAC	TATACAGCA	CTCTTGTGAA	GTATGAGGTA	2220
	CGAARAAGGG	TTCACATCTA	CTTCAATACC	CTATGAAAGC	CAGAGATNTC	CCATTAAGGA	2280
	AAATGTCTAC	GAGGCAAAAT	CATATGAGGG	GTCTGTATTG	CTATAGCTTG	CCCTGTGTGA	2340
	AGCTTCAGAA	ATTCAGATAG	TAGCAGGGCC	CAGTAAACCA	AAAGATATGG	CAGAGCTTAC	2400
80	CTTTTGAGGC	CTCTGAGCTT	TCAACCATCA	AGAGAGCTCT	GAGATCTTCT	CCGAGAGGGA	2460
	AGGAGAGGGA	TACAGTAGGT	CTGTATATCA	TAGCTTAGTG	GCTTCCAAAC	CTCAGAGGAG	2520
	TAGATATGTC	AAATGATGAG	ACTCTGTGAT	AGGATCTGAT	AGGATATGTA	TTCCTTCCCA	2580
	AGATGTCTCT	GAGAGAGACT	CTGTGAGCTT	TAAAGAGACT	GCGGAATCTT	CTTCTTCCCG	2640
85	CTCAATATCT	CTGAGATACC	AGAGGCTCTG	TGCTMAAAG	AAATCAATTT	AGCATAGAGG	2700

PCT/US02/19297

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WO 02/102235

PCT/US02/19297

Seq ID NO: 124 DNA sequence
Nucleic Acid Accession #: NM_007196
Coding sequence: 180..1962

	1	11	21	31	41	51	
5	GTCTCCAGAA	GCTCCCGAAG	CTCTAGTGCA	GGAGGAGGAG	GAGGAGGAGC	AGGAGGTGGA	180
	GATTCCCACT	TAAGAAGGCT	CGATATCTGT	TACCAAGGCG	AGAACTCGAA	TACTGGGCCC	120
	TCTCTCCAGT	GCTCGAATC	ACTAGGTGAC	CCGCGCTCTG	GATTCTGGAA	GACCTTCACZ	160
10	TGGGAGGCC	CGACACTCTG	GGGGCCAGAG	CGTGGATGTT	CTCTCTCTTG	CTGGGGGGAG	240
	CTCGGCGAAG	ACACTCCAGG	GCACAGGAGG	ACAGGTGCTC	GGGGGGTCAI	GAGTGTCCAC	300
	CCCACTTCGA	CGCTTGGCAG	GGGGGCTTGT	TCGAGGGHCA	GGAACTACTC	TGTGTGGGTG	360
	TCTCTGTGAG	TGGCATGAGG	CTCCGCTACT	TAAAGAACCT	AAATAACAG	420	
	TCTGTCTGGG	AGCACTCCAG	CTACGAAATA	AAGATGGGCC	AGAGCAAGAA	ATACTCTGTG	480
15	TTGATGCTAT	CCCAACCCCG	TGCTACACAA	CGAGCGATGT	GGGAGACCAI	ACCATGTATC	540
	TGATGCTCTT	TCAGATGGTG	GACCGAGCAT	CTCTGGGCTG	CGAATGGAAG	CCCATCAGCC	600
	TGTCGABATG	CTGCTGCGAG	AGTGGACAGA	CTAGGCTGCT	GGAGCTGTGA	660	
	CCAGTCCCGG	AGAGGATTTT	CTGACACATC	TCAACTGTGC	AGAGATAAAT	ACTCTTCCCG	720
	AGAGGAAGTG	TGAGATGCTT	TACCCGCGGC	AGATACAGA	TGGCATGGTC	TGTGAGGGCA	780
20	GCAGCAAAAG	GGCTGCACAG	TGCCAGGGCG	ATTCTGGAGG	CCCCCTGGTG	TGTGATGGTA	840
	CACTCCAGAG	CATACATCTC	TGGGGCTGAG	ACCCCTGTGG	GGAGCTCCAG	AAACTGTGGG	900
	TCATATACAA	CTCTCTCTCC	TACCTGTGAT	GGATACAGA	GACCTGGGGC	AGCAAGGCTT	960
	GATTCTAGGA	TAAAGCACTG	ATCTCCCTTA	ATAAATCTAC	AACCTCTC		

Seq ID NO: 125 Protein sequence
Protein Accession #: NP_009127

	1	11	21	31	41	51	
25	MRFRPRAAK	TMHMLLLGG	AMAGISBAGE	DNVLGGIECG	PISSQPMQAL	FOOQQLLGCS	60
	VLEVGQWVLT	AAVQLEPFTT	VPLGDRSLG	KDPEEELPV	IFVPHCPIC	SEVDEHND	120
30	LMLGLLEDGA	SLGSGVKFPI	LADHCTPQGG	KSYVSGWVTV	TPSPENFPET	LNCAEVKIFP	180
	QKKEEDAVPG	QITDGMVCAQ	SSKAGDTCCG	DSCGFLWCDG	ALQSTITSWG	DPOORSDEPG	240
	VYTRICRYLD	WIKKI1GSGK					

Seq ID NO: 126 DNA sequence
Nucleic Acid Accession #: NM_014791.1
Coding sequence: 171..2126

	1	11	21	31	41	51	
35	TTGGCGGGCG	GAAGCGGGCA	CACCCCGGCG	ATCGAAGAAG	TTCTTAGGAA	CGCCTACCA	60
	CGCCGCTCTC	TCAGGACAGC	AGGCGGCTGT	CCCTCTGTGC	GGGCGCGCTC	AGCCTGTCCC	120
40	TGCGGGGCTC	AGGTTCCTTT	TCTAATTCGA	AAATAAGCTG	CGAAGGGCTC	ATGAAGATTI	180
	TGATGTGACT	TCGTCAATAT	TCTGAATATC	ATGAAGACTT	GGGTCGAGTT	GGCTTTGCAA	240
	AGGTCAAGCT	TGCGTGCCAT	ATCTCTACTG	CAGAGATGGT	AGCTATAAAA	ATCATGGATA	300
45	AAAAACAAT	AGGGAGTGAT	TTGCGGCGGA	TCGAACCGGA	GATTGAGGCC	TTGAGAAGAC	360
	TGAGACATCA	GKATATATGT	CACTCTACCC	ATGTGCTAGA	CAGAGCCCAI	AAATATTCAA	420
	TGGTCTTGA	GTACTGGCTT	GGAGGAGGAC	TGTTTGATGA	TAAATATTTG	CGAGATGCC	480
	TGTCAAGAGA	GGAGACCGGG	GTGTCTCTCC	GTCAAGATAGT	ATCTCTGTGT	GCTTAGTGTG	540
	ACAGCCAGGG	CTATGCTCAC	AGGGACATCA	ACGCCAGAAA	TTTGCTGTGT	GATGAGATTC	600
50	ATAAATTAAA	GCTGATTGAC	TTTGGTCTCT	GTGCAAAACC	CGAAGGTAAI	AGAGGATACC	660
	ATCTCAAGAC	ATCTGTGGGG	AGGTCTGTCT	ATCGAGCACC	TGAGTTAATA	CAGGACAAIT	720
	CAATATCTGG	ATCAAGAGTA	GAGCTTTGGA	GCTATGGCAT	ACTCTATATG	GTCTTATAGT	780
	GTGGATTCTT	ACCAATTGAT	GATGATAATG	TAACTGGCTT	ATACAGAAGG	ATTATGAGAG	840
	GRAAATATGA	TGTTCCGAGG	TGGCTCTCTC	CCAGTAGCAT	TCTGTCTCTT	CACAAATGTC	900
55	TGCAAGTGA	CCCAAGAAAA	GGGATTTCTA	TGAAAATATC	ATTAGACATT	CCCTGATGTA	960
	TGCAAGATTA	CAACTATCTT	GTTCAGTGGC	AAGACAGAAA	TGCTTTATAT	CACTTCGATG	1020
	ATGATTGGCT	AACGAACTCT	TCTGTACATC	ACGAGAAACA	CAGGCAAAAC	ATGAGGGATT	1080
	TAAATTTCACT	GTGCGAGTAT	GATCACTCTA	GGGTACTACT	TCTTCTGCTT	CTAGCCAGAA	1140
	AGGCTCGGGG	AAAAACAGTT	GGTTTAGGCG	TTTCTTCTTT	CTCTGTGGGA	CAGGCGATGT	1200
60	CTACCCCTAT	CACAGACTAT	AAGTCAGATA	ATTGGATGCT	GGAGAGATGT	ACCGGATGTG	1260
	ATAAATAAT	TGGGGGGGGA	TTATATAGACT	ATGATTGGTG	TGAGAGATGT	TATACAGACG	1320
	GTGCTGCTAC	TCCCGGAACA	TCACAGTTTA	CCAGATGACTG	CAGCAATATCA	AATGGGGTGT	1380
	AATCAAAATC	ATTAAATCCA	GCCTTAGTGA	GACACCTGTG	AATAAATTA	AGAGCAAAAG	1440
	AAATATATA	TACTCTAGAG	TTTGCTGTGA	AGATCTTATG	GTCTCTTGAG	TTTCCGAGC	1500
	CAAGCACTCC	ACTTAATATG	AACCAACATA	AGAGAGAAAT	ACTCTACTAG	CCAAATGGTT	1560
65	ACACTACACC	CTCAAAAGCT	AGAAACAGGT	GCGTGAAGA	AATCCGATTT	AAATACCGAC	1620
	TAAATTCAC	AGGACACAGC	AGGTTAATGA	CAGGTGTGAT	TAGCGGTGAG	AGGCGGTGCC	1680
	GCTCAGTGA	ATGGAGATCT	ATGACAGAGC	ATGATGGAGG	AGCTCCAAA	AGAAAGGGAG	1740
	CGAATGTTG	CGAGGCTCTT	GAAGAGGGGT	TGATATAAGT	TATACATCTG	CTTACACAGA	1800
	GCAAAAGGAA	GGGTTCTGCC	AGAGACGAGC	CCAGAGACTC	AAGCTTCAC	TATAATGTGA	1860
70	CTCAACTATG	ATTATGTAAI	CCAGATCAAT	TCTTGATGTA	AATAATGCTC	ATTCTTCCAA	1920
	AGAGCATGT	TGACTTTGTA	CAGAAGGTTT	ATGACCTGGA	GTGTCAAAAT	CATTCAGATT	1980
	TTGGCAATGT	GCAATGATCT	TTTGATATCT	AGATGTGCTG	CTCTCAAAA	CCGATATGAT	2040
	TGGGATCTAG	GAGGCAAGCG	CTTAAAGGGG	ATGCTTGAGT	TTTACAAAGA	TGATGTGAAG	2100
	ACATCCATCT	TAGCTCAAG	GTATAAATGA	TGGTCTCTTC	CATCTCGCGC	GATGATGTGT	2160
75	GGTGTGATAC	AGCTCAATA	AGACCTGTGA	TGATGCTCTT	GATTTTAMG	TTGATGTGGA	2220
	CTACCAACT	GTTCATGATCT	AGCACTCTTA	AGCACTCTTA	CTCTCAAGT	TTTAAACATG	2280
	GATATTAATT	TGTGTATGAA	TCTAAATCAA	GGCCATCTGT	CATTATGTTA	CTGTCTTTTT	2340
	TAACTATGTG	GTITTTGATA	TAAATAAATG	TGACCTTCTT	TAGATTCTACT	TCCATATGTG	2400
80	AATGTAGACT	CTTAACATATG	TCTCTTTGTA	ATGTGTAAAT	TCTTTCTGAA	ATAAACCAT	2460
	TTTGTAATAT						

Seq ID NO: 127 Protein sequence
Protein Accession #: NP_055606.1

	1	11	21	31	41	51	
85							

WO 02/102235

PCT/US02/19297

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MDYDELLKY YELHETIGTG GFACVKLACH ILTCEMVAIK IMDKNTLSDG LPRKIKTIEBA 120
 LKNEHGHIC GLYHRYLETAH KIPWVLEYCP GDLLEPDYIIS QRLSESEETR VYFRQIVBAY 160
 AYVHQHQAIV DELHREKLELF DEHLEKALID HSLCAHPCW KYHLETKCCJ SLAYAPRIL 180
 GKSYSLASBA DVMSBILLY VLACQFLPFD DMWMLKXKK IMEGCKDVVK WLSPSILL 200
 QQMQLQDPEK RISMGLINAH PWIMQDZNYF VBMQSNPFI HLDDCVDTEL SVBHHNRROT 240
 NEDLIISQWY DRLATYTYLL LAKKARGEPV BLHLSFSFSC QASATPTPTI KSNMNSLEW 260
 TASHRYVUG LIDVHPCWBL LQDAKAPFT RQFTKFWES NQVSEBELP ALQCTPARKL 320
 EKHENVTPTK SAVNREYTHM PEPKTPVXK NQKHBEILIT PWTYTPSKA RNMQLCKEPI 360
 ZLPVNSTGTD KMTQVISEP RRCRSVLELH NQMHRETEP RKGAIRVGSJ ERGLQKIVTY 380
 LTRBKHKCSA RLDGPRLRLH YHVTITRLWN PQMLKEIDS ILPEKHVDVF QGYTTLKQCT 400
 QSDGFKWTK FELEBVQLQK PDVVGIRRR LEGEAWYKXK LVEDILSSCK V 440

Seq ID NO: 128 DNA sequence
 Nucleic Acid Accession #: E06 sequence
 Coding sequence: 189-1323

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 TCGGTGCGCT GGCATGGGT CTTCGGGAGT TTTCTGTGCA AGATGCTGAG CACTCTTTAT 540
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 ATACTCTTC CAGCCTCAT ACTCTCAC TCCCTTTCA TTTCTGAC ATTCAACT 4080

WO 02/102235

PCT/US02/19297

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TGAGATCTGG  AGCTACTCTC  TCTCTCACCC  AATCTTONG  AGGTGAAGCA  GATATGTGAT  4440
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Seq ID NO: 129 Protein sequence
 Protein Accession #: NP_001287.2

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STLTIMFY  CLFFSCLSL  DYLLTYVQA  PHLIRTRRA  SILLATVRA  VGLVSEIEM  180
VFVQZHENP  GTWCHADRG  GSOTIMKFL  RFQCNLLGF  LFLMLIFFY  SRICQVLEL  240
RPAGQGRALK  TAAALVAAF  VLMFPYKLT  FLTLTLDLQ  FGNCSQHL  DYALQVTEI  300
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Seq ID NO: 130 DNA sequence
 Nucleic Acid Accession #: NM_002774

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CGCCATGAA  GAGCTGATG  GTGTGTCTA  GTCTGATTC  TGACGCTGG  CGACAGGAG  300
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ACATCCACT  GGTGTCCCT  GAGAGTGTG  AGCATGCTA  CCGTGGCAG  ATACCCACA  780
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TATTTT

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Seq ID NO: 131 Protein sequence
 Protein Accession #: NP_002765

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MKLLMVLEL  LAMWATRG  KLVISGCPK  TSHPYDALK  TSHLLCGV  LELIPLVITA  60
AIKCEKPLV  FEGNLRGR  EBSGQSSRV  RAVHFDYA  ASHQDMLL  RLAPAKLEL  120
LIQPLPLED  CSNNTSCI  LWNKATDGD  FPDITQAVI  RLVSRECEH  AYPGQITGM  180
LCADSEKYK  DSCQDSQF  LVCDHLRL  VSNQIPQGS  KEKPGVYIV  CRTTMIQKT  240
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Seq ID NO: 132 DNA sequence
 Nucleic Acid Accession #: AY038071.1

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CTGCGCCCA  AGCTGGGCG  CCTTAAGCT  GCGGAGAGG  GCGGCTCTCT  TCGAGGTGG  300
CGCGCGCGG  CGCGCGCGG  GCGCGGCGG  CGCGCAAGC  CGCCCAAGC  CACCGCGCT  360
CGACGCGGG  AGCGCTCTC  GCGCTCTAC  CCAACGCTC  GCGCTGGBA  ACGGCGGAG  420
CGCGCGCGG  CGCGCGCGG  AGCGCGCGG  CCGCTGGBA  CAGCTGAG  CAGCTGAG  480
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CGCTCTGTC  CGCGCGCGT  CGCTCTGAC  GAGCTGAGG  GCGCGGGGG  GTTCAAGAC  600
CGCGAGAGC  GCTCTCTCT  GCGCGCGCG  CCGCGAGCG  CCGCGCTGC  GGTGTGTGC  660
ACCGCGAGG  CTGAGAGCT  CTGAGAGCT  CTGAGAGCT  CTGAGAGCT  CTGAGAGCT  720
GAGGAGCTC  TGAGAGAGG  CAGAGAGAG  CTGCTGAGG  AGCAAGCTC  CGCTCTCTC  780
AAGGAGCGG  GCGCGCTCT  TGTGGCGCG  CCGCGCGCG  TGGCGGAGC  AGCTCGGCT  840
CGACTGCGA  CAGAGAGCG  GAGCTCTCA  ACTAGAGAG  AGCTCTCTC  ACTCGCGGA  900
GAGCTGAGG  CAGAGAGAG  CAGAGAGAG  GTCTCTCTC  CTGCGGAGC  CAGCTGAGG  960
GAGGCGCTC  TGAAGAGCA  CAGAGAGCG  TACCGAGCA  CTTTACAGC  CTACAGCTG  1020

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WO 02/102235

PCT/US02/19297

GAGGACATGG AGCGCGCTTT CCGAAGAAGCG CACTACCGCG ACCTCTTCAC CAGGAGAGAA 1080
 GTCCGCACTGA GCGTGGACTT GACCGAGGCG CAGGTCCAGG TCTGGTTCGA GAACGCTCGG 1140
 GCGACATGCG GCGAGCGAGG GAGGCGAGCG GCGGAGACCT ACCTCCCTGCG GCTCCCTCTC 1200
 CGCGGGCGCG TCTCGCGCAC CCGACCGCTC AGCGCCCTACC TGGACCGCAG CCGCTTCCCT 1260
 CGGCAACACC CGGCGCTGGA TCTCGCTTGG ACTGCGCGCTG CCGCCCGCGCG CGCGCCCGCG 1320
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 GCGCTCGAGA CTTCCTCGCG AGCGGCGAGTG TTCTGAGCAC CAGCTTTCAT CAGCTCCGGA 1440
 TTCCGCGGCG TCTTTTTCAC AATGGCGCCCG CTGACACAGG CDTTGCACCG CGCGCCCGCTC 1500
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 CGCACGCGCG CGCGAGAGAG CAGCGCGCTCT AGCATATGCT CCGTGGAGCT CAGGCGCAGG 1620
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 GTGTGC

Seq ID NO: 133 Protein sequence
Protein Accession #: AK93901.1

1 11 21 31 41 51
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 EIAVGQYFS SSAPFAELH LPFKLRHLRG PGERLLQGR AAAAAAANA AARATATATG 120
 PRGEAPPPF PTAPGHPD GQAAAJAAJA AAAAAATLK LQAPVPEIE ERSRYLEMA 180
 FFFVPPFALD ELGSGPGVTH PSLRGLVAGG PGSAPANGGG TGTDEESEL LEDEDEDEB 240
 BELLEDEBEE LLEEDARALL KEPRKCPVAA TQAVAAAAAA AVATRGSELS PKEELLHPE 300
 DAGSGDGBDS VGLSGGSDS ECLLARIKQR YKTTFTSYGL EBLERAPQKT HYDVPVRES 360
 LAMEGLZEA RVQWQHR NRNRNRRAG AGTPPLPPT POPLEATPL SPYLDAWPP 420
 PHEPALDSAN TAAAAAANA FFELPPPPPS ASLPEGAPL GLSTGLCAN FHPAFISPA 480
 PGRFLSTYAP LLSASTAAAL LQPTPAVBG KVASGALADP ATAAADRAS SIALRLKAK 540
 EHAQGLTQLN ILPGTSTGKE VC

Seq ID NO: 134 DNA sequence
Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
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 TGCTTAGACA GTGTATAGC ACTCAGCCTT CAGGCGAAG ATAACTCTTC ACATTGTCA 120
 CAGTATGAC ACACATATTC AGCATATACA TCTGTAATGG CATACAGGA CTTGTAGAA 180
 ACGAGATAGA TTCCGTGAGA ATATCTTGG ATACTTATCA AGCTGTAAA GAGACATCA 240
 TCTTTTCTT TGTATCTTCC TTAGACCTCT CACAGAGAA GTACTAGAA ATTCTTCTC 300
 TCTTGAGAAA CCTCAGACCC TTAATGGTCT AATGTAGGTT AAGTGCCTCG CAGATCTCC 360
 TAGAATAGAA AAGCAGCTTG AACTAGTGTG TCTGACTTAA TAGACACANA TATAATGAA 420
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Seq ID NO: 135 DNA sequence
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Coding sequence: 1..963

1 11 21 31 41 51
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 GAGCGGCTA TCGCTCGCG CATCTGTGGT GCGGCGAGCG CGAACTCGG CGTGTGGG 180
 TGCGAGGAGA GCGTGCCTCT GTGCGATTCO CAGTATGCG GAGTGAAGCT CCGCAGCAC 240
 CGCTGCGCA TCAGCGGCGC GAGCTGCTTT GAAACCTATA GTGACCTTAG TGAICTCTCC 300
 GGGTGAATGG TCGAGTTTGG CAGCTGACTT TCACTCGCAT CTTCTGAGG CTTGCGGCT 360
 TACTGACCC GTACTTGT ATGAGATATC TATCTGAGCG CTGCTACTCT GGGAACTCA 420
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 CCGACTGTCT TCGAGGCTC CACATTTGAG TTGAGACCG GAGCAGACTG CTGGGTGACT 540
 GCGTGGGGT ACATCAAGA GAGTGGAGCT GCGGACCTCT CCGACACCTT CAGGAGGTT 600
 CAGGTGCA TCGTATGCG CACTATGCGC AAGCACTCTT TCTTCAAGTA CAGTGTCCG 660
 AAGGACATCT TTGAGACAT GATTGTGTCT GCGACTGCCC AAGCGGAGAA GAGTGTCTG 720
 TTGCTGACT CAGGTGGAC CTTGCGCTGT AACAGAAATG GACTGTGTTA TCGATTGGA 780
 GCTGTGACT GGGAGGTGGG CTGTGTGGCG CCGACTCGCG CCGTGTGTCA CACCAATATC 840
 AAGCACTCT TTAGTGGAT CCGAGAGCTG AGAGAGTGA GTGAGTATCT CCGAGCAG 900
 CCTCTCTGCG CTGCTCTCT TTGCTCTCT CTGAGACTCT TCGACTCTCT GGGCGGCTC 960
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1 11 21 31 41 51
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 VMSYILSPRY LGNSPYDIAL VKLSAPVTY KIIQPICLGA STEFERNRDT CWTGMYGIL 180
 EDRLSPHET LQGVQVAIN NSMCHWLFK YEFKDIIFD KVCAGNAGQS KNAIGGDSGI 240
 PLACNSHEML YGIVGVWGV GQRRPWRPV YTNISEHFM LQKLNAQSGM SDPPDSWPLL 300
 FFLLHMLAL LQPI

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Nucleic Acid Accession #: Bos sequence

1 11 21 31 41 51
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WO 02/102235

PCT/US02/19297

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CTGTGTCGAC CTGTCACTA CACTAAACAC ATCCAGGCC TCTCTCTGCA GGCTCCACAA 480
TTTGAATTTC AGAACCGGAC AGACTCTGCG GTGACTGAGT GGAGGTACAT CAANAAGAGT 540
GAGGATCTGC CACTCTGCG CACTCTCTGG GAGTCTGAT TGGCTCATAT AACACAGCTT 600
ATGTCGAACC ACTCTCTCT CAGTAAGTAT TCCGCAAGG ACATCTTTGG AAGACATGCT 660
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GGCTCTAACA AGAATGGACT GTGGTATCG ATTGAGTCCG ATGAGTGGGG ATGGTGCTGT 780
GGCTGCGCCA ATGCGGCTGG TGTCTACGCC AATATGAGCC ACCMCTTGT GTGATGACTG 840
AAGGCTATGG CTTAGAGTGG CATTCTCTGG CAGAGGCTCT CCTGGGCTAT ACTCTTTTTC 900
CCTCTCTCT GGGCTCTGCC ATCTCTGGGG CCGGCTGGA

Seq ID NO: 138 Protein sequence
Protein Accession #: E05 sequence
1 11 21 31 41 51
MGAGCALLA LLARAGLER PESQEAAPLS GPQGRVITE RIVGGEDABL GRWPWQSLR 60
LNDHFVQVS LLERHARLTA ARCTETDLE GPRWVQVQZ LTPWFSPSLG QATTFVPS 120
NYLSPRYLG NSPDIALYR LSAPTVTKH IQPLQLAST FEFNRIDCW VTGSGYIKED 180
BALPSPHTLQ EVQVAIIHNS MCHNLFLKYS FRKIDFGDW CAGNAGGQK ACPGGSGGLP 240
ACHNGLNLYQ IGVSVGVGC GRPHRPQVYT NISHFEWIG KLWAGSGMQS PDPSPLLLF 300
PLLALPLLG PV

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CGCGCGGAGC ATGGCGAGG GCGCGCGCG GCGCGCGCG CTGCGCTGCT 180
CGCGCTGGGC CTGCTCTGCG GCTGTGGGG AGGGCTCTCG CCGCGCGCGA CCGAGCTGCG 240
GGCTCTCGGG CGCGCGGAG ACCGACTGCC AGCGCGCGCG GCGCGGAGCG GCGCGCGCGC 300
CGCGCGGCTC GCTTCTGCTC TGCGCGCGCG CTGCGGCTGG GACGCGCGCG GCGGCTCTCT 360
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CGCGAGCGAG CCGAGGTGGC AGCTGTGAGC CAGCGAGGCC GCGCGCGGAG AGAGCGCGCG 480
GGTCAAGCGG GGCTCTCTCT GGAGCGCGCG CTGCGAGGAG CAGGTGCGCG GCGGCTTTTC 540
GAGCGCGCGG GCGCGCGCGT GCGTGAAGCG GCTCTGAGCG GCGCGGATGG TGCGCTCTGA 600
TGGCGGGGTT TCGCGCGGCA GCTCTCAAGC AGCTGCGCTT TTGCGCGAG CCGCGCGCGC 660
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GCGCGGCTCG CTGGGCTCTC AGCGCGAGT GCTGCGCGCT GCACTTGCTC GGGTGGAGCG 780
TGGCGGCGCG CAGTGGCGCG AGGTGCAAGG GAGCTGTGCC GCTCGGACTC GAGCAGGAGG 840
CAGGCTGGTG AGCTGACAC GCTGCGCTCG CAGCTCAAGG GAGCTGTGCG TGCGCGCGCG 900
CTGCGGCTCG GAGCGGCGCT GCTGCGCGCT CCGCGCGGAT GCGCGGCGCG AGCTGCGCA 960
CTCGAGCGAG GCGGAGCTGG TGAGCTTAGT ACAATGAGC GACTTATGCC TTTTCACTA 1020
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GCGCGAGTGG GCGGCTGTG TGCGCGCTA CCGGCTGAG GCGATGTGCG ACAGTATTA 1200
CGAGCGCTCG TTGAGTCTG TGTGCTGTT CCGCGAGCG ACCGCGCGCG GCGTCTGGA 1260
GCTGCGCGCG GAGCAGGAG CCGCGCGCGG GCTGCTGCG CTCTACCGG GCGCAGGCT 1320
TGGCTTCCCG GAGCTGGCGG CCGTCTGAGA CCGCGAGCTC CAGCTGTCTC AGCGCGCGCT 1380
GAGCTCTCT GCGCAGGCA TTTTGACTG TAAAGCGAG TACGCTCGC GGTCTGGAGC 1440
TTAGTGTGAC CGGAGAGAA AGAGAGAGT CTGCGGCTGG GTATGTGATG ATGGGAGGAA 1500
GGGCGGTGCG CTCTGCACT GTCAAGGAGC AGCGCGCGCA CGCCCAAGCG CAAGGTGTC 1560
TAAAGACTTC AGCTTTTAC CACCTGTGCC TCTCTTTCA ATCCAGAGCT GTTCTCTTC 1620
AAGATTCTGG GAGGAGGAC TCAGCGAGCG GAGAGTGTG ACATCTCTC CAGCGAGCT 1680
ATGAAGAT TTTTATCTG GCGAGGAGC GAGATCTCT GAGAGAACT GATCTCTGCG 1740
GTTTGGGCGC GAGGCGCG TCCTGTGGG AGATGAGC CATCTGTGGG CCGCGCTCAC 1800
TCCCTTTCCG AAAAGAGAA ACTTGTGTT GAGCGCTTGA GCTAATTTCT CAATTTTCTA 1860
CCAGACGAG GCTGTGTGCG CCGGAGGAG GCTGTGATCA TGGCGTGGTG GAGCGCTCTC 1920
GCTGTGCTCT CCGTGTGCTC AGCGCGGGA GCGTGTGAT ACTCTGACA GCGAGGAG 1980
GGCTTGGGAT AGCAAGAGA GAGCGAGGAC TCCAGACTCT GGGGAGGCTC GCGAGCTTGG 2040
ACAAATTTGC TGACTGATC CTGAGCTCTT GTCAATTTTG CTTGAGAGCT ACMAATTTG 2100
GGTCACTGTT ATGCACTAG CCAATATATG AATTTCTCT TCCCTCTCGC AACGAGCA 2160
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TGGTTTGAT TTTCACTTT TATTAAGAAA AATTTTAT TTACAGAAAT TACCTCTCT 2280
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GAGTTTTAAA ATTTAAGAAA AAAAAA

Seq ID NO: 140 Protein sequence
Protein Accession #: NP_055159
1 11 21 31 41 51
MGRMRGAAI TAGLMLLAG LLALAGCLL PPRTHLPSR PFEDRLPRP ASEGGAPADP 60
RFFLPPPLAN DARGGSLKTE RALLTLAAGA DGPFRGSEB PRHIVBQRP RFSEBAHVH 120
GVFNSGLEAE QVPFGFSRAQ AAHLDAARG ARHVALERG GRSNSRLAR FADTTRACVR 180
TGINPFIQGG EALSXYLARI LGLGRHVPL ALARVARGA QNQGVEBLR ANHTEGSEV 240
ELTZWNLKLF LNVDPGPMYK EDRLLRYLR AGELLARLQ ASHVDVQNF DILLRYFLTA 300
TFDRLYNSLF LSHQNDPMYK RATSNLHRP GGLAFLNE AGLVHYEYLA GMDKRYEPL 360
LQSVYFRER TARRVLELHR GQDAARLLR LYRSHPRFP ELAALADPHA QLLGRLEDFL 420
AXHLLCKAK YGRSSGT

Seq ID NO: 141 DNA sequence

WO 02/102235

PCT/US02/19297

Nucleic Acid Accession #: Bos sequence
Coding sequence: 11..574

1 11 21 31 41 51

5 GTCCGCGAAG ATGCTTGCCT CAGTCCCTCT GCTGTCTGCA GCCGAGCCTT CACCCCTCTG 60
CATGCGAATA TCGTCTACAG ACTTCTGCCC ATGCGTGTAT TCGACGACGG ACGAGACTAG 120
CAATGACCTT GCTGCGAGGT ACCTATAGGA GCTCTCTCTT TCGAGAGGAT CMTTCCGGA 180
CAATGACCTT AATGCTGCT CTTCTGCTCC CCGACCTCTT AATATCAAGA TACGCGAGAA 240
AATGCTCCTT CTTGCGAGCA AATGTGTGGT GATGCTTAC AATCAAGAA TCTTACAGTG 300
GCTGAGGCTT TCCACACTTA ACGCAAAAGC TATTCCTGGT ATTATAGAGC 360
TTCCAGAGGA AGAGATGTGG CTGCGAGAGC ACCAGACACC AGATACAT ATGAGACTAT 420
CAGCAGAGG AGAGACTAT CTGCGAGAGC CAGGCTTAT GAGGCTGTA GAGAGAGAG 480
TTTCCGAGTG GCGCTGAGAG TTGCTGAGCT TGTATTCTT ATCATCTGGG TGTATTCTTA 540
CCTGACTGTG GAAATAAGT GCGCTGTTGG TTAACTAATT TAGG

Seq ID NO: 142 Protein sequence
Protein Accession #: Bos sequence

1 11 21 31 41 51

20 MPAPVPLLSA AQPEPSCKNG SSTDFCPWLY VRTDRASND AGRYDRKPLL QDSFPFNDP 60
KCLSLPPFP NIKIAENAL LGAKCVVWFY NQKFLWPEA STTKKAVMT YCLDYKPSKG 120
RRWAJAPST RITYGTITEE RDYCAEDQTI BSWRREGPFV GLKVLAVGLF IIVVYVLTV 180
ENKSLFG

25 Seq ID NO: 143 DNA sequence
Nucleic Acid Accession #: XM_050184.6
Coding sequence: 39..365

1 11 21 31 41 51

30 GATCTACCA TCAGAAAGGA GGCGAAACTT CTATCATCAT GTTGATGTG AAGTGTCTGA 60
GTGACTGTAA ATTGCGAACA CAACTTGTGA AGCTTGGATT TTCACTGGC CCMACTACT 120
CTTCCACAGG AAGTGTGAT GAAAGAAATG TAGTACAGTT GTTGCTCTCA CTTCTCTGTG 180
CAGCAGCTCT GAGTATGGA CCGAGAGAGC TGGATGAGCT GAGCAGCTT GATGAGCTG 240
AAGTGTGGCT GCGAGACGCA CAGACACGAG AATCACTAT GGGACTATCA CCAAGAGAG 300
AGACTACTGC CGGAGAGACC AGACTATGGA GAGCTGAGA GAGAAAGTGT TCCAGTGGG 360
CTTGACAGCT GCTGCTGTGT GTATTPTCAT CATTTGAGTG TTGTCTACCC TGACTGTGGA 420
AATATGCTCT CTTGTGTGAT AGATATTTTA GAGAGAGGCA ATATCTCCA GAGAGAGCT 480
CTTCTCAGG AAGAGACCTA AACACTACCC TGAAGGCGCA GCGTACGCTG CAGCCTCTCC 540
TTGCGAGGAG CCTTCCCTTG CACTGTGCTG CTCTCAGGA TGGGTGTCTG GCGTCAAGCA 600
GTGCGAAGGA ACCCTCCCTA CCAAGCAACT GTTCTATAGA CATGATGTTT AGGAATATCC 660
CCAAGCTCAT TCAACTCTCA TTAAAGGTGC TTCTCATATT GAGCAGGCTT GAAAC

Seq ID NO: 144 Protein sequence
Protein Accession #: XP_050184.1

1 11 21 31 41 51

45 MVDVCLSDC ELQNGLEKL PEPQPLPST RKLYEKILV LLVFPFCAPP VNRQPRELDG 60
AQDSDDSEGG LQESQAPESI NGLSPKRETT ARKTLERSAG EKKVSGMA

50 Seq ID NO: 145 DNA sequence
Nucleic Acid Accession #: NM_022204.1
Coding sequence: 74..3229

1 11 21 31 41 51

55 AGGTGACAG GCTCTCAAGC CCAAGCTCCG CCGCTCAAGC GCTCTCGCG GAGCCCGGCT 60
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CTGCGGCTCT GCTCTGATGG TGGCGCGCGG GCGCTGCTCT GTCTCGGCTT TCAACTGTGA 180
TACCAAGATC CTGAGTAGGA AGGAGAGAGC GAGACCGGAG AGCTCTCTTG GCTACTCGGT 240
CGCTCTCTCT CCGAGACGCA CCAAGCTCCG CCGCTCAAGC CCGCTCTCTG GTTCTCTGCT 300
GAGCTCTCTCT GTGCGCGAGT GCTCAACCCA CCGAGCTGCT GCTCTCTGAG TGTGCGGCT 360
CAGCTCGCAC AAGATGACT GTGAGCGGAT GAGCATCTCA GTGAAAGATG ACCCTGGCCA 420
TCACTATATT GAGAGCATGT GCTCTGAGAT GACTCTGAGC AGCGAGGCTG CTGAGCGCAG 480
AATCTGCTCT TGTGCGAGC CCGTCAACCA GCTGCTGCTG TCAAGGTGAG AAGACGAGG 540
GCGCATGTGT GCGCAAGTGT ACTGTGAGG CAGTACACTA GAGCTGTGAT CAGGTGATGA 600
CTGCGAGAGC TACCAACAGC AGATGTGCTA TAGGACACA GACTACTGCG AGACGGGCT 660
CTGCGAGGCT GCGACAGAGC GTGCGCTCAC CCGAGACACT GTGTACTTGT GCGGCCCGCT 720
TCCCTACAC TCGAGAGAGA ACGCTCTCAT GAGTCTGAGC AAGGAGTGGG ACTTATTGTA 780
GTATATTTAC AAGGACCGAG ACGACAGAGG AACCTCTCAT ATTGGGTACA AGATGAGGT 840
AGGCGCTTCT ATCTGCGACC CCAAAAGCAT CACCATTTGT ACAGGTGCCC CAGCGACCG 900
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GAGACAGTAT GGTGTGAGG ACCCTCTGCT GGGGCGCCCT TACTACTTGG AAGAGGAGA 1080
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GAGTGGAGC AAGCTCTGCT ACGAGAGGCG CCGCTCTGCT ACTCTCTG ACTACTCTT 1800
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WO 02/102235

PCT/US02/19297

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 5 CACTGTGTGTG CTTCCGCGCC TGCTGCTGTC CTCAGTGGCG CCCCOCGGGG CTCGCGAAGC 2160
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 10 GGGACTATACA CTCGAGACT CGCTTAGCAT GGTAAATCAC CGGCTCAAAA GCTCTCTTGG 2400
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 15 CAACTGTCACT CTTTCTGAAC CTGGGAGACG GCGACATCC CACACAGCCA GCGCGCGACA 2700
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 20 ATTGCTCCGA ACCAGACTCC CACACATGAA CATGAGAAAG AGACACAGCT GGTTCCTCTGT 3000
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 25 CCCCACCCCG GCCACACTGT TGTGACTCTT TTAAGCGGAG CCGCTATATT CAGTGTATCC 3300
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 35 AAAGGCTCT GCAATGCTGT GACAGCTGCC CTCTCAACTC TGAGAGAGCA TGGAGAGCA 3840
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 40 AACTCGCAGG GAGTGCATGA GAGAGGAGCA AAGACAGGCA AACGCGNACG TAGCTGCGC 4140
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 45 TACGGAGGCG GCTGCTGCTC CAGGAGAGG CAGGAGAGG CTTGAGAGG TCTGAGGGA 4380
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 50 GAGCTGCGC TTGTGGCAGC CAACTGCCA GCGCCAGGCC CTTCACTGCT ACTGTAGAGC 4560
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 AACAGTCCC AGTTTGT

Seq ID NO: 146 Protein sequence
 Protein Accession #: NP_002195.1
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 55 DMHLQVTAS QGPAEGLVR AERYTQULMS GSEDCREWG KCVRENDLE LBSDDWQTY 180
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 DPEQGNLYI QYTMQGSFT LHKNTITVL GAPRIHMGMA VFLLSQRAG DLRRQVRLG 300
 SQVAYFGGA IALALAGND NQDLLWDAPI YFERKEVGG AIVFRRNGAG TSPFARBL 360
 60 LHRPDSAGP LEVASIDIN GCTPGDLAVG APFRLKRYV YTGSSKLL RQPCQVTHIE 420
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 DPALCTATSC QVVELCFAYN QAGKNPNYR NITLALTYEA DEDRRPPELR FAGSESAVFH 540
 GFPSDEPAEC QKCELELLUM MRKLQPIII SMNYSLUPRH PORFELGLES LDAYPILAGA 600
 65 GALLBIHQVY FQJLVNTRK CESMLQWNA FYRRCQGLS RLYSDFVFK LLELVNPT 660
 ETSRSEBODA HEALLTLVVF PALLLSWRP FGACQANETI FCBLSPFFKR NQSMELLIAF 720
 EIVQITLETB DLQVQLQLST SHQDNLKPM ILTLVDVDTL QTSLSMVHR LQSFPGTVM 780
 GBSGMKTVDV VQSPKYRGP VQPMGELIAG LQTLVLGLEH PLEVSGIQLH LVPTEIVHG 840
 80 NQPMGSPDP DLVAGCAVTE GDTGCRFSP QRRRLQGLV QXGFPPTVL AAASAKSET 900
 VLKACGRIAN CVNLECFID APVNTIVTVK ARVHSTFIE DYRDEFRVY NQHTALFLE 960
 SIPTINMKNH TTTFSEVDIS ELWLEPASE ELMLVLVWAG AGLLLGLLI LMLMKCFE 1020
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 Coding sequence: 74..3274
 75 1 11 21 31 41 51
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 80 CTGTGCTGTC GCTCTGATAG TGGGCGCGCG GCGCTGCTGC GTTCGCGGCT TCAACTATGA 180
 TACCCGCTGT CTTGTGATGA AGAGAGCCCG GAGACCGGCG GCTCTCTGCT GCTCTCTGCT 240
 CCGCTCTCAT CCGGACAGAC AGCGCGACGA GCGCTATGCT CTTCTGCTGCT GTGCCCCCT 300
 GAGCTGCACT GTGCGGATGT GCTACACCAA CCGAGACTGT GCTGTGTACC TTGCCCCACT 360
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 85 TCACTATTAT GAGAGCAVTE CTTGTGAGCT GACTGTGGCC GTGAGAGGCG CTGCGAGCG 480
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WO 02/102235

PCT/US02/19297

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 CATTGAGAA GCTGAGGCTA GTTCCAAAA OCTCTCTGA CCGCTGCTG TGGGAGCT 4380
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Seq ID NO: 148 Protein sequence
 Protein Accession #: NP_05492.1

70 1 11 21 31 41 51
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 DMLGVTVAS QPGAGRVLVC AERYTQVLS GSEBDQWVG KCYVRNDLE LSSDQWQY 180
 HENKNSVTD YLKTQDQLG TSGQTQNTV YPGARCAWK KNSFTMQE ENLSEYSK 240
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 SQVATFSGA ILALCLNEDS WQDLWVAPY YFENKHEVG ALLYFMNKG TSPFAPSL 360
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 GFGFENFEC QKLELLKEM LMKLEPLTI SNYLSLPMR PORELGLAS LDAYLINAQ 600
 QALENTEVQ FQKECQPNK CESHLMELAA FVSEQQKLS RLQYSVDRK LLISNVNTP 660
 RTSRBOEDA HEALTLVVF PALLLSVRP PQACQWETI FCHLGNFPR NURMELIAT 720
 EVIGTJLHR LKQVQLSLST SHQDMLPM LTLTLVYTL PTVLSWNRH LQSFQDFTV 780
 85 GSKDQVTEV VGLPLAYTFV VQPMGELGV LGTLALGLM FTVSNGKML LPTTITVHS 840

WO 02/102235

PCT/US02/19297

NGSWCRPPG DLINFLKLTLL SDPGDRPSPS QRRRQLQDPS GQGGPPVTL AAKKAKSET 900
 VLZCQVGRH CWRKCT1P9 APVDTHTTKE AFRNASTTIE DYDFDFRVVY KBNATLELEY 950
 S1PTINEMK TWFSVD1DS ELWELPARI ELMLVLAVAG AGLLLGLLI1 LLLAKCDSFK 1020
 RTRYQIMPK YIUVIRKEE RYPPGOSTLP TKRHVVTSMQ TRQYF

5

Seq ID NO: 149 DNA sequence

Nucleic Acid Accession #: NM_006424.1

Coding sequence:

	1	11	21	31	41	51	
10	GGGGCAAGT	TTCCAGGCTC	GGCGCGCGCC	TCCATCCGAG	CACCTGCGGA	GGGAGCGCTG	60
	ACCATGTGCT	CCTGGCGCTG	ATATGGAGAT	GCCCGAGCCA	ACCCCGATAA	GTACCTCGAA	120
	GGGGCGGAG	GTGACGGGCG	CACCTGCCCT	GATAAAGCA	AAGAGACCAA	CAAAACAGAT	180
15	AACAGTCAG	CACCGTACAC	CAGATGTGAA	CTTCCTGCGT	CTTACTCCAC	GGTACACATG	240
	ATAGATGAG	CCTCCTGCGG	GGAGGACATC	TGGAACTGAC	CCATCTCTCA	GGATCGGEE	300
	AGATTAGTGT	CAGAGAGACA	CACCAAAAGG	AGAGTTCTCT	GTTCCTTCCA	AGGZATTGCG	360
	AGGATGATTT	TACTTCTCGG	ATTCTCTCTC	TTTTCCTGTT	GCTCCCTGGA	TATTCCTTAG	420
	AGGCGCTCTT	AGCTGGTGGT	AGSAAAGATG	GAGGACAGGT	TCTTCAGAGC	CAGCTCTATT	480
20	ATGTCGACC	CTTTGTTGGG	CTGGGTGATC	GGGCTGTGGT	TGACCTGCTT	GCTGCGAGAG	540
	TCCGCACTT	CAAGTCCCAT	GGTGTGAGC	ATGGTGTGCT	CTTCATGCTC	CAGCTTGTGG	600
	GCTCGATCC	CAATTATCAT	GGGGGCCAAC	ATTGGAAGCT	GATCAACCAA	CACTATTGTT	660
	GCGTCTATCC	AGTGTGGAGA	TGGAGATGAG	TTCAGAGAGG	CTTTTGCAGG	AGCCCATGTC	720
	CATGACCTCT	TGAACTGGCT	CTCGGTTGTT	GTCTCTCTGC	CGGPGAGGAT	GGGCACCGTG	780
25	TACTTCGAGA	TGATAACCA	GCTTATAGTG	GAGAAGTCC	ACTTCAGGAA	TGGNAGAGAT	840
	GCCCCGATC	TCTGGAAGT	CATCACTAAG	CCCTTCAGAA	AGCTCATGTT	CCAGCTGGAT	900
	AAAAAAGTTA	TGGAGCAAA	TGCAATGAC	GATGAAAAAG	CGMAAAGCAA	GAGTCTTGTC	960
	AGATTGTTG	GCAGAACTT	TGCAACACAG	ACCGAGATA	AATGTACTGT	TCCCTGAGCT	1020
	GCTCACTCGA	CCTCCCTTTC	CCTCTGTGTC	ACGATGCGCA	TCCAAACTGC	GACCATGAAG	1080
	AATGTGACCT	ACAAAGAGAA	CATCGCCAAA	TGCCAGATA	TCTTTGTGAA	TTTCACCTTC	1140
30	CGGATCTTG	CTGTGGGAC	CATCTTGCTC	ATACTCTCCC	TCTTGCTGCT	CTGTGGTGGC	1200
	CTGATCAGA	TGTTGACAT	CGTGGGCTCT	GTGCTCAGG	GGGAGGCTCC	CACCTGTGAC	1260
	AAGAGACGA	TGCAACGAT	CTTCCGCTGC	GGTGTACTGC	GTATCTGCTC	CTACCTGGCC	1320
	ATCTCTGCTG	GGGCGGCTAT	GACCTTGATC	GTACACAGCA	GCTCTGTGTT	CAGTGTGGCC	1380
	TTGACCCCCC	TGATTGAAT	GGGCGTGATA	ACCATTAGAA	GGGCTTATCC	ACTCAAGCTG	1440
35	GGTCTCAAGA	TGGGCAACA	CACACACGCC	ATCCTGAGCC	CTTTAGCGAG	CCCTCGAGAG	1500
	CGATGATGA	GTTTCTGCTG	GGGACGCTGC	TGCCATCTCT	TTCTTCAGAT	CTCCGCGGAC	1560
	TGGCTCTGGT	ACCGCATCCC	GTTCACTGCG	CTGCCCATCC	GGATGGGCAA	GGGCGTGGGC	1620
	AACATCTCTG	CCAGATATCG	CTGGTGTGCG	CTCTTCTCAT	TGATCATCTT	CTTCTCTCTG	1680
40	GGTCCGCTGA	GGGTGTGGG	GCCTGCTGCG	GGCGGCTGGC	GGGCTGTGGT	TGGTGTGGG	1740
	CTTCCCTCTG	CTGCTGCTG	CTCTGCTGTA	CTCTGCTCTG	CTCTGCTCTG	GTCTGCTCTG	1800
	CCAGCGCTCC	TGCGAGAGAA	ACTCCAGAAC	TGGAACTTCC	TGCCGCTGTG	GATGCGCTCG	1860
	CTGAAGCCTC	GGGATGCGT	GGTCTCCAGT	TTCACCGGCT	GCTTCCAGAT	GGGCTGCTCG	1920
	TACTGTGCTC	GGGTGTGCTG	CGGCGCGTGC	TGCTTGCTGT	TGGGCTGCGC	GGGCTGTGTC	1980
45	AGCTCGACGA	AGGCTGTGCT	AGGCGGCTCT	GAGCGCGGCG	AGGCGCGGCG	TGTCTCTCTC	2040
	AGGCTGCTG	AGACTGTGTA	TGACATAAAC	ATTAGAGAG	AGGCTCAGGG	TAGAGTCTCT	2100
	GCTGTGAGCT	CAAGAGACCA	ATGCAAGGCC	TGTAGAGGGA	CGCCCCAGAT	TGTCAAGGAT	2160
	GGGCGGATGG	TGCTTGAGTT	TGTCATGCTC	TGCTCCCTCC	CAGTTCTCGA	CCCTTTCACC	2220
	ACCTCGAGGA	GATTGTGCTC	CATTAGAGGA	ATGAAATTGA	TGCAGTCTTA	AAAAAAAAAA	

50

Seq ID NO: 150 Protein sequence:

Protein Accession #: NP_006415.1

	1	11	21	31	41	51	
55	MAPNPGLGDA	QNPFDKYLEG	AAGQOFTAPD	KSKEKTNITN	TEAPVTKIEL	LPSYSTATIL	60
	DEPTEVDVDP	NLPTLQDSOI	KNSERTTGRK	ILCFPFQIIR	LILLGLGYLF	FCVSLDLS	120
	AFQVAGGGRH	QGFERSISIN	SNPLGLGVIG	VLVTVLVQSS	STFSTVIVBH	VBSLLTVRA	180
	ATPILINDAT	GTPLTGTGVA	LVGVVDSREI	BRAGAGVTH	DFRHLVSLV	LLPVEVATV	240
	LEITIGLIVE	SFRFNIGEDA	POLKEVITPK	FTKILVOLKL	XVQIOLAMBD	EKAHKLSDLP	300
	INOKTFTNKT	QINVTVSTTA	NTSPSLCHCT	DQIGNVTGSH	VTKENIAXC	QHIFVNRHLP	360
	DLAVGTILLI	LSLLVLQCLL	IMIVKILGVS	LKQVNAVTVK	KTIHTEDPFF	FAMLTGTLAI	420
60	LYGQMTFV	GRSFTVGLD	TLHLGIVHTI	GGGTFPLHLS	SLTQVTFVAL	LAAMASPIRA	480
	LSSSLQIALC	HEFFNLSIL	LVVYIPFTPL	PIRANKEGLN	ISATYKGFV	FTLLIFPFLA	540
	PLTVFGLSLA	QKRVLVGVSV	VVVFIIILVL	CLRLQLSRCP	RVLFPGLQNN	NFLPLNWSRL	600
65	KPHDAVVSFK	TPCFQKRCCT	CRVVCORACC	LLCGCPKCCR	CSKCCDLLEE	AQSGQVVPVK	660
	APETPDNITI	SREAGVEPVA	SDSKTECTAL				

Seq ID NO: 151 DNA sequence

Nucleic Acid Accession #:

Coding sequence: 1..1119

	1	11	21	31	41	51	
70	ATGAAACCGCA	GTCACCGGCA	CGGGCGCGGC	AGCGCGCTGC	TGGGCACATAT	GGAGGTGAGG	60
	ACCAAGTTTG	GAGCTGAATT	TGCTGTGATT	TGCTGTGAAA	GTCCAAACCC	TGJAAAAATT	120
	OKGAGGTTTG	ATGATATACT	ACACAGATGT	CGTAAAGCTT	CGAATGTGGA	CGTTTGCTGA	180
75	GCTATGCGAG	ACATCCATGG	AGACTTACTA	CCCTATAAAT	ATGATGATTA	TTATACAAAA	240
	GCTGTTCAA	CGGCAATCC	ACTGCTTAGG	ATTATTATAC	AAAGAAGGGA	AGAGCGAGAC	300
	TACATGTGCT	TGTGTACGA	CACGCTAATA	AAGAGAGAAG	ATGTTTAAAC	CAAGATATAT	360
	CTCTCTGACA	ACCATAGAAA	AAAGCGGCTT	ATAGTCPTTA	GTATGCCCTA	AGACCTTGGG	420
	CTGTGCTCTT	CTATATAGGA	CTGGAGATTA	CTCCACAGAA	CGATGCTGAG	GTATGCTCTT	480
80	TACAATAAGC	GACAGGAGAA	ACCCCTAGGA	TTCTACATCT	CGATATGGCT	CAGTGTGAGG	540
	GTACACACAC	ATGCTCTTGA	AAAGGTTCCA	GGATCTCTTA	TATCCAGGCT	TGTCGCCAGG	600
	GGTCTGCTCT	AAAGTACAGG	ACTATTAGCT	GTATATGATG	AGATTTTAGC	AGTAAATGTC	660
	ATGAAATTTT	CGAGGAGAG	CGTGTGATGA	GTACACAGCA	TGATGATATC	AAAGAGAGCT	720
	ANCTCATCA	TACAGGTGAG	ACCGCAACAC	CAGAGAGATA	ATGTTGTGAG	GACAGCTGCG	780
85	ACTCTGGGCA	GTTCGGTCA	GTCTACTGAT	AACAGCCTTC	TTGCTGATCC	ACAGCAGATT	840

WO 02/102235

PCT/US02/19297

5
 GRACCAAGCT TTGAGCCAGA GGAATGAAGC ACGGAGAGAG ATGACATTAT CATTGAGAAC 960
 AATGAGATGC CACAGCAGAT TCCAAAGCT GTTCTTAATA CTGAGAGCTT GAGATCATTAA 960
 ACACGATAG ACATGATCTGA GAGATCTGTA GAGATAGGCT TATATCCCTC TAATGAGATG 1020
 AACTTAGCAG CCATAGCAAG CAGCTCAAC ACGGAATTGG AAACACATGC TCCAGATCAA 1080
 AACTCTTAG AAGAGATGG AACATCATTA ACATTATGA

Seq ID NO: 152 Protein sequence
 Protein Accession #: XP_030559

10
 1 11 21 31 41 51
 | | | | |
 KRVSHSHGAG SCLGTHKEK SKTPAEFRIR SLEBSKPKGF DEFYLLQGV IKINPVVPLV 60
 GYDINHQLL PINDDNVIK AVSTANPLIE IFIOKKSEAD YSARGTDLI KKKVLTNVG 120
 RPDNRKELL IVISMPQDF PVS81IDW1 LPETHEVRVL YKVTGKPLG FYIKGSSVR 180
 VPIHGLEVPV GIPISRLVPG GLAGSTGLLA VNDVLEVING IEVSGKSLDQ VTDMMINSR 240
 NLIITVRAN QSNVYVNSR TSSSSGOSTD HSLGYPOOI EPSFEHDEP SEEDDILIED 300
 KTVPOQIFA VTESLSESL TQLELFPSSQ QNGFIPSNIV SLAAIASSSR TEFETHAPQG 360
 KLEEDGTII TL

Seq ID NO: 153 DNA sequence
 Nucleic Acid Accession #: NM_003064.2
 Coding sequence: 23..421

20
 1 11 21 31 41 51
 | | | | |
 CAGAGTCACT CTTGCCTTCA CGATGAAGTC CAGGRCCTCC TTCCCTCTGC TGTGCTGCT 60
 TGCCCTGGGA ACTCTGSCAC CTTCGGCTGT GGAAGSCTCT GGAAGTCTCT TCAAGCTGG 120
 AAGTCTCTCT CCTAGAATAT GTCGCCAGTG CTTTAGATAC AAGAAGCTGC AGTCCGAGAG 180
 TGACTGTCAG TGTCCAGGGA AAGAGAGATG TTGTCTGAC ACTTGTGCA TCAATAGCT 240
 GATCCCTTGT GACACCCCA ACCACACAG GAGAGAGGCT GGAAGATGCT CAGTACCTTA 300
 TGCCATATGT TTGATGCTTA ACCCCCCCAA TTCTCTGAG ATGAGAGGAG AGTCGACAG 360
 TGACTTGAG TTGTGATGAG GCATGTGTGG GAATCTCTGC GTTTCCTGCT TGAAGCTTG 420
 ATTTCTGCCA TATGAGAGAG GCTCTGAGAT CTTGCTCTGT GTATGCCAG TCTTTCAC 480
 CTTGAGACTT GCTCCACCA CTGATATCTT CTTTGAGGA AAGCTCTGCG ACACGACAG 540
 CTTTCAGAA GTCCGCTTG TCAATGAT AAATAACGA GCTATTCTT CTTCGAC

Seq ID NO: 154 Protein sequence
 Protein Accession #: NP_003055.1

35
 1 11 21 31 41 51
 | | | | |
 MKSSGLFFPL VLLALGTLP WAVEGSGSKF KAGVCPKKS AQCLRYKPE COSMWCPCPK 60
 KRCCPTDGTG KCLDPVDTFN PTKRKPGRKC VTYQGCLMLN PMHFCMDQG CREDLKCCKG 120
 HCKHSCVSPV KA

Seq ID NO: 155 DNA sequence
 Nucleic Acid Accession #: NM_001306.1
 Coding sequence: 199..861

45
 1 11 21 31 41 51
 | | | | |
 AATTGCGCAC GAGGCGAGT GCAGGCGCAC GGCGCGAGAG CATTATGAGC CGAGGCGCTTA 60
 GCGCGCGGCT TGCGTGAATC AGTCCCTCTG TCCCTCCCTC CBTGCGGAGG CGGAGGCTCC 120
 CGCAGAGGCG AGCGCGCGCG GCGCTCTCTG TCCCGCGCAC CGAGCGCACG CGTGTGCGAG 180
 GCGCTTGCGG CGCGACCAAT GTCCATGCGG CTGAGGATCA CGGCGACGCG GCTGCGCGTG 240
 CTGCGCTGCG TGCGACCAAT CATTGTGCTG GCGTTGCCA TGTGGCGGCT GTGCGCGCTTC 300
 ATCGCGCAGCA ACATCATCAC GTGCGCAGAC ATTGCGGAGG GCTGTGTGAT GATCTGCTTG 360
 GTGCGACGCA CGCGCGGAGT CAGATGCGAG GTGTAGGAT CCGTCTCTGCG ACTCGACAG 420
 GACTCTCAGG CGCGCGCGCG CTTCACTCTG GTGAGCATCC TATGCGCGCG CTTGCGGCTG 480
 CTAGTGGGCG CTGTTGCGCG CCAATGCGAC AACTCGGTGC AGGACGACAC GCGCAGGCGC 540
 AAGATCAACA CTGTGCGCAG GGTGCTGTTC CTTCTGCGCG CCGTCTCTAC CCTGTGCGCG 600
 GTCTCTCTGT CCGTCACTCA CATATCTCTG GACTCTTACA ACCCTGTGAT GCGCGAGGCG 660
 CAGAGCGGCG AAGATGCGCG GCGCTCTGAG GTGAGCTGCG CGCGCGCGCG GCTGCGCGCTG 720
 CTGCGCGGCG CCGTCTCTGT CTCTCTGTGT CCGCCACGCG AAGAGAGATA CAGCGCGCAC 780
 AAGGTGTCTT ACTCGCGCGC GCGCTCTCAC GGCGCGGAG CAGCGCTGCG CAGAGCTAC 840
 GAGCGCGAGT ACTCATCTCA AAGGACAGCG GCGAGGAGAC CCGACACGCA CGACACGAC 900
 CAGACCGCC ACACCGCGC CAGGCTGAG GCGCGACGAG GCGATCCAGG GTCCAGGCTT 960
 GCGCTGCGAG CGACCGCAC CCGAGAACGC AAGAGCGCCC CCGCTCTGAG TGCGCGGAGT 1020
 TCCCGACGAG CCAAGCTTTT GCGCGCGCGG CAGTGCATTT CGGCGCGCAG GAGCAACT 1080
 GCGTGTGACT TGAACCTCA CCGTCTCTCA GCGCGCGGCG TGCGGTGAGC CAGATCTGT 1140
 ACCACCGCTT CAGCGCGGCT CCGTCTCTCA TAAAGCGCTC TCGTCTTACG 1200
 GCGCTGAGAG GCGCACTTGA TATTTTTCA TAAAGCGCTC TCGTCTTACG

Seq ID NO: 156 Protein sequence
 Protein Accession #: NP_001297.1

70
 1 11 21 31 41 51
 | | | | |
 MSGLGKITGT ALAVLNLGT IVCALLPMWR VSAFISNII TSGINBGLM MKCVVSTGQ 60
 MGRVTEELL ALPDELQAR ALVFAILLA AGELLALRG AGCTNCVGTG TARKETITTA 120
 GVFLFLALL TLVTVSHSY TIEHFVPI VPEAKRREMG KGVTVGMAA ALQLLEGNLL 180
 CCBCFPREKE YATKVIYSA PRSTGPASL GTYDKKUYV

Seq ID NO: 157 DNA sequence
 Nucleic Acid Accession #: NM_005564
 Coding sequence: 1..597

80
 1 11 21 31 41 51
 | | | | |
 ATGCGCCGAG GTCTCTGTG CTTGAGGCGCTA GCGCTGTGCG GCGCTCTGCA TGCCGAGGCG 60
 CAGGACTCCA CTTGAGACT GATCCAGACC CAGCTCTGGA CGAAGGTCCC TCTCGACGAG 120

WO 02/102235

PCT/US02/19297

	AACTTCCAGG	ACAACCAATT	CCAGGGGGAG	TGGTATGTGG	TAGGCTCTGC	AGGAAATGCA	180
	ATTCCTAGAG	AGACAAAGA	CCGCCAAGG	ATGATATGCA	CCATCTATGA	GCTGAAAGAA	240
	GCACAGAGCT	ACATATGTC	CTCGCTCTGT	TTTAGAGAAA	AGAGATGTGA	CTACTGGATC	300
5	AGGACTTTTG	TTCACGGTTC	CCAGCCCGGC	GAGTTTCACT	TGGCACAATC	TAGAGATTAC	360
	CTGGATTATA	CAGATTACTC	CGTCGGAGTG	GTGGGCACCA	ACTACAACCA	GCATGCTATG	420
	GTGTCTTTCA	AGAAAGTTTC	TCAAAACAGG	GAGTACTCTCA	AGATCCACCT	CTACGGGAGAA	480
	ACCAAGAGGC	TGATCTTGGA	ACTAAAGGAG	AGCTTCACTC	GCTTCTCGCA	ATATCTGGGC	540
	CTCCCTCAAA	ACCAATCTCT	CTTCCCTGTC	CCATCTGACC	AGTGTATCGA	CGGCTGTA	
10	Seq ID NO: 158 Protein sequence						
	Protein Accession #: NP_005555						
	1	11	21	31	41	51	
	NPGLLMLGL	ALIGALRAQA	QDSTSDLIPA	PPLGRVPLQG	NPDNQPGQK	WYVVGLAGNA	60
15	ILRESDRDK	PRATTELKLE	DHSIRVPSVL	FRKRKCDWI	RTVPGCCPG	EPLGRIHST	120
	PGLTSYLVV	WSTYINQHM	VFFKRVQMR	EYFRITLYGR	TKGLTSELAE	NFRFSSKYLQ	180
	LPRNHFVFF	PIDQCIDG					
	Seq ID NO: 159 DNA sequence						
	Nucleic Acid Accession #: NM_006853.1						
	Coding sequence: 26..874						
	1	11	21	31	41	51	
	AGGAATCTGC	GCTCGGGTTC	CCGAGATGCA	CAGGTTGAGG	TGGCTCGGGG	ACTGGAAGTC	60
25	ATGGCGGAGA	GGTCTCAGAG	CAGCCAAAGA	ACCTGGGGCC	CGCTCCTCCG	CCCTCCAGGC	120
	CATGAGGATT	CTGCAGTTAA	TCTGCTCTGC	CTTGGCAACA	GGCCTTGTAG	CGGAGAGAGC	180
	CAGGATCATC	AGGCGGTTTG	AGTGCAAGCC	TCATCTCCAG	CCCTGGCAGG	CAGCCTCTTT	240
	CGAAAGAGCG	CGCTACTCT	GTSPGGCGAC	CGTCGPGGCC	CCGAGATGCG	TCTTGACAGC	300
	AGCCCACTGC	CTCAAGCCCC	GCTACATAGT	TGACTCTGGG	CAGCAACACC	TCCAGAAGGA	360
30	CGAGGGCTGT	GAGCAGACCC	GGACAGCCAC	TGAGTCTCTT	CCCAACCCCG	GCTTCAACAA	420
	CAGCTCCCCC	AACAAAGACC	ACCGCAATGA	CATCATGCTG	GTGAAGATGG	CATCGCCAGT	480
	CTCCATCAGC	TGGCGGTGCG	GACCCCTCAC	CGTCTCTCTA	CGTGTGTGCA	CTGCTGGAGC	540
	CAGCTGCTTC	ATTTCGCTCT	GGGGCAGCAC	GTCCAGCCCC	CAGTTAGGCC	TGCTTCACAC	600
	CTTGCGATGC	CCCAACATCA	CCATCATTTA	GCACCGAAGG	TGTGAGAGCG	CGTACCCCGG	660
35	CNACATCACA	GACACCATGG	TGTTTGCCAG	CGTGCAGGGA	GGGGGCAAGG	ACTCTGCGCA	720
	GGGTGACTCC	GGGGGCCCTC	TGTTCTGTAA	CGAGTCTCTT	CAGGCGATTA	TCTCTGGGGG	780
	CGAGGATGCG	TGTCGCTCTA	CCGAAAGGCG	TGGTCTCTAC	ACGAAGTCTC	GGAAATATGT	840
	GGACTGGATC	CAGGAGACGA	TGAAGAGACA	TTAGACTGGA	CCACCCCGAC	ACAGCCCATC	900
	ACCTCCCATT	TCCACTTGGT	GTTTGGTTCC	TGTTCACTCT	GTTAATAGA	AACCTTAAGC	960
40	CAGAGCCCTC	TAGGACATTT	CTTTGGGCTC	CTGGACTACG	AGAGATGCTC	GTCACTTAAT	1020
	ATATGACTTG	GGTTGCGAAG	TGAGAGAGAC	CTGGATTTGA	ATTCCTGCTT	GAATATTTGT	1080
	GACTCTGGGA	ATGACACAGC	CTGGTTTGGT	CTCTGTTGTA	TCCCCAGGCC	CAAGACAGGC	1140
	TCTTGCCAT	ATATCAAGGT	TTCATATAAT	ATTTCGTAAA	TGAGTG		
45	Seq ID NO: 160 Protein sequence						
	Protein Accession #: NP_006844.1						
	1	11	21	31	41	51	
	NPILGLILLA	LATGAGVST	RIIKFBCPK	BSQWQAALF	ETRELLCGAT	LIAEPNLLTA	60
50	ARCLKPRVIV	HLGGHNLQKE	BCEBQTZTAT	ESPPHKGFIN	SLRWEDHMD	IMLVKMASPU	120
	SITWAPRPLT	LSSRCVTAGT	SLGISGKST	SSPQLALEPH	LRCANITIEE	HQKCNATVPG	180
	NITDINVCAS	VGGGKIDSCQ	GDGGGLVCH	QSLQGIISNG	QDPCATRKP	GVYTRVCEVY	240
	DWIGETNNNN						

55 It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

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WHAT IS CLAIMED IS:

1 1. A method of detecting an ovarian cancer-associated transcript in a cell
2 from a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence
4 as shown in Tables 1-26.

1 2. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.

1 3. The method of claim 2, wherein the nucleic acids are mRNA.

1 4. The method of claim 2, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.

1 5. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1-26.

1 6. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.

1 7. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat ovarian cancer.

1 8. The method of claim 1, wherein the patient is suspected of having
2 ovarian cancer.

1 9. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1-26.

1 10. The nucleic acid molecule of claim 9, which is labeled.

1 11. An expression vector comprising the nucleic acid of claim 9.

1 12. A host cell comprising the expression vector of claim 11.

1 13. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1-26.

- 1 14. An antibody that specifically binds a polypeptide of claim 13.
- 1 15. The antibody of claim 14, further conjugated to an effector component.
- 1 16. The antibody of claim 15, wherein the effector component is a
2 fluorescent label.
- 1 17. The antibody of claim 15, wherein the effector component is a
2 radioisotope or a cytotoxic chemical.
- 1 18. The antibody of claim 15, which is an antibody fragment.
- 1 19. The antibody of claim 15, which is a humanized antibody
- 1 20. A method of detecting an ovarian cancer cell in a biological sample
2 from a patient, the method comprising contacting the biological sample with an antibody of
3 claim 14.
- 1 21. The method of claim 20, wherein the antibody is further conjugated to
2 an effector component.
- 1 22. The method of claim 21, wherein the effector component is a
2 fluorescent label.
- 1 23. A method for identifying a compound that modulates an ovarian
2 cancer-associated polypeptide, the method comprising the steps of:
3 (i) contacting the compound with an ovarian cancer-associated polypeptide,
4 the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least
5 80% identical to a sequence as shown in Tables 1-26; and
6 (ii) determining the functional effect of the compound upon the polypeptide.
- 1 24. A drug screening assay comprising the steps of
2 (i) administering a test compound to a mammal having ovarian cancer or a cell
3 isolated therefrom;
4 (ii) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26 in a

WO 02/102235

PCT/US02/19297

- 6 treated cell or mammal with the level of gene expression of the polynucleotide in a control
7 cell or mammal, wherein a test compound that modulates the level of expression of the
8 polynucleotide is a candidate for the treatment of ovarian cancer.